Multi-ancestry genome-wide association study of lipid levels incorporating gene-alcohol interactions

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This work was funded by the National Heart, Lung, and Blood Institute grant R01HL118305. Infrastructure for the CHARGE Consortium is supported in part by the National Heart, Lung, and Blood Institute grant R01HL105756. American Heart Association Grant #17POST33350042 made it possible for Dr. de Vries to lead this project. Study-specific funding is provided in the acknowledgement section.

Conflict of interest: The authors declare no competing financial interests except for the following. Bruce M Psaty serves on the DSMB of a clinical trial funded by the manufacturer (Zoll LifeCor) and on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson. Oscar H Franco received grants from Metagenics (on women's health and epigenetics) and from Nestle (on child health). Mike A. Nalls' participation is supported by a consulting contract between Data Tecnica International and the National Institute on Aging, National Institutes of Health, Bethesda, MD, USA, and Dr. Nalls also consults for Illumina Inc, the Michael J. Fox Foundation and University of California Healthcare among others. Neil Poulter has received financial support and consultancy fees from several pharmaceutical companies that manufacture either blood pressure-lowering or lipid lowering agents or both. Peter Sever has received research awards from Pfizer Inc. Jost Bruno Jonas serves as a consultant for Mundipharma Co. (Cambridge, UK), patent holder with Biocompatibles UK Ltd. (Franham, Surrey, UK) (Title: Treatment of eye diseases using encapsulated cells encoding and secreting neuroprotective factor and / or anti-angiogenic factor; Patent number: 20120263794), and Patent applicant with University of Heidelberg (Heidelberg, Germany) (Title: Agents for use in the

therapeutic or prophylactic treatment of myopia or hyperopia; Europäische Patentanmeldung 15 000 771.4).

Running head: Gene-alcohol interactions and lipid levels

Abbreviations: low-density lipoprotein cholesterol (LDL-C), high-density lipoprotein cholesterol (HDL-C), triglycerides (TG), degrees of freedom (DF), genome-wide association study (GWAS), false discovery rate (FDR).

ABSTRACT

An individual's lipid profile is influenced by genetic variants and alcohol consumption, but the contribution of interactions between these exposures has not been studied. We therefore incorporated gene-alcohol interactions into a multi-ancestry genome-wide association study of levels of high-density lipoprotein cholesterol, low-density lipoprotein cholesterol, and triglycerides. We included 45 studies in Stage 1 (genome-wide discovery) and 66 studies in Stage 2 (focused follow-up), for a total of 394,584 individuals from five ancestry groups. Genetic main and interaction effects were jointly assessed by a 2 degrees of freedom (DF) test, and a 1 DF test was used to assess the interaction effects alone. Variants at 495 loci were at least suggestively associated ($P<1\times10^{-6}$) with lipid levels in Stage 1 and were evaluated in Stage 2, followed by combined analyses of Stage 1 and Stage 2. In the combined analysis of Stage 1 and Stage 2, 147 independent loci were associated with lipid levels at $P<5\times10^{-8}$ using 2 DF tests, of which 18 were novel. No genome-wide significant associations were found testing the interaction effect alone. The novel loci included several genes (*PCSK5*, *VEGFB*, and *A1CF*) with a putative role in lipid metabolism based on existing evidence from cellular and experimental models.

Keywords: Alcohol consumption, gene-environment interactions, gene-lifestyle interactions, genome-wide association study, lipid levels, cholesterol, triglycerides

Serum concentrations of high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), and triglycerides (TG) are modifiable risk factors for cardiovascular disease, the leading cause of death globally (1). Lipid levels are influenced by multiple exposures, including genetic and lifestyle factors. The genetic factors influencing lipid levels have been widely studied (2-8), and large-scale genome-wide association studies (GWAS) have identified 236 loci associated with HDL-C, LDL-C, and TG, which account for up to ~12 percent of the total trait variance in the studied populations (5, 7).

Lifestyle factors, such as alcohol consumption, also associate considerably with lipid levels: in epidemiologic studies, higher alcohol consumption is associated with improved lipid profile, including associations with HDL-C levels, HDL particle concentration, and HDL-C subfractions (9, 10). The relationship between alcohol use and LDL-C or TG is less clear, with some studies reporting positive while others reported negative associations (11-20). A causal role of low-to-moderate alcohol consumption in improving overall lipid profile is supported by intervention studies (19), and more recently by Mendelian randomization studies (21, 22).

Potential modification of genetic effects on lipid levels by lifestyle exposures, including alcohol consumption, is relatively unexplored (23). Genetic association studies accounting for potential gene-alcohol interactions may lead to the identification of novel lipid loci and may reveal new biological insights that can potentially be explored for treatment or prevention of dyslipidemia. In order to investigate the potential modulating role of alcohol consumption in the genetic architecture of lipid levels, and identify novel HDL-C, LDL-C, and TG loci, we performed genome-wide gene-alcohol interaction meta-analyses of LDL-C, HDL-C and TG.

METHODS

Overall design

Table 1 shows the overall design of this study, conducted within the setting of the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Gene-Lifestyle Interactions Working Group (24, 25). In order to decrease the computational burden we carried out genome-wide analyses in Stage 1, and followed up suggestively associated variants in Stage 2, with the combined analysis of Stage 1 and Stage 2 serving as the primary analysis (26). We used two complementary approaches to model interactions: 1) a 2 degrees of freedom (DF) test was used to jointly assess both the genetic main effect and interaction effect on lipid levels, and 2) a 1 DF test was used to assess the effect of interactions alone. The 2 DF test is more powerful when there is both a genetic main and interaction effect, and it may thus help identify interaction effects for which the 1 DF test is underpowered (27).

Overview of participating studies

This study includes men and women between the ages of 18-80 from five ancestry groups: European, African, Asian, Hispanic, and Brazilian. Each study obtained informed consent from participants and approval from the appropriate institutional review boards. Although the participating studies are based on different study designs and populations, all of them have data on lipid levels, alcohol consumption, and genotypes across the genome.

In total, this study comprises 394,584 individuals. Stage 1 included 89,893 European, 20,989 African, 12,450 Asian, and 3,994 Hispanic ancestry participants for an overall total of 127,326 individuals from 45 studies (Web Table 1), namely: Age Gene/Environment Susceptibility Reykjavik Study (AGES: 1967 - Reykjavik, Iceland), Atherosclerosis Risk in Communities study (ARIC: 1987-1989 - Washington County, MD; Forsyth County, NC; Jackson, MS; and

Minneapolis, MN), Coronary Artery Risk Development in Young Adults (CARDIA: 1985-1986 - Birmingham, AL; Chicago, IL; Minneapolis, MN; and Oakland, CA), Cardiovascular Health Study (CHS: 1989-1990 and 1992-1993 - Forsyth County, NC; Sacramento County, CA; Washington County, MD and Pittsburgh, PA), CROATIA-Korcula (2007 - Korcula, Croatia), CROATIA-Vis (2003-2004 - Vis, Croatia), Erasmus Rucphen Family study (ERF: 2002-2005 - Rotterdam, the Netherlands), FamHS (FamHS: 1992-1995 - Salt Lake City, UT; Forsyth County, NC; Minneapolis, MN; and Framingham, MA), Framingham Heart Study (Framingham: 1948 - Framingham, MA), Genetic Epidemiology Network of Arteriopathy (GENOA: 1995-2000 - Rochester, MN and Jackson, MS), Genetic Epidemiology Network of Salt Sensitivity (GenSalt: 2003-2005 - Hebei; Henan; Shandong; Shaanxi; and Jiangsu, China), Generation Scotland: Scottish Family Health Study (GS:SFHS: 2006-2011 - Scotland), Health, Aging and Body Composition *Study* (HABC: 1997-1998 - Pittsburgh, PA and Memphis, TN), Healthy Aging in Neighborhoods of Diversity across the Life Span (HANDLS: 2004-2009 - Baltimore, MD), Health, Risk Factors, Exercise Training and Genetics (HERITAGE: 1995-2000 - AZ; IN; MN; TX; and Quebec, Canada), Howard University Family Study (HUFS: 2001-2008 - Washington, DC), Hypertension Genetic Epidemiology Network (HyperGEN: 1996-1999 - Birmingham, AL; Salt Lake City, UT; Forsyth County, NC; Minneapolis, MN; and Framingham, MA), Jackson Heart Study (JHS: 2000-2004 - Jackson, MS), Multi-Ethnic Study of Atherosclerosis (MESA: 2000-2002 - Los Angeles, CA; St. Paul, MN; Chicago, IL; Winston-Salem, NC; Baltimore, MD and New York, NY), Netherlands Epidemiology of Obesity study (NEO: 2008-2012 - Leiden, the Netherlands), Rotterdam Study 1 (RS1: 1990 - Rotterdam, the Netherlands), Rotterdam Study 2 (RS2: 2000-2001 - Rotterdam, the Netherlands), Rotterdam Study 3 (RS3: 2006-2008 - Rotterdam, the Netherlands), Singapore Chinese Eye Study (SCES: 2009-2011 - Singapore),

Singapore Chinese Health Study (SCHS: 1993-1998 - Singapore), Singapore Malay Eye Study (SiMES: 2004-2006 - Singapore), Singapore Indian Eye Study (SINDI: 2007-2009 - Singapore), Singapore 2 (SP2-1M: 1982-1998 - Singapore), Women's Genome Health Study (WGHS: 1992-1995 - USA), and Women's Health Initiative (WHI: 1993-1998 - USA).

Stage 2 included 136,986 European, 4,475 African, 108,431 Asian, 13,714 Hispanic, and 3,652 Brazilian ancestry individuals for an overall total of 267,258 individuals from the following studies (**Web Table 2**): 1982 Pelotas Birth Cohort Study (1982 - Pelotas, Brazil), African American Diabetes Heart Study (AA-DHS: 1998-2005 - Winston-Salem, NC), Anglo-Scandinavian Cardiac Outcomes Trial (ASCOT: 1998-2000 - Denmark; Finland; Ireland; Norway; Sweden; UK), Baependi Heart Study (2010 - Baependi, Brazil), BBJ (2003-2008 - Japan), Beijing Eye Study (2001 - Beijing, China), British Genetics of Hypertension (BRIGHT: 1995 - UK), Cardio-metabolic Genome Epidemiology Network, Amagasaki Study (CAGE-Amagasaki: 2002-2003 - Amagasaki, Japan), Data from an Epidemiological Study on the Insulin Resistance (DESIR-1: 1994-1996 - France), Dongfeng-Tongji Cohort Study (DF-TJ: 2008 - Shiyan city, China), Diabetes Heart Study (DHS: 1998-2005 - Winston-Salem, NC), Dose Responses to Exercise Training (DR's EXTRA: 2005-2006 - Kuopio, Finland), Estonian Genome Center - University of Tartu (EGCUT: 2002-2010 - Estonia), European Prospective Investigation into Cancer and Nutrition (EPIC: 1992-1997 - France; Italy; Spain; UK; the Netherlands; Germany; Sweden; Denmark; Norway; and Greece), Fenland Study (FENLAND-GWAS: 1950-1975 - Cambridgeshire, England), Finland-United States Investigation of NIDDM Genetics (FUSION: 1994 - Finland), Genetic Studies of Atherosclerosis Risk (GeneSTAR: 1983-2006 - Baltimore, MD), Gene x Lifestyle Interactions and Complex Traits Involved in Elevated Disease Risk (GLACIER: 1985-2004 - Sweden), Genetic Regulation of Arterial Pressure of Humans in

the Community (GRAPHIC: 2003-2005 - Leicestershire, UK), Hispanic Community Health Study/ Study of Latinos (HCHS/SOL: 2008-2011 - Chicago, IL; Miami, FL; New York City, NY; and San Diego, CA), Health & Retirement Study (HRS: 2006-2010 - USA), Hypertension Genetic Epidemiology Network (HyperGEN-AXIOM: 1996-1999 - Birmingham, AL; Salt Lake City, UT; Forsyth County, NC; Minneapolis, MN; and Framingham, MA), Italian Network Genetic Isolates - Carlantino (INGI-CARL: 2005-2006 - Carlantino, Italy), Italian Network Genetic Isolates - Friuli-Venezia Giulia (INGI-FVG: 2013 - Friuli-Venezia Giulia, Italy), EPIC-InterAct Case-Cohort Study (InterAct: 1991-2007 - France; Italy; Spain; UK; the Netherlands; Germany; Sweden; and Denmark), Insulin Resistance Atherosclerosis Study (IRASC and IRASFS: 1999-2005 - San Antonio, TX; San Luis Valley, CO), Cooperative Health Research in the Augsburg Region S3 (KORA_S3: 1994-1995 - Augsburg, Germany), Cooperative Health Research in the Augsburg Region S4 (KORA_S4: 1991-2001 - Augsburg, Germany), Lothian Birth Cohort 1936 (LBC1936: 2004-2007 - Lothian, Scotland), LifeLines (2006-2013 - the Netherlands), London Life Sciences Prospective Population study (LOLIPOP: 2003-2007 - London, England), Long Life Family Study (LLFS: 2006-2009 - Boston, MA; New York City, NY; Pittsburgh PA; and Denmark), Kingston Gene-by-environment (Loyola GxE: 1994-1995 - Kingston, Jamaica), Spanish Town (Loyola SPT: 1994-1995 - Kingston, Jamaica), Metabolic Syndrome In Men (METSIM: 2005-2010 - Kuopio, Finland), Netherlands Study of Depression and Anxiety (NESDA: 2004-2007 - the Netherlands), French obese cases (OBA: 2005 - France), Prevention of REnal and Vascular ENd stage Disease study (PREVEND: 1997-1998 - Groningen, Netherlands), Precocious Coronary Artery Disease (PROCARDIS: 2004-2008 - UK; Italy; Sweden; and Germany), Ragama Health Study (RHS: 2007 - Ragama, Sri Lanka), Stockholm Heart Epidemiology Program (SHEEP: 1992-1994 - Stockholm county, Sweden),

Study of Health in Pomerania (SHIP-0: 1997-2001 - Greifswald, Stralsund and Anklam Germany), Study of Health in Pomerania - Trend (SHIP-Trend: 2008-2012 - Greifswald, Stralsund and Anklam Germany), Shanghai Women's Health Study/ Shanghai Men's Health Study (SWHS/SMHS: 1997-2000 - Shanghai, China), TwinGene of the Swedish Twin Registry (TWINGENE: 2004-2008 - Sweden), and Cardiovascular Risk in Young Finns Study (YFS: 1980 - Finland).

Phenotype and lifestyle variables

Three lipids traits were analyzed separately: HDL-C (mg/dL), LDL-C (mg/dL), and TG (mg/dL). HDL-C and TG were directly assayed, while LDL-C was either directly assayed or estimated using the Friedewald equation: LDL-C = TC – HDL-C – (TG / 5) (28). Only fasting samples (≥ 8 hours) were used to assay TG, and the Friedewald equation was only used in samples with fasting TG ≤ 400 mg/dL. LDL-C values were adjusted for use of statins (**Web Appendix**). HDL-C and TG were natural log transformed prior to analyses.

Alcohol consumption was assessed using two dichotomized alcohol consumption variables: ‘current drinking’ status, defined as any recurrent drinking behavior, and ‘regular drinking’ status, as the subset of current drinkers who consume at least two drinks per week. Because the standard pure ethanol content in one alcoholic drink may vary among countries, for this study a standard drink was defined to contain approximately 13g of pure ethanol, and this measure was used to standardize the definitions across studies.

Genotyping and imputation

Information on genotyping and imputation for each of the Stage 1 and Stage 2 studies are presented in **Web Table 3** and **Web Table 4**, respectively. For imputation, most studies used the

1000 Genomes Project Phase I Integrated Release Version 3 Haplotypes (2010-11 data freeze, 2012-03-14 haplotypes), which contain haplotypes for 1,092 individuals from multiple ancestry groups (29).

Study-specific analysis

Study-specific regression analyses were performed for each variant, using models containing the genetic variant, alcohol consumption variable (current drinking or regular drinking status), and their interaction. Variants were coded according to the additive model, so that the beta coefficient represents the effect size per copy of the coded allele. These regressions were adjusted for age, sex, ancestry-informative principal components, and study-specific variables where appropriate (such as center for multi-center studies). Information on principal components and study-specific variables adjusted for in each study-specific analysis is provided in **Web Tables 3-4**.

Each study in Stage 1 performed genome-wide association analyses within each ancestry and provided the estimated genetic main effect, estimated interaction effect and a robust estimate of the corresponding covariance matrix. Each study in Stage 2 performed analyses only for the selected variants identified in Stage 1. Study-specific association analyses were performed using various software (**Web Appendix** and **Web Tables 3-4**). Extensive quality control using the R package EasyQC was performed for all study-specific GWAS results, as described in the **Web Appendix** (30).

Meta-analysis

We implemented METAL to meta-analyze the genetic main and interaction effects jointly using the 2 DF approach by Manning *et al*. (27, 31), and to meta-analyze the interaction coefficients

alone using inverse-variance weighted meta-analysis (1 DF test). For each meta-analysis, results were obtained from Wald tests, calculated using genetic main effect estimates, interaction effect estimates, and robust estimates of the corresponding covariance matrix.

In Stage 1 ancestry-specific meta-analyses were performed for each of the 12 analyses (3 lipids × 2 alcohol consumption exposures × 2 tests). Genomic control correction was applied twice (32), first to the study-specific GWAS results (**Web Table 5**), and then to the ancestry-specific meta-analysis results. The results from each ancestry group were then combined in a trans-ancestry meta-analysis.

The variants that were at least suggestively associated (P-value < 1×10^{-6}) in any of Stage 1 interaction analyses were pursued for Stage 2 analysis. In Stage 2, we used the same approaches as in Stage 1 to perform ancestry-specific and trans-ancestry meta-analyses. Finally, ancestry-specific and trans-ancestry meta-analyses were performed to combine Stage 1 results with Stage 2 results. Variants with *P*-value < 5×10^{-8} for either the 2 DF joint test of genetic main and interaction effects or the 1 DF test of interaction effects were considered genome-wide significant. False discovery rate (FDR) *q*-values were calculated using the Benjamini and Hochberg method implemented in the "p.adjust" function in R, correcting for the number of tests performed in Stage 1. FDR *q*-values < 0.05 thus indicate a < 5% false discovery rate even after considering the multiple testing introduced by performing genome-wide analyses on multiple outcomes using multiple models. An independent locus was defined as the ±1 Mbp region surrounding an index variant. For each locus the closest genes were determined based on proximity to the index variant. For loci with intergenic index variants we provided the closest gene in each direction.

Additional analyses

The percent of variance explained in HDL-C, LDL-C, and TG by all previously known and novel variants was evaluated in ten studies from multiple ancestries (**Web Appendix**). HaploReg, RegulomeDB, and Genotype-Tissue Expression (GTEx) were used to annotate variants at significant loci (33-35). We also used the Data-driven Expression Prioritized Integration for Complex Traits (DEPICT) software to prioritize genes at the loci associated with lipid levels in the combined analysis of Stage 1 and 2. More details on gene prioritization using DEPICT can be found in the **Web Appendix**.

Lastly, we examined the association of index variants at the 147 significant loci with coronary artery disease and myocardial infarction using publicly available summary association results from a large GWAS of these phenotypes performed by the CARDIoGRAMplusC4D consortium (36).

RESULTS

Descriptive statistics of the studies participating in Stage 1 are shown in **Web Table 1**: 56.1 percent of Stage 1 participants were current drinkers and 39.9 percent were regular drinkers. The Stage 1 genome-wide analyses identified 25,115 variants in 495 independent loci that were at least suggestively associated (P-value $< 1\times10^{-6}$) with HDL-C, LDL-C, or TG using either the 1 DF test of the interaction or the 2 DF test that jointly assesses genetic main and interaction effects. The 1 DF interaction test identified 356 suggestively associated variants, while the 2 DF joint test identified an additional 24,759. Manhattan and quantile-quantile plots are shown in **Web Figures 1 and 2, respectively**.

The 25,115 variants were then evaluated in Stage 2. Descriptive statistics of the studies participating in Stage 2 are shown in **Web Table 2**: 58.5 percent of Stage 2 participants were current drinkers and 41.0 percent were regular drinkers. The combined analysis of Stage 1 and Stage 2 identified 22,590 variants at 147 independent loci at genome-wide significance (*P*-value $< 5\times10^{-8}$, **Web Table 6**). All genome-wide significant associations were identified through the 2 DF joint tests of main and interaction effects. There were no genome-wide significant 1 DF interaction associations in the combined analysis of Stage 1 and Stage 2. At genome-wide significance, 95 of the 147 loci were associated with HDL-C, 66 were associated with LDL-C, and 58 were associated with TG. Out of the 147 loci, 60 loci were associated with more than one lipid trait, as shown in a Venn diagram in **Figure 1**.

Novel loci

Of the 147 identified genome-wide significant loci, 18 are novel lipid loci that have not been previously identified by other association studies for HDL-C, LDL-C, TG, or total cholesterol (**Table 2** and **Web Figure 3**) (2-8). A concurrent genetic association study of exonic variants also identified four of these 18 novel loci (37), as indicated in **Table 2**. Eight of the novel loci involved HDL-C, eight involved LDL-C, and seven involved TG, as shown in the heatmap in **Figure 2**. The most significant associations at each of the 18 novel loci all had FDR *q*-values < 0.05 (**Table 2**), indicating that they are unlikely to be false positives introduced by multiple testing. As shown in forest plots (**Web Figure 4**), the 2 DF associations at the novel loci were predominantly driven by genetic main effects, with a smaller contribution from interaction effects. Furthermore, of the 18 index variants, 15 had at least suggestively significant ($P < 1\times10^{-6}$) genetic main effects in Stage 1 (**Web Appendix** and **Web Table 7**). None of the associations at the 18 novel loci displayed heterogeneity across ancestry groups (**Table 2**).

Known loci

The remaining 129 of the 147 significant loci had been identified in previous GWAS of lipid traits (**Web Table 6**) (2-8). This is a subset of all known lipid loci: **Web Table 8** shows the significance of 314 reported index variants in all 236 known lipid loci among all 2 DF joint tests and 1 DF interaction tests of the combined analysis of Stage 1 and Stage 2, or Stage 1 alone for variants not meeting the Stage 2 inclusion criteria (2-8). Considering only the 314 known variants, no 1 DF interactions were significant in the European, African, or trans-ancestry meta-analyses (*P*-value < 8.8×10^{-6}, corresponding to 0.05 / [314 variants × 3 lipid traits × 2 alcohol consumption variables × 3 ancestry groups]).

Additional analyses

The percentage of variance in LDL-C, HDL-C, and TG explained by various loci was calculated in individual studies from multiple ancestries. Across ancestry groups, the mean variance explained by known lipid loci was 9.1 percent for HDL-C, 10.4 percent for LDL-C, and 7.5 percent for TG. The total percentage of additional variance explained by the 18 novel loci, including both genetic main and interaction effects, was 0.2 for HDL-C, 0.3 for LDL-C, and 0.4 for TG. Ancestry-specific and study-specific estimates are shown in **Web Table 9**.

Functional annotations using HaploReg (33) and RegulomeDB (34) for variants at the 147 loci that were associated in the combined analysis of Stage 1 and 2 are presented in **Web Table 10**, and associations of these variants with gene expression levels from the GTEx database (35) in a variety of tissues are shown in **Web Table 11**. A total of 443 variants were associated with gene expression levels, of which 27 variants were indicated by RegulomeDB as having strong evidence for an effect on enhancer function.

Our gene prioritization analyses with DEPICT highlighted (FDR *q*-values < 5 percent) 165 genes at HDL-C associated loci, 110 genes at LDL-C associated loci and 87 genes at TG associated loci (**Web Tables 11-14**). Thus, at some loci multiple potential causal genes were prioritized. DEPICT identified 656, 877 and 497 reconstituted gene sets that were significantly enriched (FDR *q*-values < 5 percent) for genes at HDL-C, LDL-C and TG loci, respectively (**Web Table 15**). This large number of processes and enriched gene sets underscores the complex genetic, biological and physiological mechanisms underlying lipid traits. Among the most significantly enriched gene sets were processes related to "total amount of body fat" and "abnormal liver morphology". Finally, DEPICT revealed that genes at associated HDL-C, LDL-C or TG loci were significantly enriched (FDR *q*-values < 5 percent) for association with gene expression in 23 tissues, 14 cell-types and 12 physiological systems (**Web Table 16**). We found a compelling enrichment of genes acting in hepatocytes and liver processes at associated loci for each of the three traits and of genes acting in adipose tissues for HDL-C and TG loci (**Web Table 16, Web Figure 5**).

Fourteen index variants at known lipid loci were associated with coronary artery disease with P-value < 1.7×10^{-4} (0.05 / [147 variants × 2 disease outcomes]), and eleven of these were also associated with myocardial infarction (**Web Table 17**) (36). None of the index variants at novel loci were significantly associated with these clinical endpoints.

DISCUSSION

We performed a genome-wide association study of lipid levels incorporating interactions with alcohol consumption and identified 147 genome-wide significant lipid loci of which 18 are novel.

Despite the large sample of 394,584 individuals, which is comparable to other successful genetic interaction studies (38, 39), genome-wide significant interactions were not found in the present study. Gene-alcohol interactions also do not appear to have contributed substantially to the discovery of the 18 novel loci, given that the genetic main effect of index variants at 15 of the 18 novel loci passed the Stage 1 suggestive significance threshold. We highlight three of the novel loci below that harbor especially promising candidate genes with putative roles in lipid metabolism based on existing evidence from cellular and experimental models.

One of the newly identified associations for LDL-C maps to Proprotein Convertase Subtilisin/Kexin Type 5 *(PCSK5)*, a member of the same gene family as *PCSK9*, which is targeted by new drugs that successfully lower LDL-C levels (40, 41). Several independent lines of evidence support the involvement of *PCSK5* in the regulation of lipid levels. First, a candidate gene study found that variants in *PCSK5* were associated with levels of HDL-C levels (42). Additionally, *in vitro* studies of cell lines show that PCSK5 inactivates endothelial lipase directly through cleavage, and that it may also inactivate endothelial lipase and lipoprotein lipase indirectly through activation of Angiopoietin-like 3 (43). Endothelial lipase, lipoprotein lipase, and Angiopoietin-like 3 have all been robustly implicated in the regulation of lipid levels, likely with primary roles in the metabolism of HDL-C and triglycerides (3, 44-46). In our study, the *PCSK5* locus was only associated at genome-wide significance with LDL-C levels, and at nominal significance (P-value < 0.05) with TG levels.

One novel locus for TG mapped to the *A1CF* gene, which encodes APOBEC1 Complementation Factor. Liu *et al*. also identified the same index variant (rs41274050) in association with TG in a concurrent study (37). They showed that introducing the minor allele of rs41274050 in mice led to increased TG levels, confirming the functional role of this missense variant in the regulation

of TG levels (37). APOBEC1 Complementation Factor forms an enzymatic complex with APOBEC1 and deaminates Apolipoprotein B mRNA (47). This site specific deamination of C to U results in the production of the apoB48 isoform as opposed to the apoB100 isoform (47). The apoB48 isoform is critical in the assembly and secretion of chylomicrons, which mainly carry dietary-derived triglycerides (48). Interestingly, a recent GWAS in individuals of East Asian ancestry identified the *APOBEC1* locus for HDL-C levels (5), an association that we confirmed in our analysis (index variant: 12:7725904:ID). At nominal significance both the index variants near *A1CF* and *APOBEC1* were associated with all three lipid traits (*P*-value < 0.05). Given the role of apoB100 in atherosclerosis, promoting the synthesis of apoB48 instead of apoB100 may represent a possible therapeutic strategy for the prevention of cardiovascular disease (49). Neither the index variant at *A1CF* nor *APOBEC1* is significantly associated with coronary artery disease or myocardial infarction in the largest GWAS of these outcomes. However, further studies are needed to characterize their role in cardiovascular disease, given our multi-ancestry design and the European-driven design of the available GWAS data on cardiovascular disease outcomes **(Web Table 17)**.

Variants closest to the MACRO Domain Containing 1 *(MACROD1)* gene were associated with HDL-C levels and TG levels. This locus was also reported in the concurrent study by Liu *et al.* (37), although the index variant in their study was located in the Phospholipase C Beta 3 *(PLCB3)* gene, around 120 Kbp away from the index variant in the present study. We found that variants at this locus were associated with expression levels of another nearby gene, Vascular Endothelial Growth Factor B *(VEGFB),* in adipose and heart tissue (**Web Table 11**). VEGF-B is reportedly involved in endothelial fatty acid transport, with $Vegfb^{-/-}$ mice showing less accumulation of lipids in muscle, heart, and brown adipose tissue, but a greater uptake of fatty

acids in white adipose tissue, and higher body weight (50). Additionally, inhibition of VEGF-B in a mouse model of type 2 diabetes resulted in improved glycemic profile as well as a reduction of dyslipidemia (51). Mice lacking VEGF-B had lower levels of TG and LDL-C accompanied by higher levels of HDL-C. Subsequent studies on other mouse models did not corroborate these findings: Dijkstra *et al.* found in an independent strain of mice that knocking out VEGF-B had no effect on TG and total cholesterol levels (52), while Rubciuc *et al.* reported that transduction of the human *VEGFB* gene into mice led to increased vascularity in adipose tissue, and improved lipid profile (53, 54). Our results provide insight into the effects of VEGF-B in humans to complement the divergent reports from rodent studies. The A allele of index variant rs190528931 is associated with decreased expression of *VEGFB* in adipose and heart tissue, decreased levels of HDL-C and increased levels of TG. Additionally, rs190528931 was also associated with nominally significant increased levels of LDL-C (P-value < 0.05). Hence, evidence from our study suggests that inhibition of VEGF-B does not improve lipid profile, but instead promotes dyslipidemia.

The strengths of this study include the large sample size and diverse ancestral composition of the sample, and the use of a dense reference panel for genotype imputation (55). A limitation of this study is the imbalance in ancestry groups between Stage 1 and Stage 2. African ancestry individuals were well-represented in Stage 1 but underrepresented in Stage 2. In contrast, Asian and Hispanic ancestry individuals were relatively underrepresented in Stage 1 compared to Stage 2. A more balanced division of participants across Stage 1 and Stage 2 may have led to the identification of additional loci. Additionally, alcohol consumption may be underreported in both self-administered questionnaires and interviews, leading to a loss of statistical power due to misclassification (56). Similarly, the classification of alcohol consumption into categories such

as regular drinkers and current drinkers may have reduced power relative to treating it as a fully quantitative variable (57). Nevertheless, the use of such categories was necessary for harmonizing data from 111 studies with heterogeneous measurement of alcohol consumption. It is plausible that more comprehensive characterization of alcohol consumption could reveal interactions that were missed in our study.

In conclusion, we identified 18 novel loci that were significantly associated with lipid traits, and these include several loci with genes (*PCSK5*, *VEGFB*, and *A1CF*) that have a putative role in lipid metabolism based on existing evidence from cellular and experimental models. The associations identified in this study appear to be driven by genetic main effects and it remains uncertain whether alcohol consumption modifies the effect of genetic variants on lipid levels.

ACKNOWLEDGEMENTS

Affiliations: Human Genetics Center, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston, Houston, Texas (Paul S de Vries, Michael R Brown, Megan L Grove, Zhe Wang, Bing Yu, Myriam Fornage, Alanna C Morrison); Center for Research on Genomics and Global Health, National Human Genome Research Institute, National Institutes of Health, Bethesda, Maryland (Amy R Bentley, Charles N Rotimi); Division of Biostatistics, Washington University School of Medicine, St. Louis, Missouri (Yun Ju Sung, Karen Schwander, Lisa de las Fuentes, C Charles Gu, Yize Li, Treva K Rice, Dabeeru C Rao); Department of Genetic Epidemiology, University of Regensburg, Regensburg, Germany (Thomas W Winkler); Clinical Pharmacology, William Harvey Research Institute, Barts and The London School of Medicine and Dentistry, Queen Mary University of London, London, United Kingdom (Ioanna Ntalla, Patricia B Munroe); Division of Statistical Genomics, Department of Genetics, Washington

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Epidemiology and Biostatistics, Imperial College London, London, United Kingdom (Evangelos Evangelou, Weihua Zhang, Saima Afaq, Benjamin Lehne, Marie Loh, Raha Pazoki, William R Scott, John C Chambers, Paul Elliott); Department of Hygiene and Epidemiology, University of Ioannina Medical School, Ioannina, Greece (Evangelos Evangelou); Estonian Genome Center, University of Tartu, Tartu, Estonia (Maris Alver, Reedik Mägi, Andres Metspalu, Lili Milani, Tõnu Esko); CNRS UMR 8199, European Genomic Institute for Diabetes (EGID), Institut Pasteur de Lille, University of Lille, Lille, France (Mathilde Boissel, Mickaël Canouil, Philippe Froguel); Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Stockholm, Sweden (Xu Chen, Nancy L Pedersen, Patrik KE Magnusson); Biostatistical Sciences, Public Health Sciences, Wake Forest School of Medicine, Winston-Salem, North Carolina (Jasmin Divers, Fang-Chi Hsu, Carl D Langefeld); Department of Medical Sciences, University of Trieste, Trieste, Italy (Ilaria Gandin, Dragana Vuckovic, Paolo Gasparini); Molecular Genetics and Genomics Program, Molecular Genetics and Genomics Program, Wake Forest School of Medicine, Winston-Salem, North Carolina (Chuan Gao); Division of Cardiovascular Medicine, Radcliffe Department of Medicine, University of Oxford, Oxford, Oxfordshire, United Kingdom (Anuj Goel, Martin Farrall, Hugh Watkins); Wellcome Centre for Human Genetics, University of Oxford, Oxford, Oxfordshire, United Kingdom (Anuj Goel, Martin Farrall, Hugh Watkins); Department of Cardiology, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands (Yanick Hagemeijer, M Abdullah Said, Ruben N Eppinga, Pim van der Harst); Centre for Cognitive Ageing and Cognitive Epidemiology, The University of Edinburgh, Edinburgh, United Kingdom (Sarah E Harris, John M Starr, Ian J Deary); Medical Genetics Section, University of Edinburgh Centre for Genomic and Experimental Medicine and MRC Institute of Genetics and Molecular

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Wareham); Department of Clinical Chemistry, Fimlab Laboratories, Tampere, Finland (Leo-Pekka Lyytikäinen, Terho Lehtimäki); Department of Clinical Chemistry, Finnish Cardiovascular Research Center - Tampere, Faculty of Medicine and Health Technology, Tampere University, Tampere, Finland (Leo-Pekka Lyytikäinen, Terho Lehtimäki); Laboratory for Statistical Analysis, Center for Integrative Medical Sciences, RIKEN, Yokohama, Japan (Nana Matoba, Yoichiro Kamatani); Department of Epidemiology, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands (Ilja M Nolte, Peter J van der Most, Marzyeh Amini, Harold Snieder); Institute of Clinical Chemistry and Laboratory Medicine, University Medicine Greifswald, Greifswald, Germany (Maik Pietzner, Matthias Nauck); DZHK (German Centre for Cardiovascular Health), Partner Site Greifswald, Greifswald, Germany (Maik Pietzner, Matthias Nauck); Department of Cardiovascular Sciences, University of Leicester, Leicester, United Kingdom (Muhammad Riaz, Christopher P Nelson, Nilesh J Samani); NIHR Leicester Biomedical Research Centre, Glenfield Hospital, Leicester, United Kingdom (Muhammad Riaz, Christopher P Nelson, Nilesh J Samani); Division of Sleep and Circadian Disorders, Brigham and Women's Hospital, Boston, Massachusetts (Tamar Sofer); Institute of Clinical Medicine, Internal Medicine, University of Eastern Finland, Kuopio, Finland (Alena Stančáková, Sami Heikkinen, Johanna Kuusisto, Markku Laakso); Department of Gene Diagnostics and Therapeutics, Research Institute, National Center for Global Health and Medicine, Tokyo, Japan (Fumihiko Takeuchi, Norihiro Kato); Department of Public Health Sciences, Loyola University Chicago, Maywood, Illinois (Bamidele O Tayo); Department of Clinical Sciences, Genetic and Molecular Epidemiology Unit, Lund University Diabetes Centre, Skåne University Hospital, Malmö, Sweden (Tibor V Varga, Paul W Franks); Department of Population and Quantitative Health and Sciences, Case Western Reserve University, Cleveland,

Ohio (Yajuan Wang, Jingjing Liang, Xiaofeng Zhu); Survey Research Center, Institute for Social Research, University of Michigan, Ann Arbor, Michigan (Erin B Ware, Jessica D Faul, Jennifer A Smith, David R Weir); Division of Epidemiology, Department of Medicine, Vanderbilt University School of Medicine, Nashville, Tennessee (Wanqing Wen, Xiao-Ou Shu, Wei Zheng); Division of General Internal Medicine, Department of Medicine, Johns Hopkins University School of Medicine, Baltimore, Maryland (Lisa R Yanek, Diane M Becker); Department of Cardiology, Ealing Hospital, Middlesex, United Kingdom (Weihua Zhang, John C Chambers, Jaspal S Kooner); McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, Maryland (Dan E Arking); Ophthalmology & Visual Sciences Academic Clinical Program (Eye ACP), Duke-NUS Medical School, Singapore, Singapore (Tin Aung, Tien Yin Wong); Section of Cardiovascular Research, Baylor College of Medicine, Houston, Texas (Christie Ballantyne); Houston Methodist Debakey Heart and Vascular Center, Houston, Texas (Christie Ballantyne); Department of Epidemiology, Human Genetics, and Environmental Sciences, The University of Texas School of Public Health, Houston, Texas (Eric Boerwinkle, James E Hixson); Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas (Eric Boerwinkle); Section of Genomic Pediatrics, Department of Pediatrics, Medicine and Physiology, Medical College of Wisconsin, Milwaukee, Wisconsin (Ulrich Broeckel); Centre for Genomic & Experimental Medicine, Institute of Genetics & Molecular Medicine, University of Edinburgh, Edinburgh, United Kingdom (Archie Campbell); Ninewells Hospital & Medical School, University of Dundee, Dundee, Scotland, United Kingdom (John M Connell); Cardiovascular Division, Department of Medicine, Washington University, St. Louis, Missouri (Lisa de las Fuentes); Clinical Epidemiology, Leiden University Medical Center, Leiden, Netherlands (Renée de Mutsert, Dennis O Mook-Kanamori);

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Institute (UK-DRI) at Imperial College London, London, United Kingdom (Paul Elliott); Carolina Center of Genome Sciences, University of North Carolina, Chapel Hill, North Carolina (Kari E North); Public Health Sciences, Epidemiology and Prevention, Wake Forest University Health Sciences, Winston-Salem, North Carolina (Yongmei Liu); Cardiovascular Health Research Unit, Epidemiology, Medicine and Health Services, University of Washington, Seattle, Washington (Bruce Psaty); Kaiser Permanente Washington, Health Research Institute, Seattle, Washington Bruce Psaty); Harvard Medical School, Boston, Massachusetts (Paul M Ridker, Daniel I Chasman); Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, Singapore, Singapore (Jianjun Liu, Rob M van Dam, E Shyong Tai); Public Health and Primary Care, Leiden University Medical Center, Leiden, Leiden (Dennis O Mook-Kanamori); Epidemiology, Tulane University School of Public Health and Tropical Medicine, New Orleans, Louisiana (Tanika N Kelly); Cardiology, Medicine, University of Mississippi Medical Center, Jackson, Mississippi (Ervin R Fox); WHI CCC, Fred Hutchinson Cancer Research Center, Seattle, Washington Jingmin Liu); Biostatistics, Preventive Medicine, University of Southern California, Los Angeles, California (W James Gauderman); NIHR Barts Cardiovascular Biomedical Research Unit, Queen Mary University of London, London, United Kingdom (Patricia B Munroe); and NHLBI Framingham Heart Study, Framingham, Massachusetts (L Adrienne Cupples).

Equal contributions: Paul S de Vries, Michael R Brown, Amy R Bentley, Yun J Sung, Thomas W Winkler, Ioanna Ntalla contributed equally to the manuscript as junior authors. Patricia B Munroe, Kenneth Rice, Daniel I Chasman, L Adrienne Cupples, Dabeeru C Rao, Alanna C Morrison contributed equally to the manuscript as senior authors.

Funding: This work was supported by the National Heart, Lung, and Blood Institute grant R01HL118305. Infrastructure for the CHARGE Consortium is supported in part by the National Heart, Lung, and Blood Institute grant R01HL105756. American Heart Association Grant #17POST33350042 made it possible for Dr. de Vries to lead this project. Study-specific funding sources are provided below, starting with Stage 1 studies followed by Stage 2.

AGES (Age Gene/Environment Susceptibility Reykjavik Study): This study has been funded by NIH contract N01-AG012100, the NIA Intramural Research Program, an Intramural Research Program Award (ZIAEY000401) from the National Eye Institute, an award from the National Institute on Deafness and Other Communication Disorders (NIDCD) Division of Scientific Programs (IAA Y2-DC_1004-02), Hjartavernd (the Icelandic Heart Association), and the Althingi (the Icelandic Parliament). The study is approved by the Icelandic National Bioethics Committee, VSN: 00-063.

ARIC (Atherosclerosis Risk in Communities) Study: The ARIC study is carried out as a collaborative study supported by National Heart, Lung, and Blood Institute contracts (HHSN268201100005C, HHSN268201100006C, HHSN268201100007C, HHSN268201100008C, HHSN268201100009C, HHSN268201100010C, HHSN268201100011C, and HHSN268201100012C), R01HL087641, R01HL59367 and R01HL086694; National Human Genome Research Institute contract U01HG004402; and National Institutes of Health contract HHSN268200625226C. Infrastructure was partly supported by Grant Number UL1RR025005, a component of the National Institutes of Health and NIH Roadmap for Medical Research.

Baependi Heart Study (Brazil): The Baependi Heart Study was supported by Fundação de Amparo a Pesquisa do Estado de São Paulo (FAPESP) (Grant 2013/17368-0), Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) and Hospital Samaritano Society (Grant 25000.180.664/2011-35), through Ministry of Health to Support Program Institutional Development of the Unified Health System (SUS-PROADI).

CARDIA (Coronary Artery Risk Development in Young Adults): The CARDIA Study is conducted and supported by the National Heart, Lung, and Blood Institute in collaboration with the University of Alabama at Birmingham (HHSN268201300025C & HHSN268201300026C), Northwestern University (HHSN268201300027C), University of Minnesota (HHSN268201300028C), Kaiser Foundation Research Institute (HHSN268201300029C), and Johns Hopkins University School of Medicine (HHSN268200900041C). CARDIA is also partially supported by the Intramural Research Program of the National Institute on Aging. Genotyping was funded as part of the NHLBI Candidate-gene Association Resource (N01-HC-65226) and the NHGRI Gene Environment Association Studies (GENEVA) (U01-HG004729, U01-HG04424, and U01-HG004446). This manuscript has been reviewed and approved by CARDIA for scientific content.

CHS (Cardiovascular Health Study): This CHS research was supported by NHLBI contracts HHSN268201200036C, HHSN268200800007C, HHSN268200960009C, N01HC55222, N01HC85079, N01HC85080, N01HC85081, N01HC85082, N01HC85083, N01HC85086; and NHLBI grants U01HL080295, R01HL085251, R01HL087652, R01HL105756, R01HL103612, R01HL120393 and R01HL130114 with additional contribution from the National Institute of Neurological Disorders and Stroke (NINDS). Additional support was provided through R01AG023629 from the National Institute on Aging (NIA). The provision of genotyping data

was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR000124, and the National Institute of Diabetes and Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center.

ERF (Erasmus Rucphen Family study): The ERF study as a part of EUROSPAN (European Special Populations Research Network) was supported by European Commission FP6 STRP grant number 018947 (LSHG-CT-2006-01947) and also received funding from the European Community's Seventh Framework Programme (FP7/2007-2013)/grant agreement HEALTH-F4-2007-201413 by the European Commission under the programme "Quality of Life and Management of the Living Resources" of 5th Framework Programme (no. QLG2-CT-2002-01254). The ERF study was further supported by ENGAGE consortium and CMSB. High-throughput analysis of the ERF data was supported by joint grant from Netherlands Organisation for Scientific Research and the Russian Foundation for Basic Research (NWO-RFBR 047.017.043). ERF was further supported by the ZonMw grant (project 91111025).

FamHS (Family Heart Study): The FamHS is funded by R01HL118305 and R01HL117078 NHLBI grants, and 5R01DK07568102 and 5R01DK089256 NIDDK grant.

FHS (Framingham Heart Study): This research was conducted in part using data and resources from the Framingham Heart Study of the National Heart Lung and Blood Institute of the National Institutes of Health and Boston University School of Medicine. The analyses reflect intellectual input and resource development from the Framingham Heart Study investigators participating in the SNP Health Association Resource (SHARe) project. This work was partially supported by the National Heart, Lung and Blood Institute's Framingham Heart Study (Contract

Nos. N01-HC-25195 and HHSN268201500001I) and its contract with Affymetrix, Inc for genotyping services (Contract No. N02-HL-6-4278). A portion of this research utilized the Linux Cluster for Genetic Analysis (LinGA-II) funded by the Robert Dawson Evans Endowment of the Department of Medicine at Boston University School of Medicine and Boston Medical Center. This research was partially supported by grant R01-DK089256 from the National Institute of Diabetes and Digestive and Kidney Diseases (MPIs: Ingrid B. Borecki, L. Adrienne Cupples, Kari North).

GENOA (Genetic Epidemiology Network of Arteriopathy): Support for GENOA was provided by the National Heart, Lung and Blood Institute (HL119443, HL118305, HL054464, HL054457, HL054481, HL071917 and HL087660) of the National Institutes of Health. Genotyping was performed at the Mayo Clinic (Stephen T. Turner, MD, Mariza de Andrade PhD, Julie Cunningham, PhD).

GenSalt (Genetic Epidemiology Network of Salt Sensitivity): The Genetic Epidemiology Network of Salt Sensitivity is supported by research grants (U01HL072507, R01HL087263, and R01HL090682) from the National Heart, Lung, and Blood Institute, National Institutes of Health, Bethesda, MD.

HANDLS (Healthy Aging in Neighborhoods of Diversity across the Life Span): The Healthy Aging in Neighborhoods of Diversity across the Life Span (HANDLS) study was supported by the Intramural Research Program of the NIH, National Institute on Aging and the National Center on Minority Health and Health Disparities (project # Z01-AG000513 and human subjects protocol number 09-AG-N248). Data analyses for the HANDLS study utilized the high-

performance computational resources of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, MD (http://biowulf.nih.gov; http://hpc.nih.gov)).

Health ABC (Health, Aging, and Body Composition): Health ABC was funded by the National Institutes of Aging. This research was supported by NIA contracts N01AG62101, N01AG62103, and N01AG62106. The GWAS was funded by NIA grant 1R01AG032098-01A1 to Wake Forest University Health Sciences and genotyping services were provided by the Center for Inherited Disease Research (CIDR). CIDR is fully funded through a federal contract from the National Institutes of Health to The Johns Hopkins University, contract number HHSN268200782096C. This research was supported in part by the Intramural Research Program of the NIH, National Institute on Aging.

HERITAGE (Health, Risk Factors, Exercise Training and Genetics): The HERITAGE Family Study was supported by National Heart, Lung, and Blood Institute grant HL-45670.

HUFS (Howard University Family Study): The Howard University Family Study was supported by National Institutes of Health grants S06GM008016-320107 to Charles Rotimi and S06GM008016-380111 to Adebowale Adeyemo. Participant enrollment was carried out at the Howard University General Clinical Research Center, supported by National Institutes of Health grant 2M01RR010284. This research was supported in part by the Intramural Research Program of the Center for Research on Genomics and Global Health (CRGGH). The CRGGH is supported by the National Human Genome Research Institute, the National Institute of Diabetes and Digestive and Kidney Diseases, the Center for Information Technology, and the Office of the Director at the National Institutes of Health (Z01HG200362). Genotyping support was provided by the Coriell Institute for Medical Research.

HyperGEN (Hypertension Genetic Epidemiology Network): The hypertension network is funded by cooperative agreements (U10) with NHLBI: HL54471, HL54472, HL54473, HL54495, HL54496, HL54497, HL54509, HL54515, and 2 R01 HL55673-12. The study involves: University of Utah: (Network Coordinating Center, Field Center, and Molecular Genetics Lab); Univ. of Alabama at Birmingham: (Field Center and Echo Coordinating and Analysis Center); Medical College of Wisconsin: (Echo Genotyping Lab); Boston University: (Field Center); University of Minnesota: (Field Center and Biochemistry Lab); University of North Carolina: (Field Center); Washington University: (Data Coordinating Center); Weil Cornell Medical College: (Echo Reading Center); National Heart, Lung, & Blood Institute. For a complete list of HyperGEN Investigators: http://www.biostat.wustl.edu/hypergen/Acknowledge.html

CROATIA-Korcula: CROATIA-Korcula (CR-Korcula) was funded by the Medical Research Council UK, The Croatian Ministry of Science, Education and Sports (grant 216-1080315-0302), the European Union framework program 6 EUROSPAN project (contract no. LSHG-CT-2006-018947) and the Croatian Science Foundation (grant 8875). The SNP genotyping for the CROATIA-Korcula cohort was performed in Helmholtz Zentrum München, Neuherberg, Germany.

CROATIA-Vis: CROATIA-Vis (CR-Vis) was funded by the Medical Research Council UK, The Croatian Ministry of Science, Education and Sports (grant 216-1080315-0302), the European Union framework program 6 EUROSPAN project (contract no. LSHG-CT-2006-018947) and the Croatian Science Foundation (grant 8875). The SNP genotyping for the CROATIA-Vis cohort was performed in the core genotyping laboratory of the Wellcome Trust Clinical Research Facility at the Western General Hospital, Edinburgh, Scotland.

GS:SFHS: Generation Scotland received core support from the Chief Scientist Office of the Scottish Government Health Directorates [CZD/16/6] and the Scottish Funding Council [HR03006]. Genotyping of the GS:SFHS samples was carried out by the Genetics Core Laboratory at the Wellcome Trust Clinical Research Facility, Edinburgh, Scotland and was funded by the Medical Research Council UK and the Wellcome Trust (Wellcome Trust Strategic Award "STratifying Resilience and Depression Longitudinally" (STRADL) Reference 104036/Z/14/Z). Ethics approval for the study was given by the NHS Tayside committee on research ethics (reference 05/S1401/89).

JHS (Jackson Heart Study): The Jackson Heart Study is supported by contracts HSN268201300046C, HHSN268201300047C, HHSN268201300048C, HHSN268201300049C, HHSN268201300050C from the National Heart, Lung, and Blood Institute on Minority Health and Health Disparities.

MESA (Multi-Ethnic Study of Atherosclerosis): This research was supported by the Multi-Ethnic Study of Atherosclerosis (MESA) contracts N01-HC-95159, N01-HC-95160, N01-HC-95161, N01-HC-95162, N01-HC-95163, N01-HC-95164, N01-HC-95165, N01-HC-95166, N01-HC-95167, N01-HC-95168, N01-HC-95169, by grant HL071205 and by UL1-DR-001079 from NCRR . Funding for MESA SHARe genotyping was provided by NHLBI Contract N02-HL-6-4278. This publication was partially developed under a STAR research assistance agreement, No. RD831697 (MESA Air), awarded by the U.S Environmental Protection Agency. The provision of genotyping data was supported in part by the National Center for Advancing Translational Sciences, CTSI grant UL1TR001881, and the National Institute of Diabetes and

Digestive and Kidney Disease Diabetes Research Center (DRC) grant DK063491 to the Southern California Diabetes Endocrinology Research Center.

NEO (The Netherlands Epidemiology of Obesity study): The genotyping in the NEO study was supported by the Centre National de Génotypage (Paris, France), headed by Jean-Francois Deleuze. The NEO study is supported by the participating Departments, the Division and the Board of Directors of the Leiden University Medical Center, and by the Leiden University, Research Profile Area Vascular and Regenerative Medicine. Dennis Mook-Kanamori is supported by Dutch Science Organization (ZonMW-VENI Grant 916.14.023).

Pelotas Birth Cohort Study (The 1982 Pelotas Birth Cohort Study, Brazil): The 1982 Pelotas Birth Cohort Study is conducted by the Postgraduate Program in Epidemiology at Universidade Federal de Pelotas with the collaboration of the Brazilian Public Health Association (ABRASCO). From 2004 to 2013, the Wellcome Trust supported the study. The International Development Research Center, World Health Organization, Overseas Development Administration, European Union, National Support Program for Centers of Excellence (PRONEX), the Brazilian National Research Council (CNPq), and the Brazilian Ministry of Health supported previous phases of the study.

Genotyping of 1982 Pelotas Birth Cohort Study participants was supported by the Department of Science and Technology (DECIT, Ministry of Health) and National Fund for Scientific and Technological Development (FNDCT, Ministry of Science and Technology), Funding of Studies and Projects (FINEP, Ministry of Science and Technology, Brazil), Coordination of Improvement of Higher Education Personnel (CAPES, Ministry of Education, Brazil).

RS (Rotterdam Study): The Rotterdam Study is funded by Erasmus Medical Center and Erasmus University, Rotterdam, Netherlands Organization for the Health Research and Development (ZonMw), the Research Institute for Diseases in the Elderly (RIDE), the Ministry of Education, Culture and Science, the Ministry for Health, Welfare and Sports, the European Commission (DG XII), and the Municipality of Rotterdam. The generation and management of GWAS genotype data for the Rotterdam Study was executed by the Human Genotyping Facility of the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, Rotterdam, The Netherlands. The GWAS datasets are supported by the Netherlands Organisation of Scientific Research NWO Investments (nr. 175.010.2005.011, 911-03-012), the Genetic Laboratory of the Department of Internal Medicine, Erasmus MC, the Research Institute for Diseases in the Elderly (014-93-015; RIDE2), the Netherlands Genomics Initiative (NGI)/Netherlands Organisation for Scientific Research (NWO) Netherlands Consortium for Healthy Aging (NCHA), project nr. 050-060-810.

SCHS-CHD (Singapore Chinese Health Study - Coronary Heart Disease): The Singapore Chinese Health Study is supported by the National Institutes of Health, USA (RO1 CA144034 and UM1 CA182876), the nested case-control study of myocardial infarction by the Singapore National Medical Research Council (NMRC 1270/2010) and genotyping by the HUJ-CREATE Programme of the National Research Foundation, Singapore (Project Number 370062002).

SCES (Singapore Chinese Eye Study), SiMES (Singapore Malay Eye Study), (SINDI) Singapore Indian Eye Study: The Singapore Malay Eye Study (SiMES), the Singapore Indian Eye Study (SINDI), and the Singapore Chinese Eye Study (SCES) are supported by the National Medical Research Council (NMRC), Singapore (grants 0796/2003, 1176/2008, 1149/2008, STaR/0003/2008, 1249/2010, CG/SERI/2010, CIRG/1371/2013, and CIRG/1417/2015), and

Biomedical Research Council (BMRC), Singapore (08/1/35/19/550 and 09/1/35/19/616). Ching-Yu Cheng is supported by an award from NMRC (CSA/033/2012). The Singapore Tissue Network and the Genome Institute of Singapore, Agency for Science, Technology and Research, Singapore provided services for tissue archival and genotyping, respectively.

SP2 (Singapore Prospective Study Program): SP2 is supported by the individual research grant and clinician scientist award schemes from the National Medical Research Council and the Biomedical Research Councils of Singapore.

WGHS (Women's Genome Health Study): The WGHS is supported by the National Heart, Lung, and Blood Institute (HL043851 and HL080467) and the National Cancer Institute (CA047988 and UM1CA182913), with collaborative scientific support and funding for genotyping provided by Amgen.

WHI (Women's Health Initiative): The WHI program is funded by the National Heart, Lung, and Blood Institute, National Institutes of Health, U.S. Department of Health and Human Services through contracts HHSN268201100046C, HHSN268201100001C, HHSN268201100002C, HHSN268201100003C, HHSN268201100004C, and HHSN271201100004C.

AA-DHS (African American Diabetes Heart Study): The investigators acknowledge the cooperation of our Diabetes Heart Study (DHS) and AA-DHS participants. This work was supported by NIH R01 DK071891, R01 HL092301 and the General Clinical Research Center of Wake Forest School of Medicine M01-RR-07122.

Airwave (The Airwave Health Monitoring Study): The study is funded by the Home Office (Grant number 780-TETRA) with additional support from the National Institute for Health

Research (NIHR), Imperial College Healthcare NHS Trust (ICHNT) and Imperial College Biomedical Research Centre (BRC). The study has ethical approval from the National Health Service Multi-site Research Ethics Committee (MREC/13/NW/0588). This work used computing resources provided by the MRC- funded UK MEDical Bioinformatics partnership programme (UK MED-BIO) (MR/L01632X/1). P.E. would like to acknowledge support from the Medical Research Council and Public Health England for the MRC-PHE Centre for Environment and Health (MR/L01341X/1) and from the NIHR Health Protection Research Unit in Health Impact of Environmental Hazards (HPRU-2012-10141).

ASCOT (Anglo-Scandinavian Cardiac Outcomes Trial): The ASCOT study was supported by Pfizer, New York, NY, USA for the ASCOT study and the collection of the ASCOT DNA repository; by Servier Research Group, Paris, France; and by Leo Laboratories, Copenhagen, Denmark. We thank all ASCOT trial participants, physicians, nurses, and practices in the participating countries for their important contribution to the study. In particular we thank Clare Muckian and David Toomey for their help in DNA extraction, storage, and handling. Genotyping was funded by the CNG, MRC and the National Institutes of Health Research (NIHR). This work forms part of the research programme of the NIHR Cardiovascular Biomedical Research Unit at Barts and The London, QMUL. H.R.W, M.J.C and P.B.M. wishes to acknowledge the NIHR Cardiovascular Biomedical Research Unit at Barts and The London, Queen Mary University of London, UK for support.

BBJ (Biobank Japan Project): BioBank Japan project is supported by the Japan Agency for Medical Research and Development and by the Ministry of Education, Culture, Sports, Sciences and Technology of the Japanese government.

BES (Beijing Eye Study): BES was supported by the National Key Laboratory Fund, Beijing, China.

BRIGHT (British Genetics of Hypertension): This work was supported by the Medical Research Council of Great Britain (grant number G9521010D) and the British Heart Foundation (grant number PG/02/128). The BRIGHT study is extremely grateful to all the patients who participated in the study and the BRIGHT nursing team. This work forms part of the research program of the National Institutes of Health Research (NIHR Cardiovascular Biomedical Research) Cardiovascular Biomedical Unit at Barts and The London, QMUL.

CAGE-Amagasaki (Cardio-metabolic Genome Epidemiology Network, Amagasaki Study): The CAGE Network studies were supported by grants for the Core Research for Evolutional Science and Technology (CREST) from the Japan Science Technology Agency; the Program for Promotion of Fundamental Studies in Health Sciences, National Institute of Biomedical Innovation Organization (NIBIO); and the Grant of National Center for Global Health and Medicine (NCGM).

DESIR (Data from an Epidemiological Study on the Insulin Resistance): The DESIR Study Group is composed of Inserm-U1018 (Paris: B. Balkau, P. Ducimetière, E. Eschwège), Inserm-U367 (Paris: F. Alhenc-Gelas), CHU d'Angers (A. Girault), Bichat Hospital (Paris: F. Fumeron, M. Marre, R. Roussel), CHU de Rennes (F. Bonnet), CNRS UMR-8199 (Lille: A. Bonnefond, P. Froguel), Medical Examination Services (Alençon, Angers, Blois, Caen, Chartres, Chateauroux, Cholet, LeMans, Orléans and Tours), Research Institute for General Medicine (J. Cogneau), the general practitioners of the region and the Cross- Regional Institute for Health (C. Born, E. Caces, M. Cailleau, N. Copin, J.G. Moreau, F. Rakotozafy, J. Tichet, S. Vol). The DESIR study

was supported by Inserm contracts with CNAMTS, Lilly, Novartis Pharma and Sanofi-aventis, and by Inserm (Réseaux en Santé Publique, Interactions entre les déterminants de la santé, Cohortes Santé TGIR 2008), the Association Diabète Risque Vasculaire, the Fédération Française de Cardiologie, La Fondation de France, ALFEDIAM, ONIVINS, Société Francophone du Diabète, Ardix Medical, Bayer Diagnostics, Becton Dickinson, Cardionics, Merck Santé, Novo Nordisk, Pierre Fabre, Roche and Topcon.

DFTJ (Dongfeng-Tongji Cohort Study): This work was supported by grants from the National Basic Research Program grant (2011CB503800), the Programme of Introducing Talents of Discipline, the grants from the National Natural Science Foundation (grant NSFC-81473051, 81522040 and 81230069), and the Program for the New Century Excellent Talents in University (NCET-11-0169).

DHS (Diabetes Heart Study): This study was supported by the National Institutes of Health through HL67348 and HL092301.

DR's EXTRA (Dose Responses to Exercise Training): The study was supported by grants from Ministry of Education and Culture of Finland (722 and 627; 2004-2010); Academy of Finland (102318, 104943, 123885, 211119); European Commission FP6 Integrated Project (EXGENESIS), LSHM-CT-2004-005272; City of Kuopio; Juho Vainio Foundation; Finnish Diabetes Association; Finnish Foundation for Cardiovascular Research; Kuopio University Hospital; Päivikki and Sakari Sohlberg Foundation; Social Insurance Institution of Finland 4/26/2010.

EGCUT (Estonian Genome Center - University of Tartu (Estonian Biobank)): This study was supported by EU H2020 grants 692145, 676550, 654248, Estonian Research Council Grant

IUT20-60, NIASC, EIT – Health and NIH-BMI Grant No: 2R01DK075787-06A1 and EU through the European Regional Development Fund (Project No. 2014-2020.4.01.15-0012 GENTRANSMED.

EPIC (European Prospective Investigation into Cancer and Nutrition): The EPIC Norfolk Study is funded by Cancer Research, United Kingdom, British Heart Foundation, the Medical Research Council, the Ministry of Agriculture, Fisheries and Food, and the Europe against Cancer Programme of the Commission of the European Communities.

FENLAND (The Fenland Study): The Fenland Study is funded by the Wellcome Trust and the Medical Research Council (MC_U106179471). We further acknowledge support from the Medical research council (MC_UU_12015/1).

FUSION (Finland-United States Investigation of NIDDM Genetics): The FUSION study was supported by DK093757, DK072193, DK062370, and ZIA-HG000024. Genotyping was conducted at the Genetic Resources Core Facility (GRCF) at the Johns Hopkins Institute of Genetic Medicine.

GeneSTAR (Genetic Studies of Atherosclerosis Risk): GeneSTAR was supported by National Institutes of Health grants from the National Heart, Lung, and Blood Institute (HL49762, HL59684, HL58625, HL071025, U01 HL72518, HL087698, HL092165, HL099747, and K23HL105897), National Institute of Nursing Research (NR0224103), National Institute of Neurological Disorders and Stroke (NS062059), and by grants from the National Center for Research Resources to the Johns Hopkins General Clinical Research Center (M01-RR000052) and the Johns Hopkins Institute for Clinical & Translational Research (UL1 RR 025005).

GLACIER (Gene x Lifestyle Interactions and Complex Traits Involved in Elevated Disease Risk): The current study was supported by Novo Nordisk (PWF), the Swedish Research Council (PWF), the Swedish Heart Lung Foundation (PWF), the European Research Council (PWF), and the Skåne Health Authority (PWF).

GRAPHIC (Genetic Regulation of Arterial Pressure of Humans in the Community): The GRAPHIC Study was funded by the British Heart Foundation (BHF/RG/2000004). This work falls under the portfolio of research supported by the NIHR Leicester Cardiovascular Biomedical Research Unit. CPN and NJS are funded by the BHF and NJS is a NIHR Senior Investigator.

HCHS/SOL (Hispanic Community Health Study/ Study of Latinos): The baseline examination of HCHS/SOL was supported by contracts from the National Heart, Lung, and Blood Institute (NHLBI) to the University of North Carolina (N01-HC65233), University of Miami (N01-HC65234), Albert Einstein College of Medicine (N01-HC65235), Northwestern University (N01-HC65236), and San Diego State University (N01-HC65237). The National Institute on Minority Health and Health Disparities, National Institute on Deafness and Other Communication Disorders, National Institute of Dental and Craniofacial Research (NIDCR), National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), National Institute of Neurological Disorders and Stroke, and NIH Office of Dietary Supplements additionally contributed funding to HCHS/SOL. The Genetic Analysis Center at the University of Washington was supported by NHLBI and NIDCR contracts (HHSN268201300005C AM03 and MOD03). Additional analysis support was provided by 1R01DK101855-01 and 13GRNT16490017. Genotyping was also supported by National Center for Advancing Translational Sciences UL1TR000124 and NIDDK DK063491 to the Southern California

Diabetes Endocrinology Research Center. This research was also supported in part by the Intramural Research Program of the NIDDK, contract no. HHSB268201200054C, and Illumina.

HRS (Health & Retirement Study): HRS is supported by the National Institute on Aging (NIA U01AG009740 and R03 AG046389). Genotyping was funded separately by NIA (RC2 AG036495, RC4 AG039029). Our genotyping was conducted by the NIH Center for Inherited Disease Research (CIDR) at Johns Hopkins University. Genotyping quality control and final preparation of the data were performed by the Genetics Coordinating Center at the University of Washington.

HyperGEN-AXIOM (Hypertension Genetic Epidemiology Network): The study was support by the National Institutes of Health, the National Heart, Lung, Blood Institute grant HL086718.

INGI-CARL (Italian Network Genetic Isolates): This study was partially supported by Regione FVG (L.26.2008) and Italian Ministry of Health (GR-2011-02349604).

INGI-FVG (Italian Network Genetic Isolates): This study was partially supported by Regione FVG (L.26.2008) and Italian Ministry of Health (GR-2011-02349604).

InterAct (The EPIC-InterAct Case-Cohort Study): The InterAct study received funding from the European Union (Integrated Project LSHM-CT-2006-037197 in the Framework Programme 6 of the European Community).

IRAS (Insulin Resistance Atherosclerosis Study): The IRAS is supported by the National Heart Lung Institute (HL047887, HL047889, HL047890, and HL47902). Genotyping for this study was supported by the GUARDIAN Consortium with grant support from the National Institute of

Diabetes and Digestive and Kidney Diseases (NIDDK; DK085175) and in part by UL1TR000124 (CTSI) and DK063491 (DRC).

IRAS Family Study (Insulin Resistance Atherosclerosis Study): The IRASFS is supported by the National Heart Lung and Blood Institute (HL060944, HL061019, and HL060919). Genotyping for this study was supported by the GUARDIAN Consortium with grant support from the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK; DK085175) and in part by UL1TR000124 (CTSI) and DK063491 (DRC).

KORA (Cooperative Health Research in the Augsburg Region): The KORA study was initiated and financed by the Helmholtz Zentrum München – German Research Center for Environmental Health, which is funded by the German Federal Ministry of Education and Research (BMBF) and by the State of Bavaria. Furthermore, KORA research was supported within the Munich Center of Health Sciences (MC-Health), Ludwig-Maximilians-Universität, as part of LMUinnovativ.

LBC1936 (Lothian Birth Cohort 1936): Phenotype collection was supported by Age UK (The Disconnected Mind project). Genotyping was funded by the BBSRC (BB/F019394/1). The work was undertaken by The University of Edinburgh Centre for Cognitive Ageing and Cognitive Epidemiology, part of the cross council Lifelong Health and Wellbeing Initiative (MR/K026992/1). Funding from the BBSRC and Medical Research Council (MRC) is gratefully acknowledged.

LifeLines (Netherlands Biobank): The Lifelines Cohort Study, and generation and management of GWAS genotype data for the Lifelines Cohort Study is supported by the Netherlands Organization of Scientific Research NWO (grant 175.010.2007.006), the Economic Structure

Enhancing Fund (FES) of the Dutch government, the Ministry of Economic Affairs, the Ministry of Education, Culture and Science, the Ministry for Health, Welfare and Sports, the Northern Netherlands Collaboration of Provinces (SNN), the Province of Groningen, University Medical Center Groningen, the University of Groningen, Dutch Kidney Foundation and Dutch Diabetes Research Foundation.

LLFS (The Long Life Family Study): The study is supported by the National Institute on Aging (NIA) grant U01AG023746.

LOLIPOP (London Life Sciences Prospective Population Study): The LOLIPOP study is supported by the National Institute for Health Research (NIHR) Comprehensive Biomedical Research Centre Imperial College Healthcare NHS Trust, the British Heart Foundation (SP/04/002), the Medical Research Council (G0601966, G0700931), the Wellcome Trust (084723/Z/08/Z), the NIHR (RP-PG-0407-10371), European Union FP7 (EpiMigrant, 279143), and Action on Hearing Loss (G51).

Loyola GxE (Kingston Gene-by-environment; subset of International Collaborative Study of Hypertension in Blacks (ICSHIB)): The Loyola GxE project was supported by NIH Grant R01HL53353.

Loyola SPT (Spanish Town; subset of International Collaborative Study of Hypertension in Blacks (ICSHIB)): The Loyola SPT project was supported by NIH Grant R01HL53353.

METSIM (Metabolic Syndrome In Men): The METSIM study was supported by the Academy of Finland (contract 124243), the Finnish Heart Foundation, the Finnish Diabetes Foundation, Tekes (contract 1510/31/06), and the Commission of the European Community (HEALTH-F2-

2007 201681), and the US National Institutes of Health grants DK093757, DK072193, DK062370, and ZIA- HG000024. Genotyping was conducted at the Genetic Resources Core Facility (GRCF) at the Johns Hopkins Institute of Genetic Medicine.

NESDA (Netherlands Study of Depression and Anxiety): The infrastructure for the NESDA study is funded through the Geestkracht programme of the Dutch Scientific Organization (ZON-MW, grant number 10-000-1002) and matching funds from participating universities and mental health care organizations. Genotyping in NESDA was funded by the Genetic Association Information Network (GAIN) of the Foundation for the US National Institutes of Health. Statistical analyses were carried out on the Genetic Cluster Computer (http://www.geneticcluster.org), which is financially supported by the Netherlands Scientific Organization (NWO 480-05-003) along with a supplement from the Dutch Brain Foundation.

OBA (French obese cases): The obese French adults were recruited by the laboratory "Integrated Genomics and Metabolic Diseases Modeling" (UMR 8199 CNRS / Université de Lille 2 / Institut Pasteur de Lille) of Pr. Philippe Froguel.

PREVEND (The Prevention of REnal and Vascular ENd stage Disease study): PREVEND genetics is supported by the Dutch Kidney Foundation (Grant E033), the EU project grant GENECURE (FP-6 LSHM CT 2006 037697), the National Institutes of Health (grant 2R01LM010098), The Netherlands organization for health research and development (NWO-Groot grant 175.010.2007.006, NWO VENI grant 916.761.70, ZonMw grant 90.700.441).

PROCARDIS (Precocious Coronary Artery Disease): PROCARDIS was supported by the European Community Sixth Framework Program (LSHM-CT- 2007-037273), AstraZeneca, the British Heart Foundation, the Swedish Research Council, the Knut and Alice Wallenberg

Foundation, the Swedish Heart-Lung Foundation, the Torsten and Ragnar Söderberg Foundation, the Strategic Cardiovascular Program of Karolinska Institutet and Stockholm County Council, the Foundation for Strategic Research and the Stockholm County Council (560283). M.F and H.W acknowledge the support of the Wellcome Trust core award (090532/Z/09/Z) and the BHF Centre of Research Excellence. A.G and H.W acknowledge European Union Seventh Framework Programme FP7/2007-2013 under grant agreement no. HEALTH-F2-2013-601456 (CVGenes@Target) & and A.G, the Wellcome Trust Institutional strategic support fund.

RHS (Ragama Health Study): The RHS was supported by the Grant of National Center for Global Health and Medicine (NCGM).

SHEEP (Stockholm Heart Epidemiology Program): This study was supported by grants from the Swedish Research Council for Health, Working Life and Welfare (http://www.forte.se/en/), the Stockholm County Council (http://www.sll.se/om-landstinget/Information-in-English1/), the Swedish Research Council (http://www.vr.se/inenglish.4.12fff4451215cbd83e4800015152.html), the Swedish Heart and Lung Foundation (https://www.hjart-lungfonden.se/HLF/Om-Hjart-lungfonden/About-HLF/), and the Cardiovascular Programme at Karolinska Institutet (http://ki.se/en/mmk/cardiovascular-research-networks).

SHIP (Study of Health in Pomerania): SHIP is part of the Community Medicine Research net of the University of Greifswald, Germany, which is funded by the Federal Ministry of Education and Research (grants no. 01ZZ9603, 01ZZ0103, and 01ZZ0403), the Ministry of Cultural Affairs as well as the Social Ministry of the Federal State of Mecklenburg-West Pomerania, and the network ‘Greifswald Approach to Individualized Medicine (GANI_MED)’ funded by the

Federal Ministry of Education and Research (grant 03IS2061A). Genome-wide data were supported by the Federal Ministry of Education and Research (grant no. 03ZIK012) and a joint grant from Siemens Healthcare, Erlangen, Germany and the Federal State of Mecklenburg- West Pomerania. The University of Greifswald is a member of the 'Center of Knowledge Interchange' program of the Siemens AG.

SWHS/SMHS (Shanghai Women's Health Study/ Shanghai Men's Health Study): The Shanghai Women's Health Study and the Shanghai Men's Health Study are supported by research grants UM1CA182910 and UM1CA173640 from the U.S. National Cancer Institute, respectively.

TWINGENE (TwinGene of the Swedish Twin Registry): TwinGene received funding from the Swedish Research Council (M-2005-1112), GenomEUtwin (EU/QLRT-2001-01254; QLG2-CT-2002-01254), NIH DK U01-066134, The Swedish Foundation for Strategic Research (SSF) and the Heart and Lung foundation no. 20070481. TwinGene is part of the Swedish Twin Registry which is managed by Karolinska Institutet and receives funding through the Swedish Research Council (2017–00641).

YFS (The Cardiovascular Risk in Young Finns Study): The Young Finns Study has been financially supported by the Academy of Finland: grants 286284, 134309 (Eye), 126925, 121584, 124282, 129378 (Salve), 117787 (Gendi), and 41071 (Skidi); the Social Insurance Institution of Finland; Kuopio, Tampere and Turku University Hospital Medical Funds (grant X51001); Juho Vainio Foundation; Paavo Nurmi Foundation; Finnish Foundation for Cardiovascular Research ; Finnish Cultural Foundation; Tampere Tuberculosis Foundation; Emil Aaltonen Foundation; Yrjö Jahnsson Foundation; Signe and Ane Gyllenberg Foundation; and Diabetes Research Foundation of Finnish Diabetes Association.

We thank the participants of all of the included studies for their important contributions. Similarly, we thank all the people who have contributed to each of these studies, including volunteers, physicians, pharmacists, administrative staff, laboratory staff, recruitment center staff, and data managers, among others. We thank Matthew Brown for his help in tracking authorship information. In relation to the ERF study, we are grateful to P. Veraart for her help in genealogy, J. Vergeer for the supervision of the laboratory work, P. Snijders for his help in data collection and E.M. van Leeuwen for genetic imputation. In relation to the CROATIA-Vis and CROATIA-Korcula studies, we would like to acknowledge the staff of several institutions in Croatia that supported the field work, including but not limited to The University of Split and Zagreb Medical Schools, the Institute for Anthropological Research in Zagreb and Croatian Institute for Public Health. We are grateful to the Scottish School of Primary Care for their help in subject recruitment for the Generation Scotland study. The authors acknowledge the Jackson Heart Study team institutions (University of Mississippi Medical Center, Jackson State University and Tougaloo College) and participants for their long-term commitment that continues to improve our understanding of the genetic epidemiology of cardiovascular and other chronic diseases among African Americans. The authors thank the MESA study Coordinating Center, MESA investigators, and study staff for their valuable contributions. We thank the NEO study group, Petra Noordijk, Pat van Beelen and Ingeborg de Jonge for the coordination, lab and data management of the NEO study. In relation to the Rotterdam Study we thank Pascal Arp, Mila Jhamai, Marijn Verkerk, Lizbeth Herrera, Marjolein Peters and Carolina Medina-Gomez for their help in creating the GWAS database, and Karol Estrada, Yurii Aulchenko and Carolina Medina-Gomez for the creation and analysis of imputed data. The authors thank the WHI investigators and staff for their dedication and for making the program possible. In relation to the

ASCOT study, we would also like to acknowledge the Barts and The London Genome Centre staff for genotyping. In relation to the EPIC study we thank staff from the Technical, Field Epidemiology and Data Functional Group Teams of the Medical Research Council Epidemiology Unit in Cambridge, UK, for carrying out sample preparation, DNA provision and quality control, genotyping and data handling work. We specifically thank Sarah Dawson for coordinating the sample provision for biomarker measurements, Abigail Britten for coordinating DNA sample provision and genotyping of candidate markers, Nicola Kerrison, Chris Gillson and Abigail Britten for data provision and genotyping quality control, Matt Sims for writing the technical laboratory specification for the intermediate pathway biomarker measurements and for overseeing the laboratory work. We thank the Fenland Study Investigators, Fenland Study Co-ordination team and the Epidemiology Field, Data and Laboratory teams. In relation to the GLACIER study we thank the health professionals and data managers involved in the Västerbottens Intervention Project. We are also grateful to the staff of the Northern Sweden Biobank for preparing materials and to K Enqvist and T Johansson (Västerbottens County Council, Umeå, Sweden) for DNA preparation. The authors wish to acknowledge the services of the Lifelines Cohort Study, as well as the contributing research centers delivering data to Lifelines. In relation to the YFS, the expert technical assistance in the statistical analyses by Irina Lisinen is gratefully acknowledged.

Study group membership: The following individuals are members of the LifeLines Cohort Study: Behrooz Z Alizadeh, H Marike Boezen, Lude Frank, Pim van der Harst, Gerjan Navis, Marianne Rots, Harold Snieder, Morris Swertz, Bruce HR Wolffenbuttel, and Cisca Wijmenga. Department of Epidemiology, University of Groningen, University Medical Center Groningen, the Netherlands (Behrooz Z Alizadeh, H Marike Boezen, and Harold Snieder); Department of

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Presented at: The American Society of Human Genetics Annual Meeting, October 17-21, 2017, Orlando, FL.

Disclaimers: This manuscript has not been formally reviewed by the EPA. The views expressed in this document are solely those of the authors and the EPA does not endorse any products or commercial services mentioned in this publication. The contents of this publication are solely the responsibility of the authors and do not necessarily represent the official view of the National Institutes of Health.

Conflict of interest: The authors declare no competing financial interests except for the following. Bruce M Psaty serves on the DSMB of a clinical trial funded by the manufacturer

(Zoll LifeCor) and on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson. Oscar H Franco received grants from Metagenics (on women's health and epigenetics) and from Nestle (on child health). Mike A. Nalls' participation is supported by a consulting contract between Data Tecnica International and the National Institute on Aging, National Institutes of Health, Bethesda, MD, USA, and Dr. Nalls also consults for Illumina Inc, the Michael J. Fox Foundation and University of California Healthcare among others. Neil Poulter has received financial support and consultancy fees from several pharmaceutical companies that manufacture either blood pressure-lowering or lipid lowering agents or both. Peter Sever has received research awards from Pfizer Inc. Jost Bruno Jonas serves as a consultant for Mundipharma Co. (Cambridge, UK), patent holder with Biocompatibles UK Ltd. (Franham, Surrey, UK) (Title: Treatment of eye diseases using encapsulated cells encoding and secreting neuroprotective factor and / or anti-angiogenic factor; Patent number: 20120263794), and Patent applicant with University of Heidelberg (Heidelberg, Germany) (Title: Agents for use in the therapeutic or prophylactic treatment of myopia or hyperopia; Europäische Patentanmeldung 15 000 771.4).

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TABLES

Table 1. Layout of the Overall Study Design.

Stage	No. in Each Ancestry Group					
	European	**African**	**Asian**	**Hispanic**	**Brazilian**	**Meta-Analysis**
1	89,893	20,989	12,450	3,994	0	127,326
2[a]	136,986	4,475	108,431	13,714	3,652	267,258
Total[b]	226,879	25,464	120,881	17,708	3,652	394,584

For each lipid trait, association analyses were performed, accounting for the two alcohol consumption variables: “current drinker” status and “regular drinker”. For each ancestry group, study-specific results were combined to perform the 1 degree of freedom (DF) test for an interaction effect and the 2 DF joint test of genetic main effect and interaction with drinking exposure. Individuals from five ancestry groups were included: European, African, Asian, Hispanic, and Brazilian. [a]Variants selected for follow-up at $P \leq 1x10\text{-}6$ using 1 DF interaction and 2 DF joint tests. [b]Variants significant at $P \leq 5x10\text{-}8$ using 2 DF joint or 1 DF interaction test.

Table 2. Novel Loci Discovered in the Combined Analysis of Stages 1 and 2 Using the 2 DF Model that Jointly Tests Main and Interaction Effects.

rsID	Chr:Position	Alleles[a]	Freq	Closest Gene(s)	Main Effect[b]	Interaction Effect[b]	Joint *P*-value[b]	Joint FDR *q*-value[b]	Interaction *P*-value[c]	Heterogeneity *P*-value[d]	Most Significant 2 DF Model
rs190528931[e]	11:63911273	A/C	0.04	*MACROD1*	0.0109	-0.0023	1.9×10^{-16}	3.6×10^{-11}	0.32	0.96	META - HDL-C – CURDRINK
rs7904973[e]	10:124693587	T/G	0.55	*C10orf88*	0.9200	-0.1500	1.9×10^{-15}	3.5×10^{-10}	0.38	0.89	META - LDL-C - CURDRINK
rs73729083	7:137559799	C/T	0.91	*CREB3L2*	4.0100	0.6500	8.2×10^{-15}	1.4×10^{-9}	0.57	0.22	META - LDL-C - CURDRINK
rs80080062	3:185812169	G/C	0.87	*ETV5*	0.0061	0.0031	1.1×10^{-12}	1.7×10^{-7}	0.38	0.85	META - HDL-C - REGDRINK
rs7140110	13:114544024	C/T	0.73	*GAS6-AS1*	-0.0100	-0.0040	3.4×10^{-12}	5.1×10^{-7}	0.19	0.42	META - TG - CURDRINK
rs34311866	4:951947	C/T	0.83	*TMEM175*	-0.0200	0.0040	1.5×10^{-11}	2.1×10^{-6}	0.42	0.90	EUR - TG – CURDRINK
rs2911971	8:6607634	G/C	0.34	*AGPAT5*	-0.7500	0.0100	7.5×10^{-11}	1.1×10^{-5}	0.53	0.49	META - LDL-C - CURDRINK
rs56076449	5:132442190	G/T	0.79	*HSPA4* / *FSTL4*	0.0130	-0.0020	9.3×10^{-11}	1.3×10^{-5}	0.80	0.80	META - TG - REGDRINK
rs41274050[e]	10:52573772	T/C	0.01	*A1CF*	0.1080	-0.0310	9.6×10^{-10}	1.3×10^{-4}	0.62	1.00	EUR - TG – REGDRINK
rs7035578	9:78745177	A/G	0.15	*PCSK5*	-1.2700	0.0800	1.2×10^{-9}	1.6×10^{-4}	0.70	0.82	EUR - LDL-C - CURDRINK
rs201445483	2:17890087	I/D	0.83	*SMC6*	1.4300	0.6800	4.7×10^{-9}	6.0×10^{-4}	0.17	0.46	META - LDL-C - CURDRINK
rs72729610	4:154190965	G/A	0.86	*TRIM2*	0.0075	-0.0036	5.6×10^{-9}	7.2×10^{-4}	0.08	0.26	META - HDL-C - REGDRINK
rs143528679	4:124558378	G/A	0.10	*SPRY1* / *LINC01091*	-1.2000	-5.6300	6.3×10^{-9}	8.0×10^{-4}	6.4×10^{-4}	0.10	AFR - LDL-C - CURDRINK
rs2111622[e]	2:53984823	G/A	0.77	*ASB3* / *GPR75-ASB3*	0.0008	-0.0072	7.9×10^{-9}	9.9×10^{-4}	0.01	0.12	EUR - HDL-C - CURDRINK
rs13284665	9:131513370	G/A	0.88	*ZER1*	1.9900	-0.8900	1.1×10^{-8}	1.3×10^{-3}	0.35	0.89	EUR - LDL-C - CURDRINK
rs4898521	12:49755162	A/T	0.95	*DNAJC22* / *SPATS2*	0.0179	-0.0107	1.3×10^{-8}	1.7×10^{-3}	0.06	1.00	EUR - HDL-C - REGDRINK
rs6063050	20:45604240	C/T	0.75	*EYA2*	0.0110	0.0000	2.9×10^{-8}	3.6×10^{-3}	0.30	0.39	META - TG - CURDRINK
rs2963472	5:157999022	A/G	0.21	*LOC101927697* / *EBF1*	0.0140	-0.0020	3.5×10^{-8}	4.2×10^{-3}	0.96	0.23	EUR - TG – REGDRINK

rsID: Reference SNP ID. Chr: Chromosome number. Freq: Frequency of the coded allele. FDR: False discovery rate. DF: Degrees of freedom. HDL-C: High-density lipoprotein cholesterol. LDL-C: Low-density lipoprotein cholesterol. TG: Triglycerides. AFR: African ancestry. EUR: European ancestry. META: trans-ancestry meta-analysis. CURDRINK: alcohol consumption categorized into drinkers

and non-drinkers. REGDRINK: alcohol consumption categorized into regular drinkers and not regular drinkers. [a]The Alleles column reports the coded/non-coded alleles. [b]These estimates pertain to the 2 DF joint test of main and interaction effects. [c]These *P*-values pertain to 1 DF tests of interaction effects. [d]The Heterogeneity *P*-value column indicates the significance of the Stage 1 heterogeneity across ancestry groups in the most significant 2 DF Model. [e]These loci were also discovered by a concurrent association study focused on exonic variants (37).

FIGURE LEGENDS

Figure 1. Venn Diagram Showing the Distribution of Genome-wide Significant Associations at the 147 Identified Loci Among Lipid Traits. HDL-C: High-density lipoprotein cholesterol. LDL-C: Low-density lipoprotein cholesterol.

Figure 2. Heat Map of the Significance and Effect Direction of Index Variants at the 18 Novel Loci for the Three Lipid Traits.

For each combination of index variant and lipid trait, the effect direction and *P*-value of the most significant association is shown. For example: the 11:63911273 variant was most significantly associated with high-density lipoprotein cholesterol in the trans-ancestry meta-analysis, using the current drinker alcohol consumption variable. Shades of purple and yellow represent negative and positive directions of effect, respectively, while associations of either direction with *P*-value > 0.05 are white. Effect +: the direction of effect is greater than or equal to zero. Effect –: the direction of effect is less than zero.

Web Appendix

Multi-ancestry genome-wide association study of lipid levels incorporating gene-alcohol interactions

Paul S. de Vries et al.

Contents

Web Methods

Adjustment of LDL-C for statin use

If information on statin-specific use was unavailable, LDL-C values were adjusted for use of unspecified lipid-lowering medication, but only when lipid measurements were performed after 1994. When LDL-C values were directly assayed, LDL-C values were adjusted for lipid-lowering medication use by dividing the original values by 0.7. When LDL-C values were not directly assayed, LDL-C values were adjusted by first dividing total cholesterol by 0.8, and then using the corrected total cholesterol value in the Friedewald equation.

Study-specific analyses: software

To obtain robust estimates of covariance matrices and robust standard errors (1, 2), studies of unrelated subjects used either the sandwich R package or ProbABEL (3, 4). To account for relatedness in families, family studies used the generalized estimating equations (GEE) approach, treating each family as a cluster, with the geepack package in R (5), or a linear mixed effect model approach with a random polygenic component (for which the covariance matrix depends on the kinship matrix) with GenABEL or R (6).

Quality control

Extensive quality control (QC) using the R package EasyQC was performed for all study-specific GWAS results (7). We performed QC at two levels. The "study-level" QC reviewed result files from each study individually, which includes checking the provided allele frequencies against the ancestry-specific 1000 Genomes reference panel and harmonizing marker names to ensure consistencies across studies. To exclude unstable study-specific results that reflect low minor allele count (MAC) within alcohol consumption exposure categories or low imputation quality measures, variants were excluded from study-level results if min ($MAC_{exposed}$, $MAC_{unexposed}$) × imputation quality measure < 20. Variants were further excluded if the imputation quality measure was < 0.5 (8). The "meta-level" QC reviewed result files from each specific analysis across all studies and this included: 1) visually comparing summary statistics (mean, median, standard deviation, inter-quartile range, minimum, maximum) on all effect estimates, standard errors and *P*-values; and 2) examining SE-N and QQ plots to reveal any issues with trait transformation or other analytical problems (7). A SE-N plot examines the ratio of a study's standard deviation with the median standard error on one axis with the square root of the

study's sample size on the other axis for deviations from the 45-degree line relative to the other studies in the meta-analysis.

After meta-analysis was performed, a variant was excluded if the sample size was below 5000 or if the number of studies with the variant measured was less than 3. Given the limited availability of data on individuals of Hispanic ancestry, we excluded variants from the Hispanic ancestry analysis if the sample size was below 3000 or the numbers of studies with the variant measured was less than 2.

Genetic main effect

The study-specific analyses were not adjusted for alcohol intake or for the interaction term, and were performed only for the lipid trait that each variant was most significantly associated to in the main analysis. METAL was used to meta-analyse results across studies within each ancestry group, and subsequently to meta-analyse results across ancestry groups (9).

Variance explained

The percent of variance explained in HDL-C, LDL-C, and TG by all previously known and novel variants was evaluated using participant-level data in ten studies from multiple ancestries. These analyses were performed stratified by ancestry group. The 314 variants (Web Table 8) previously identified for lipid traits in any ancestry were considered as "known" variants (10-16), while the index variants at the 18 novel loci were considered "novel" variants.

We calculated percent variance using a series of five nested standard linear regression models. In hierarchical order, these include Model 1, adjusting for study-specific covariates; Model 2, adjusting for Model 1 and additionally adjusting for alcohol exposure; Model 3, adjusting for Model 2 and additionally adjusting for known variants; Model 4 adjusting for Model 3 and additionally adjusting for novel variants; and finally Model 5, adjusting for Model 4 and additionally adjusting for gene-alcohol interaction terms of novel variants. To select a subset of variants and interaction terms to include in Models 3, 4, and 5, for each lipid trait, we performed a stepwise regression procedure with significance tests for inclusion of one variant at a time and for backward elimination of redundant variants. From one model to the next, we kept the significant variants from the previous model before adding the next nested model's variants or interaction terms. The r^2 values obtained at each nested level were used as measures of the percent variance explained by the respective models. Through sequential subtraction of appropriate r^2 values, we determined the additional percent variance explained

by a given set of variants. For example, for a given lipid trait, the variance explained by known variants was calculated as the Model 3 r^2 subtracted by the Model 2 r^2, and the variance explained by novel variants was calculated as the Model 4 r^2 subtracted by the Model 3 r^2.

Variance explained estimates obtained using this method may be overestimates due to bias arising from the use of backwards elimination and from the estimation of variance explained in samples that were also included in the genetic association study itself.

Gene Prioritization using DEPICT

We used the Data-driven Expression Prioritized Integration for Complex Traits (DEPICT) software to prioritize genes at the 147 loci associated in the combined analysis of Stage 1 and 2.

Separate DEPICT analyses were performed for variants associated at genome-wide significance with each of the three lipid traits (HDL-C, LDL-C and TG) in the combined analysis of Stages 1 and 2 (17). For each trait, we first created a subset of non-overlapping variants (>500 kb flanking regions and LD $r^2 > 0.1$) between the associated variants and the 1000 Genomes reference data (18). Next, DEPICT obtained lists of overlapping genes by applying an LD based threshold ($r^2 > 0.5$) between the non-overlapping variants and known functional coding or cis-acting regulatory variants (of the respective genes). The major histocompatibility complex region on chromosome 6 (base position 25,000,000 - 35,000,000) was removed for further analyses. Using DEPICT, we compared the functional similarity of overlapping genes across loci using a gene score that was adjusted for varying confounders, such as gene length. To derive an experiment-wide False-Discovery-Rate (FDR) for the gene prioritization, the scoring step was repeated 50 times utilizing index variants from 500 pre-compiled null GWAS. Our DEPICT gene-set enrichment analyses were based on a total of 14,461 pre-compiled reconstituted gene sets - including 737 Reactome database pathways (19), 2,473 phenotypic gene sets (derived from the Mouse Genetics Initiative (20)), 184 Kyoto Encyclopedia of Genes and Genomes (KEGG) database pathways (21), 5,083 Gene Ontology database terms (22), and 5,984 protein molecular pathways (derived from protein-protein interactions) (23). Our DEPICT tissue, cell type and physiological system specificity analyses utilize expression data in any of the 209 MeSH annotations for 37,427 microarrays of the Affymetrix U133 Plus 2.0 Array platform.

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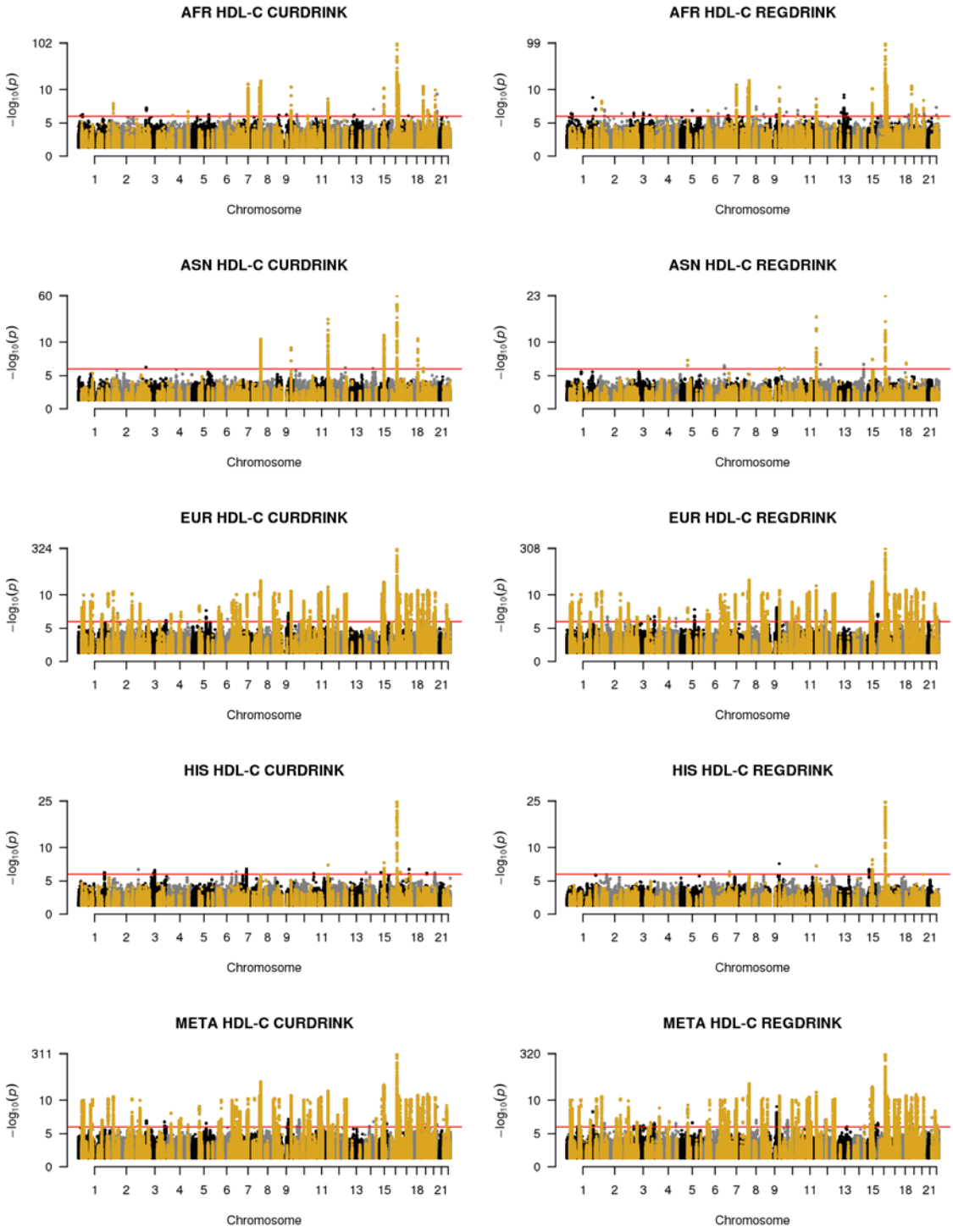
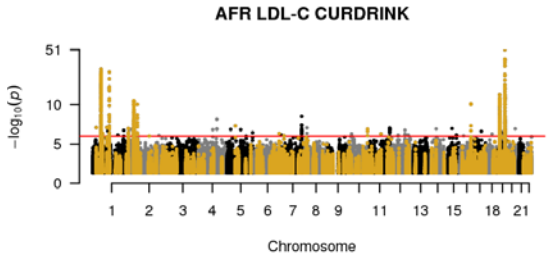
Web Figures

Web Figure 1

Manhattan plots for each of the lipid-alcohol consumption combinations by ethnicity for Stage 1. The -$\log_{10}$(*P*-values) for each variant are plotted against its chromosomal position. The line indicating suggestive significance at 1×10^{-6} is shown in red. Variants within ±1Mbp of a published known locus are highlighted in gold.

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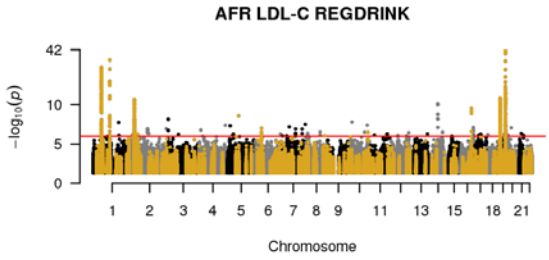
−log10(p)
51
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome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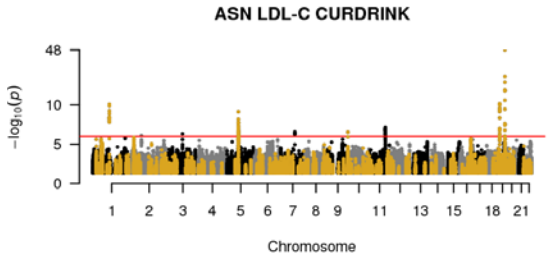
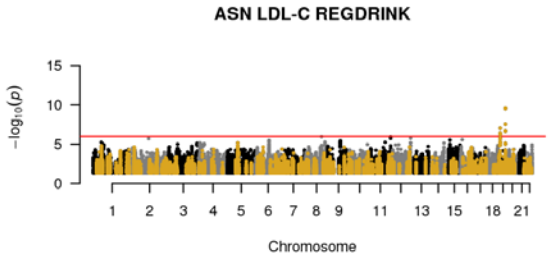
−log10(p)
42
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


ASN LDL-C CURDRINK
−log10(p)
48
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome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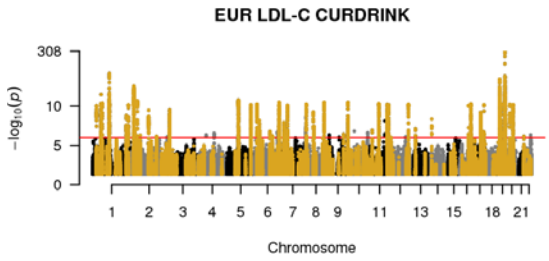
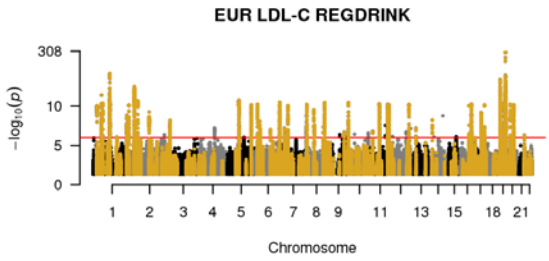
−log10(p)
15
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


EUR LDL-C CURDRINK
−log10(p)
308
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome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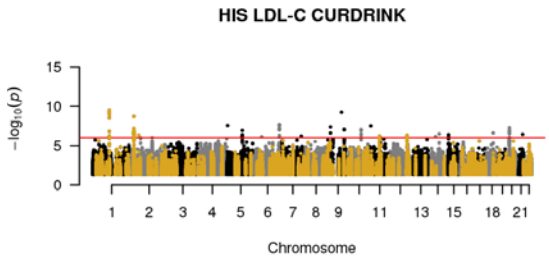
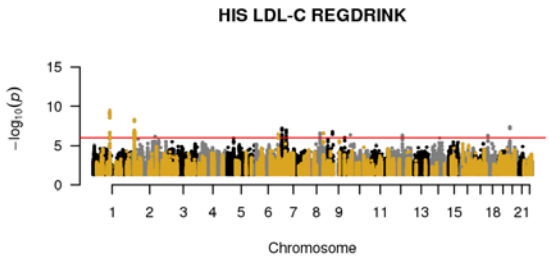
−log10(p)
308
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


HIS LDL-C CURDRINK
−log10(p)
15
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome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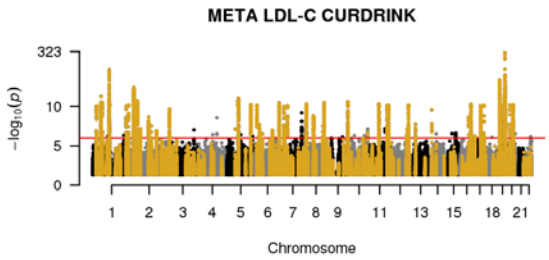
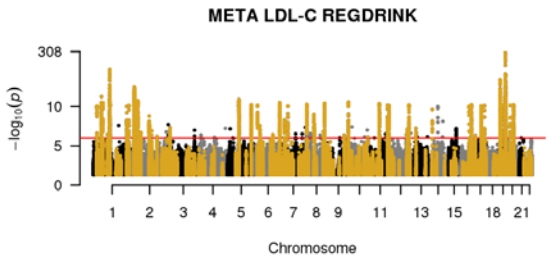
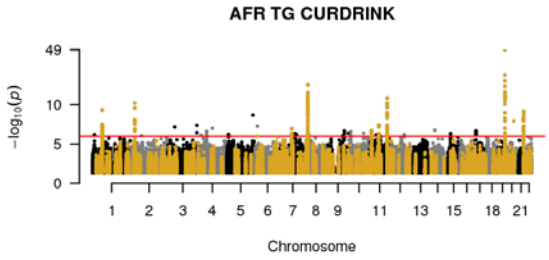
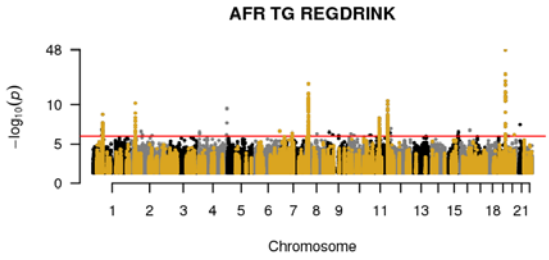
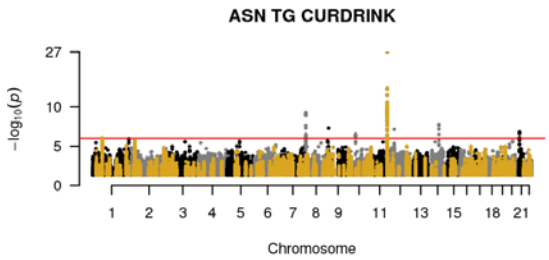
−log10(p)
15
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome

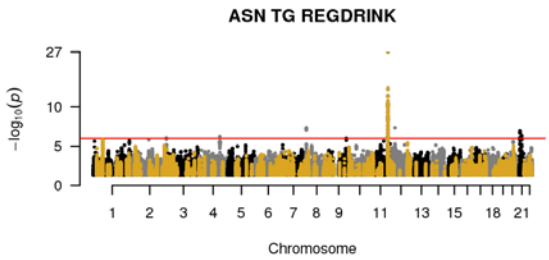

META LDL-C CURDRINK
−log10(p)
323
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome

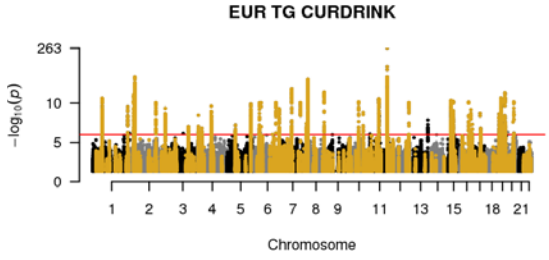

META LDL-C REGDRINK
−log10(p)
308
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome

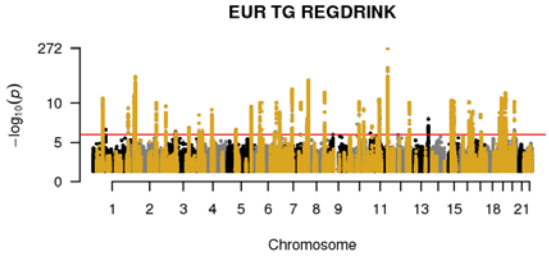

AFR TG CURDRINK
−log10(p)
49
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


AFR TG REGDRINK
−log10(p)
48
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


ASN TG CURDRINK
−log10(p)
27
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


ASN TG REGDRINK
−log10(p)
27
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


EUR TG CURDRINK
−log10(p)
263
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


EUR TG REGDRINK
−log10(p)
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10
5
0
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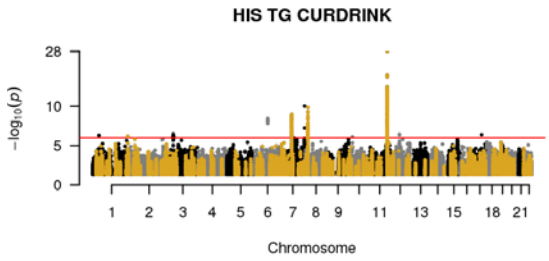
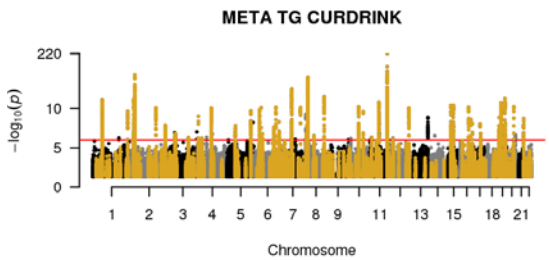
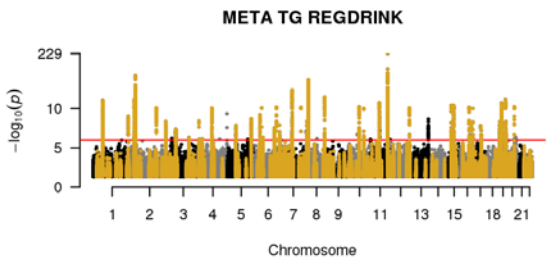
Chromosome


HIS TG CURDRINK
−log10(p)
28
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome

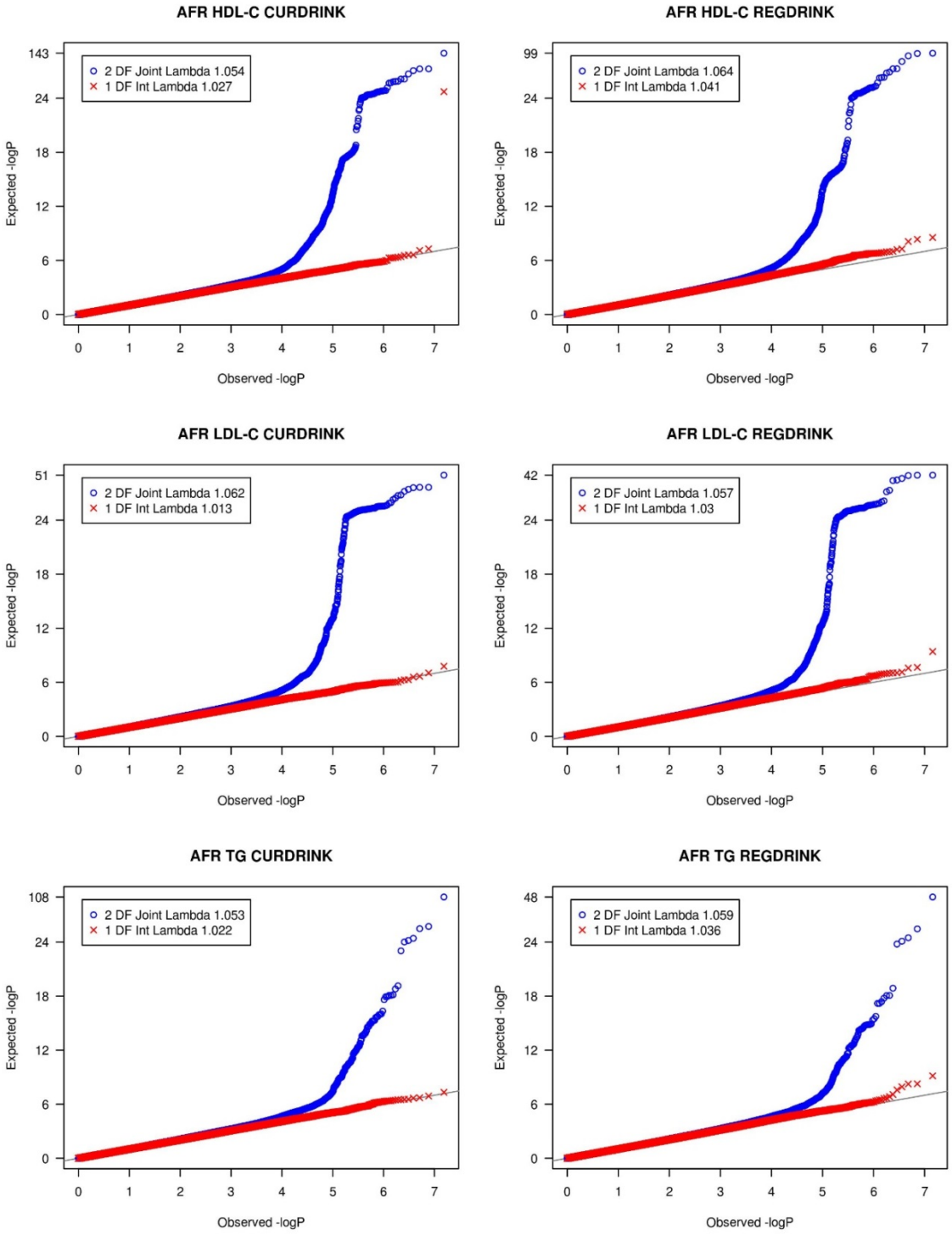

HIS TG REGDRINK
−log10(p)
27
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome

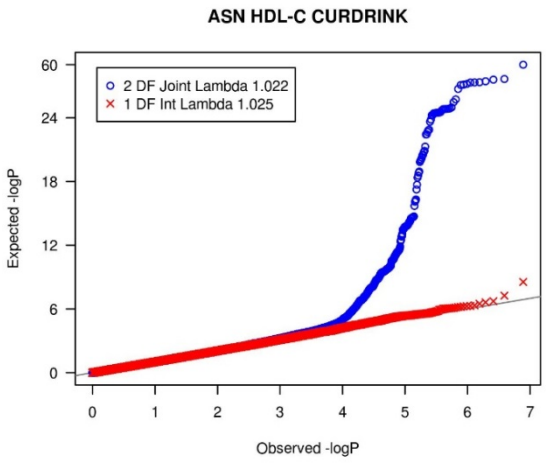

META TG CURDRINK
−log10(p)
220
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome


META TG REGDRINK
−log10(p)
229
10
5
0
1 2 3 4 5 6 7 8 9 11 13 15 18 21
Chromosome

Web Figure 2

Quantile-quantile (QQ) plots for each of the lipid-alcohol consumption combinations by ethnicity for Stage 1. The observed -$\log_{10}$(*P*-values) are plotted against the expected -$\log_{10}$(*P*-values). Here the blue circles denote the joint 2 DF test *P*-values. The red "X"s denote the 1 DF interaction *P*-values.

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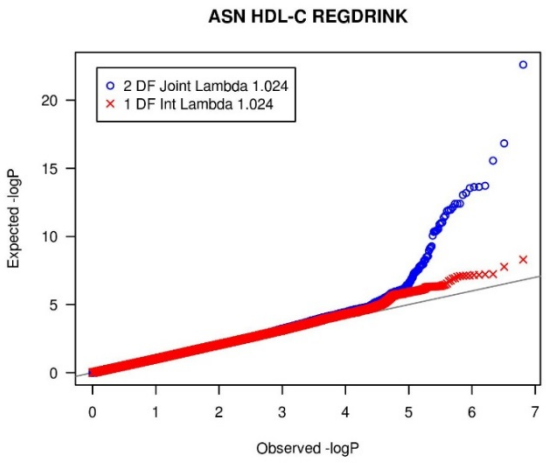
1 DF Int Lambda 1.025
Expected -logP
Observed -logP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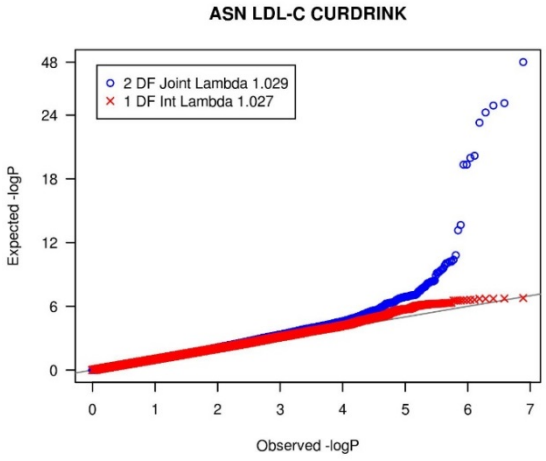
Expected -logP
Observed -logP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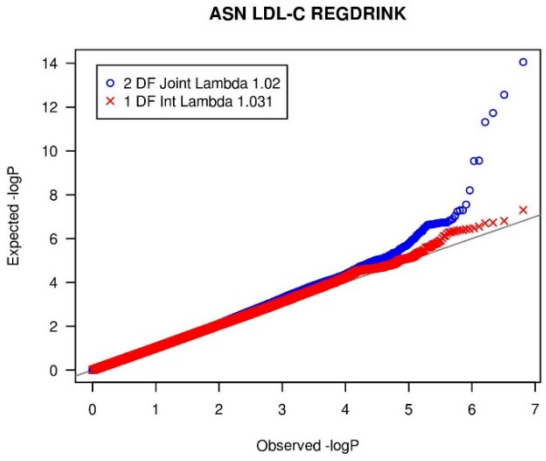
Expected -logP
Observed -logP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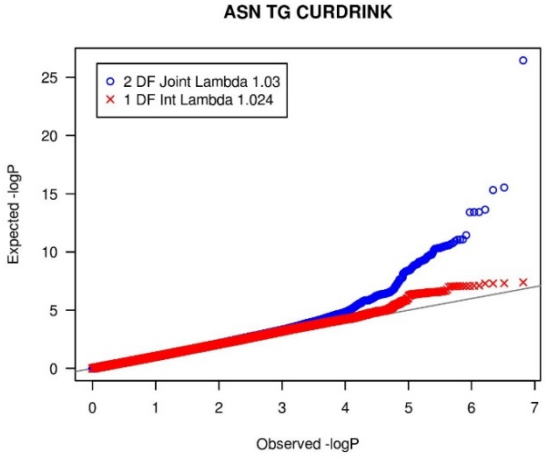
1 DF Int Lambda 1.031
Expected -logP
Observed -logP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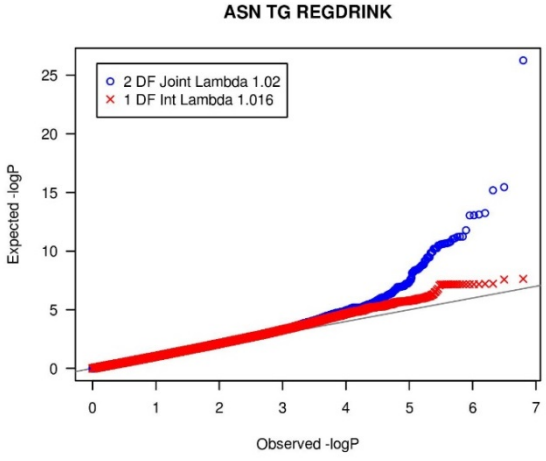
Expected -logP
Observed -logP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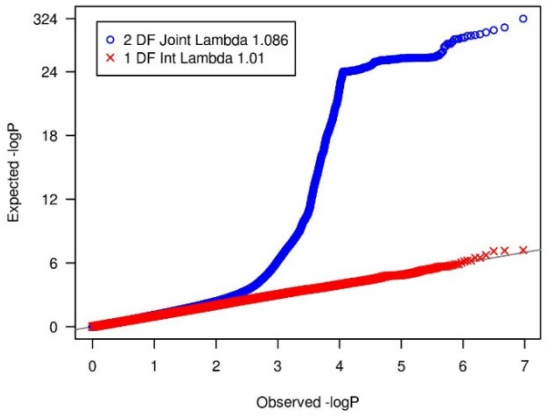
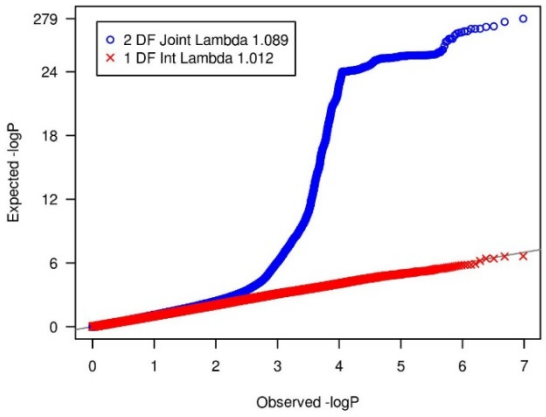
Expected -logP
Observed -logP

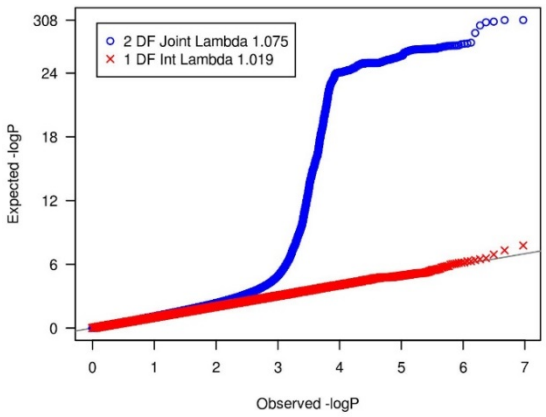
EUR HDL-C CURDRINK



EUR HDL-C REGDRINK



EUR LDL-C CURDRINK



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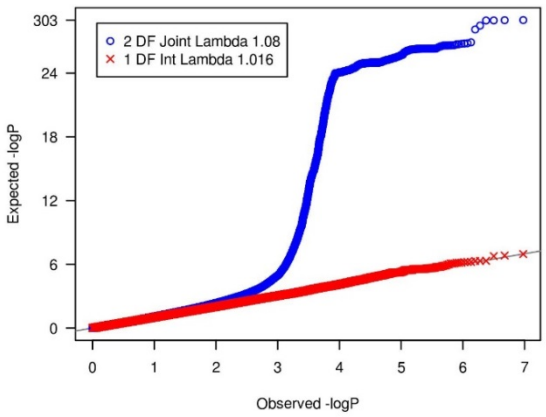
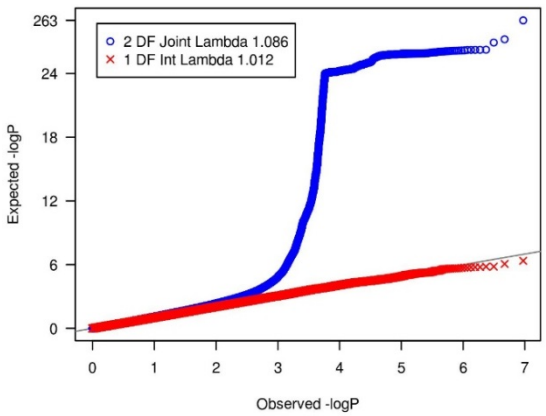
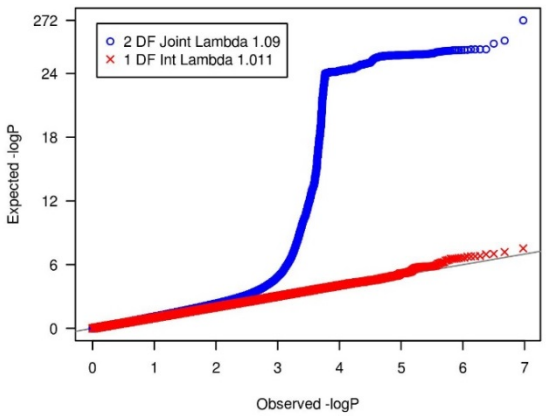
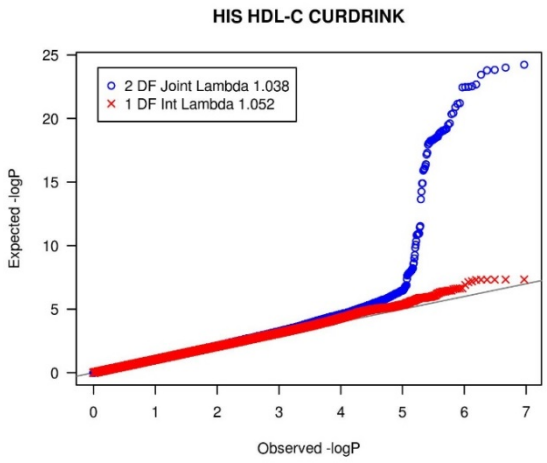


EUR TG CURDRINK



EUR TG REGDRINK

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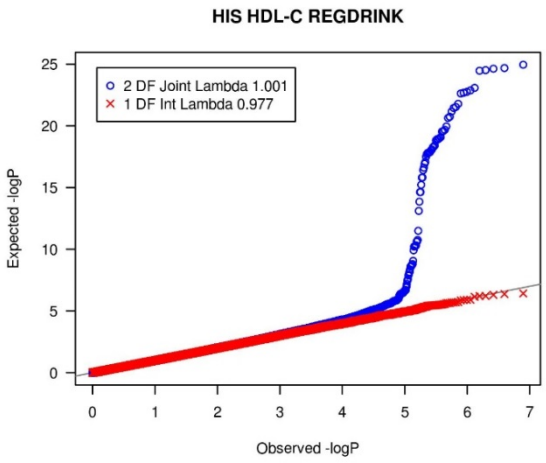
Observed -logP


HIS HDL-C REGDRINK
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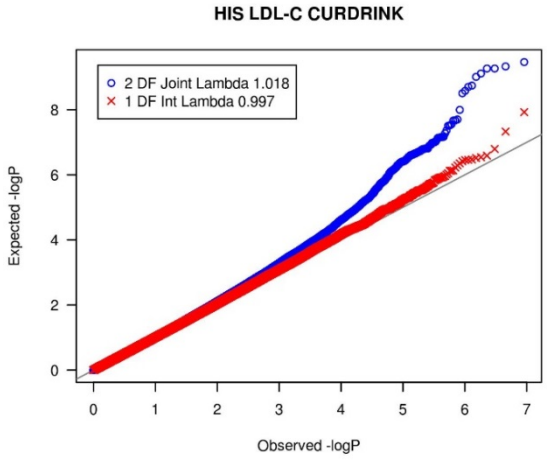
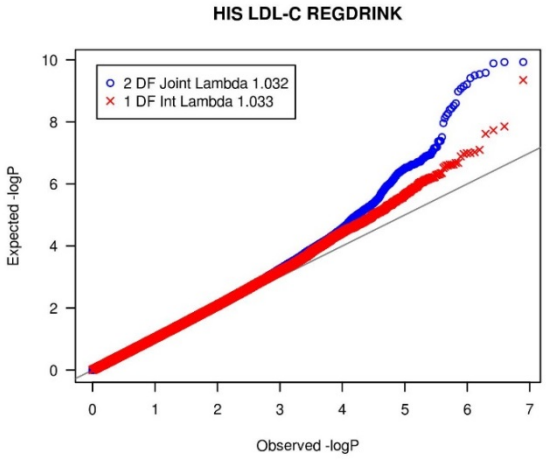
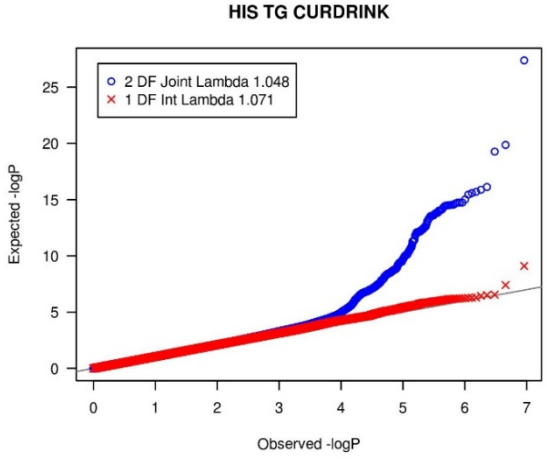
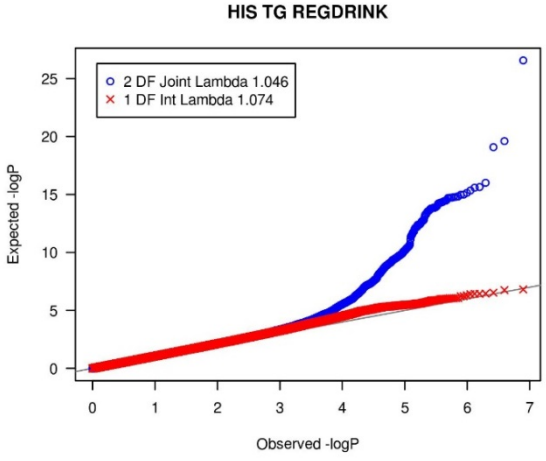
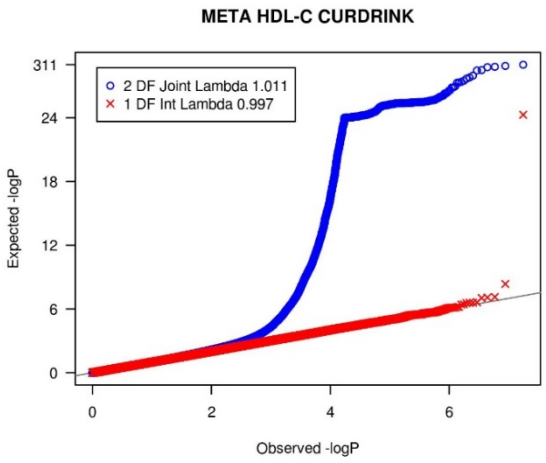
1 DF Int Lambda 0.977
Expected -logP
Observed -logP

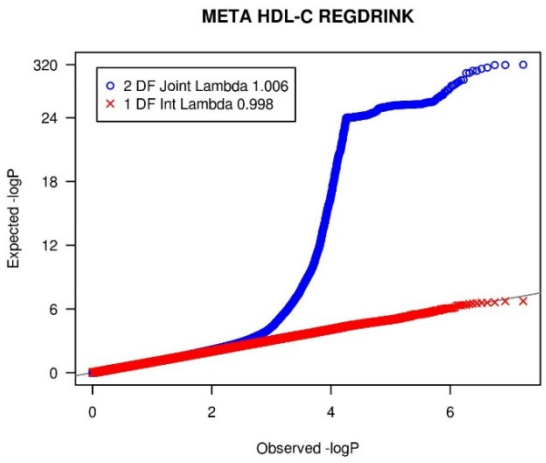

HIS LDL-C CURDRINK
2 DF Joint Lambda 1.018
1 DF Int Lambda 0.997
Expected -logP
Observed -logP

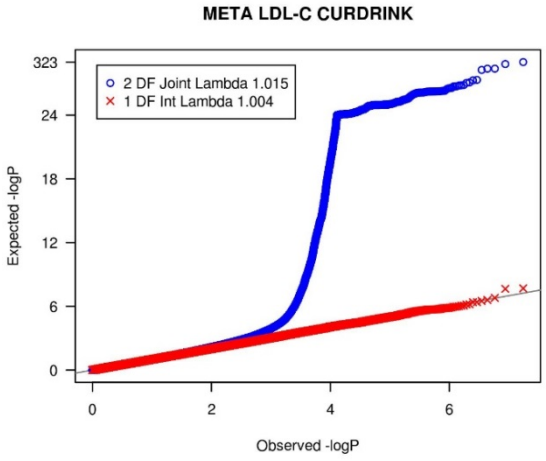

HIS LDL-C REGDRINK
2 DF Joint Lambda 1.032
1 DF Int Lambda 1.033
Expected -logP
Observed -logP

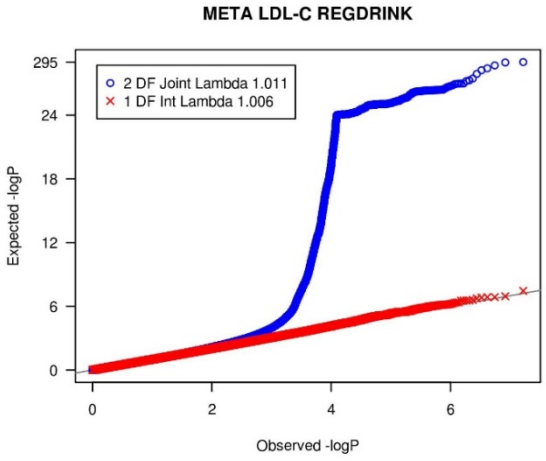

HIS TG CURDRINK
2 DF Joint Lambda 1.048
1 DF Int Lambda 1.071
Expected -logP
Observed -logP

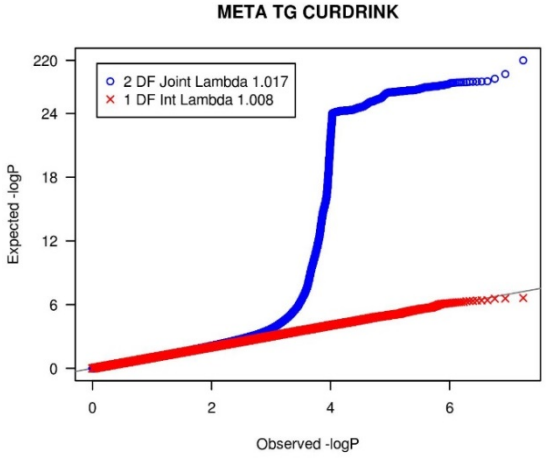

HIS TG REGDRINK
2 DF Joint Lambda 1.046
1 DF Int Lambda 1.074
Expected -logP
Observed -logP

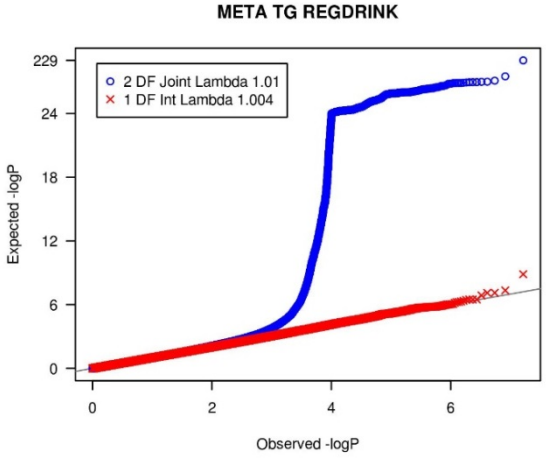

META HDL-C CURDRINK
2 DF Joint Lambda 1.011
1 DF Int Lambda 0.997
Expected -logP
Observed -logP


META HDL-C REGDRINK
2 DF Joint Lambda 1.006
1 DF Int Lambda 0.998
Expected -logP
Observed -logP


META LDL-C CURDRINK
2 DF Joint Lambda 1.015
1 DF Int Lambda 1.004
Expected -logP
Observed -logP


META LDL-C REGDRINK
2 DF Joint Lambda 1.011
1 DF Int Lambda 1.006
Expected -logP
Observed -logP

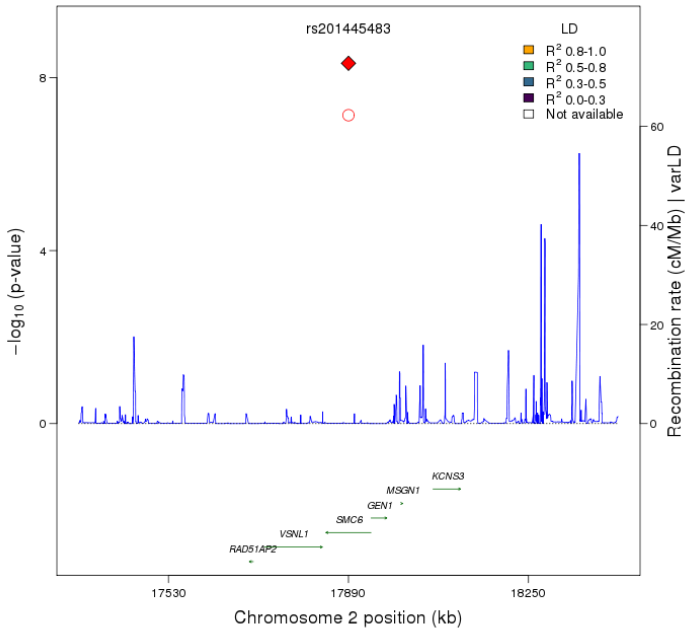

META TG CURDRINK
2 DF Joint Lambda 1.017
1 DF Int Lambda 1.008
Expected -logP
Observed -logP


META TG REGDRINK
2 DF Joint Lambda 1.01
1 DF Int Lambda 1.004
Expected -logP
Observed -logP

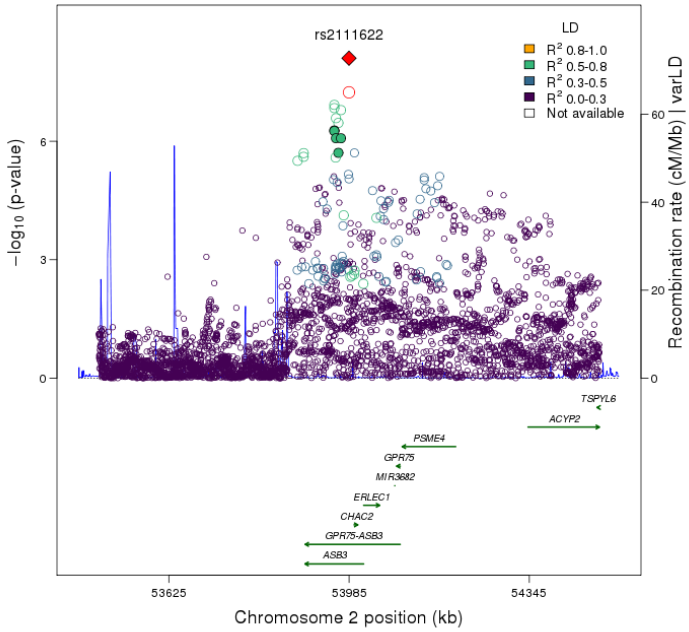
Web Figure 3

Regional plots for 18 novel loci, with *P*-values from the joint 2 DF test. Variants are identified from trans-ethnic meta-analyses (META), as well as European (EUR) and African (AFR) ancestry-specific meta-analyses. Unfilled circles represent variants that were included only Stage 1 and not Stage 2. Filled circles represent variants that were included in the combined analysis of Stage 1 and Stage 2.

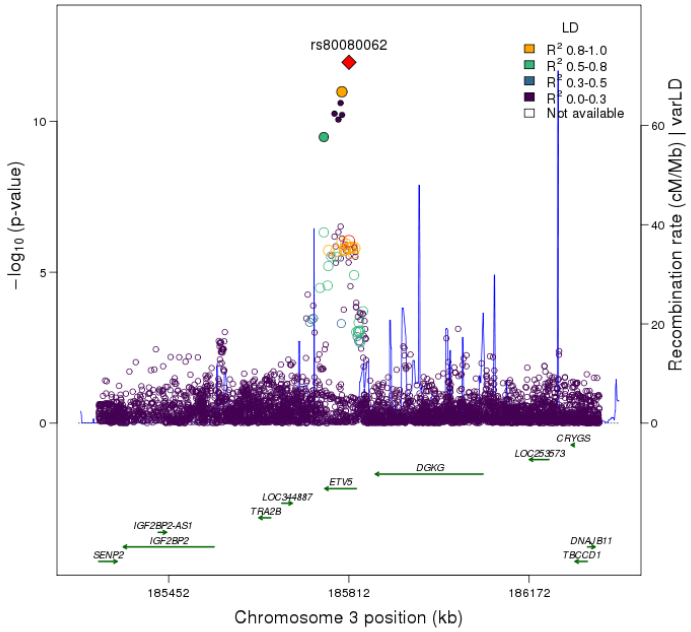
3a. Variant rs201445483 at chromosome 2, position 17890087. LDL-C Current Drinker (META)



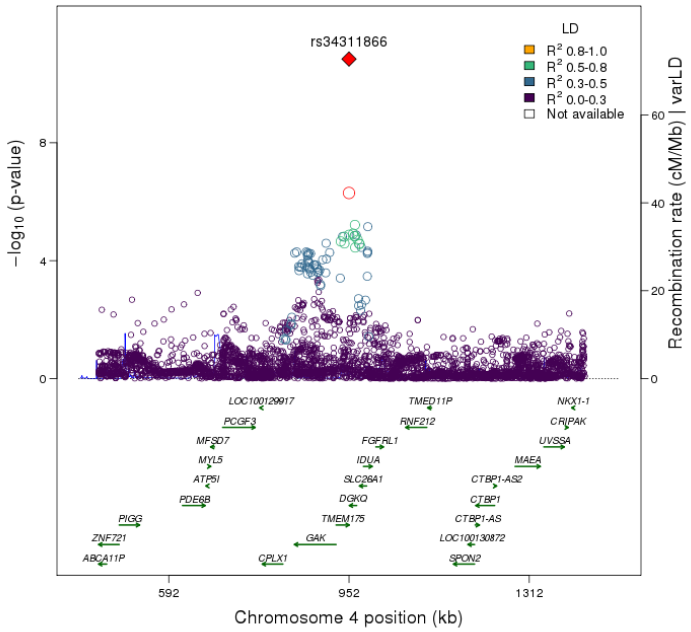
3b. Variant rs2111622 at chromosome 2, position 53984823. HDL-C Current Drinker (EUR)



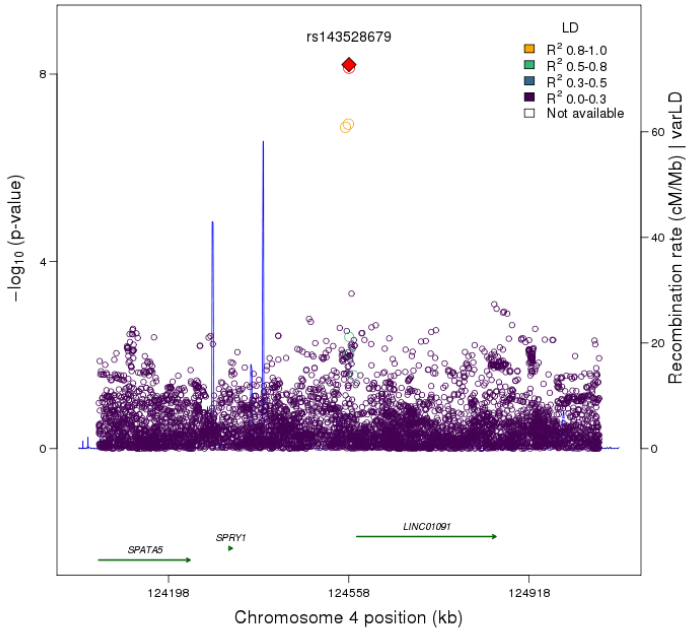
3c. Variant rs80080062 at chromosome 3, position 185812169. HDL-C Regular Drinker (META)



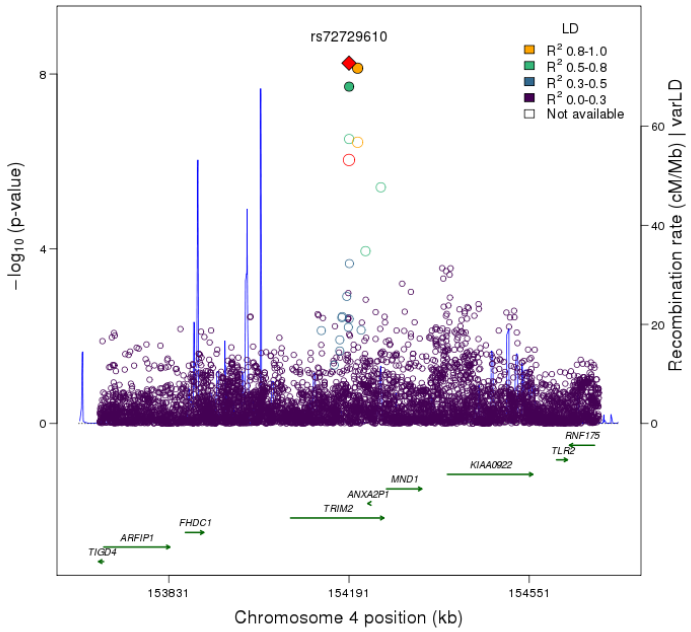
3d. Variant rs34311866 at chromosome 4, position 951947. TG Current Drinker (EUR)



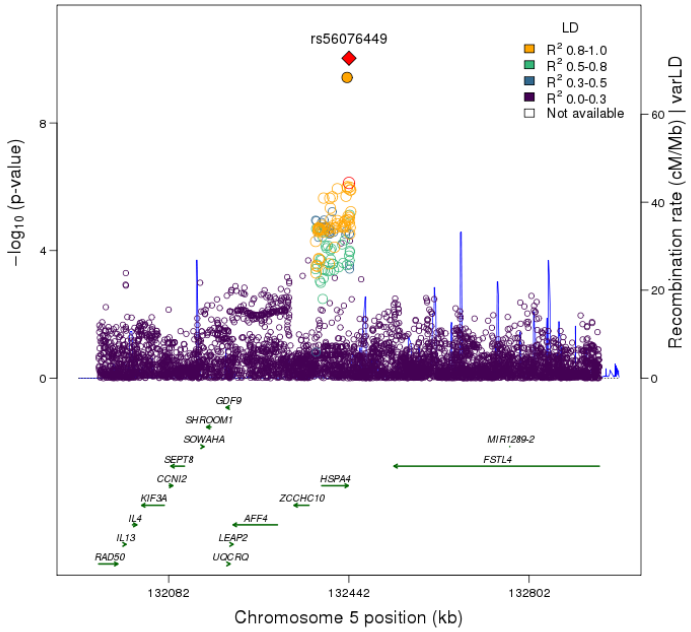
3e. Variant rs143528679 at chromosome 4, position 124558378. LDL-C Current Drinker (AFR)



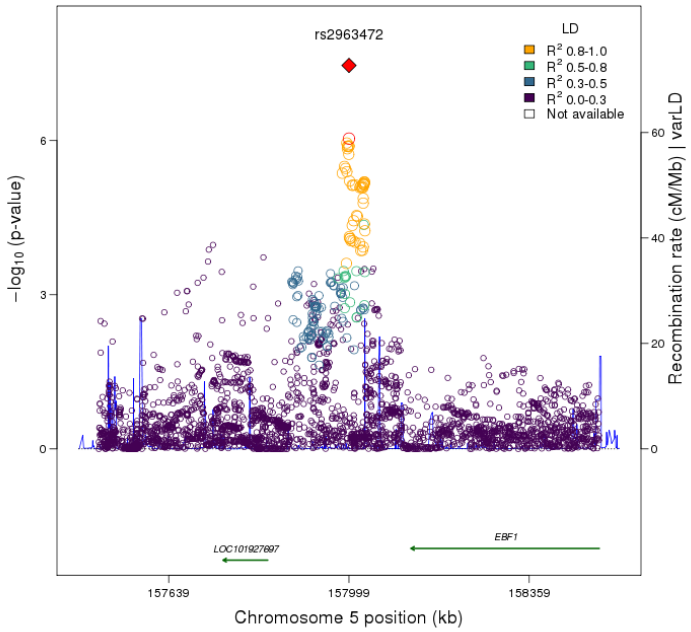
3f. Variant rs72729610 at chromosome 4, position 154190965. HDL-C Regular Drinker (META)



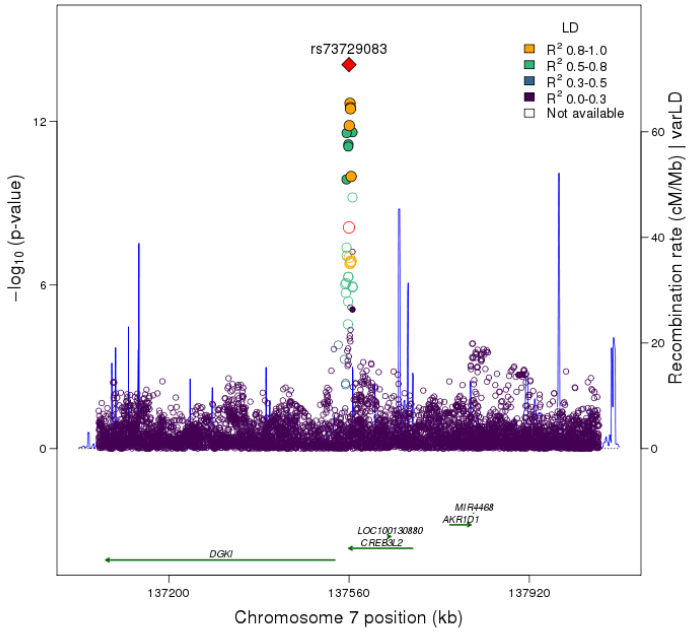
3g. Variant rs56076449 at chromosome 5, position 132442190. TG Regular Drinker (META)



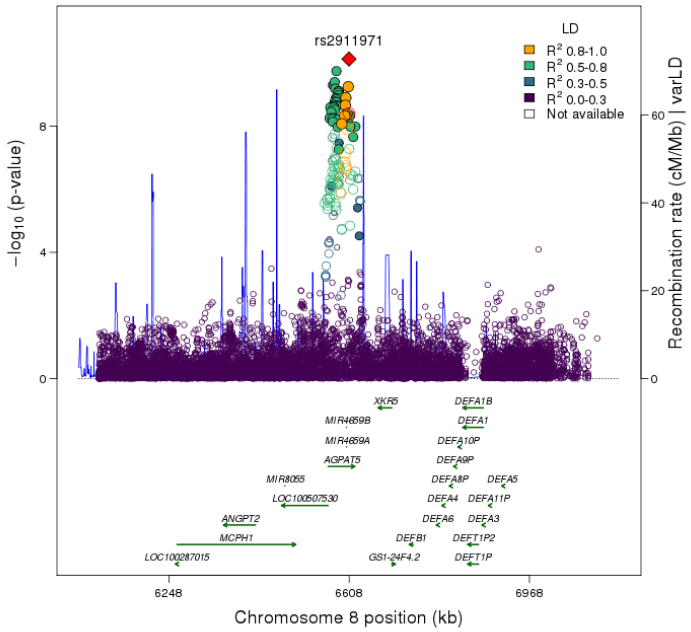
3h. Variant rs2963472 at chromosome 5, position 157999022. TG Regular Drinker (EUR)



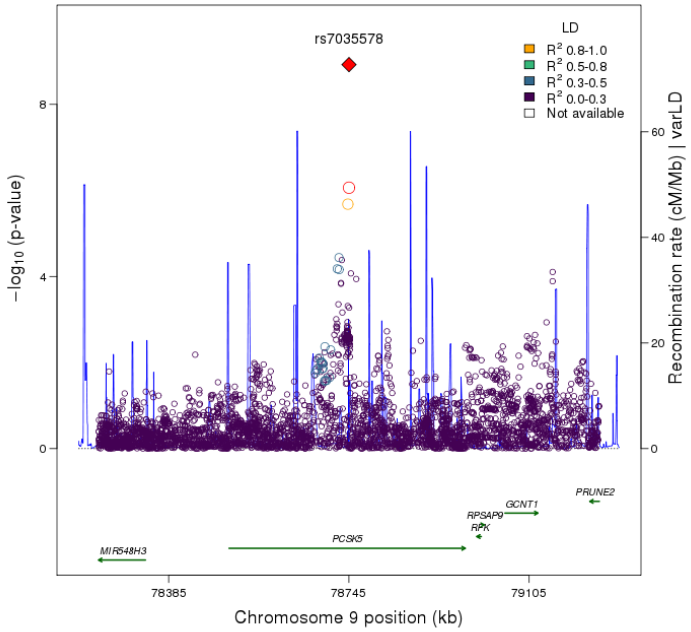
3i. Variant rs73729083 at chromosome 7, position 137559799. LDL-C Current Drinker (META)



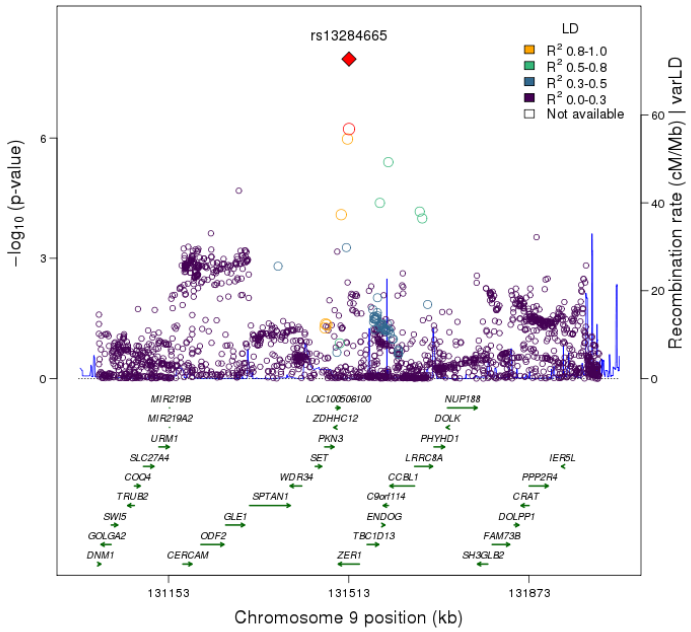
3j. Variant rs2911971 at chromosome 8, position 6607634. LDL-C Current Drinker (META)



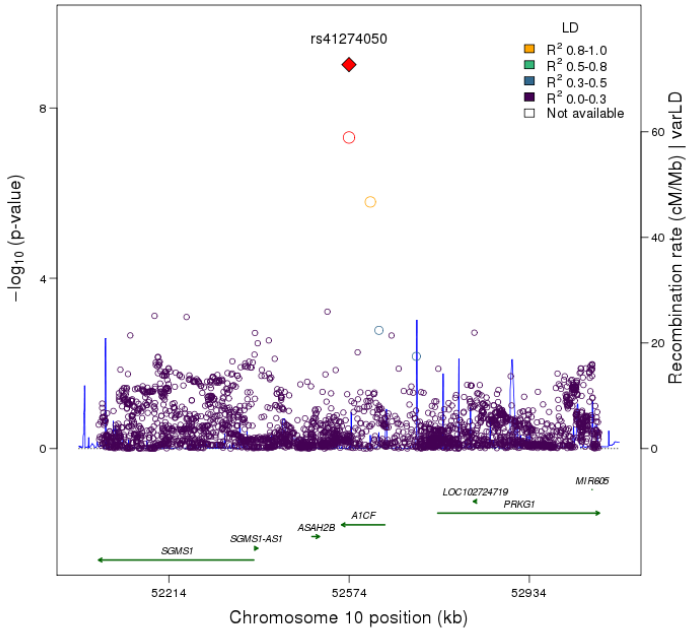
3k. Variant rs7035578 at chromosome 9, position 78745177. LDL-C Current Drinker (EUR)



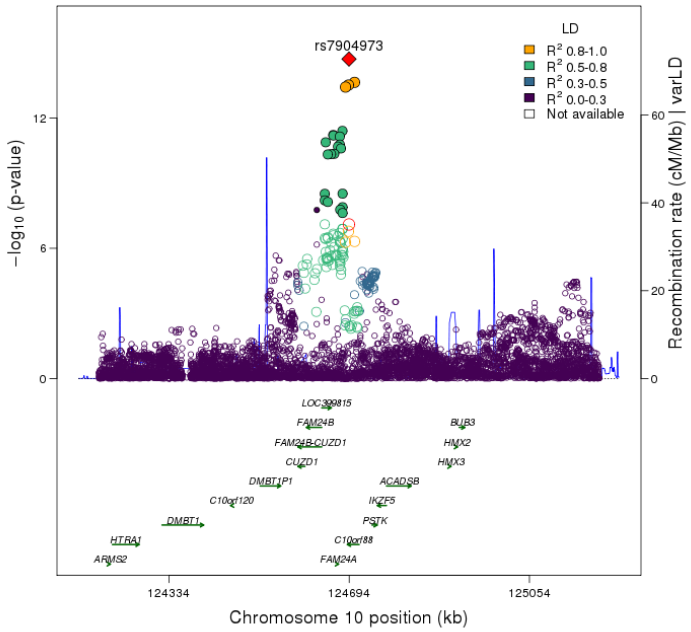
3l. Variant rs13284665 at chromosome 9, position 131513370. LDL-C Current Drinker (EUR)



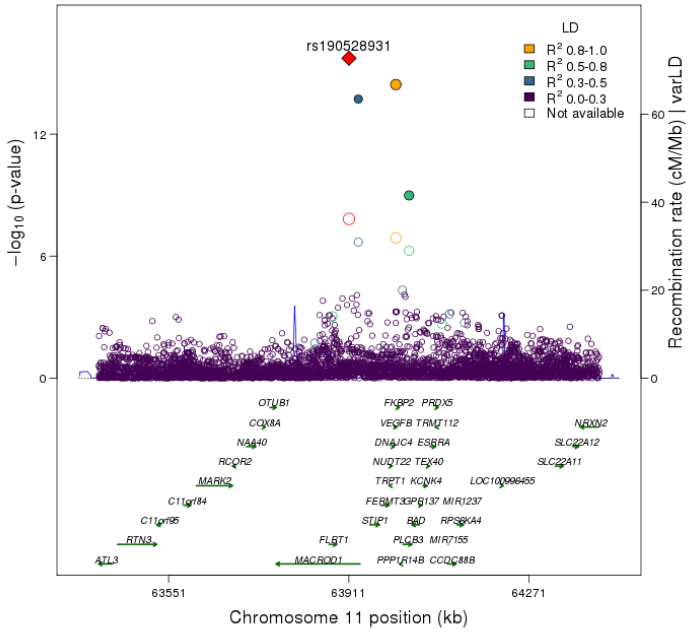
3m. Variant rs41274050 at chromosome 10, position 52573772. TG Regular Drinker (EUR)



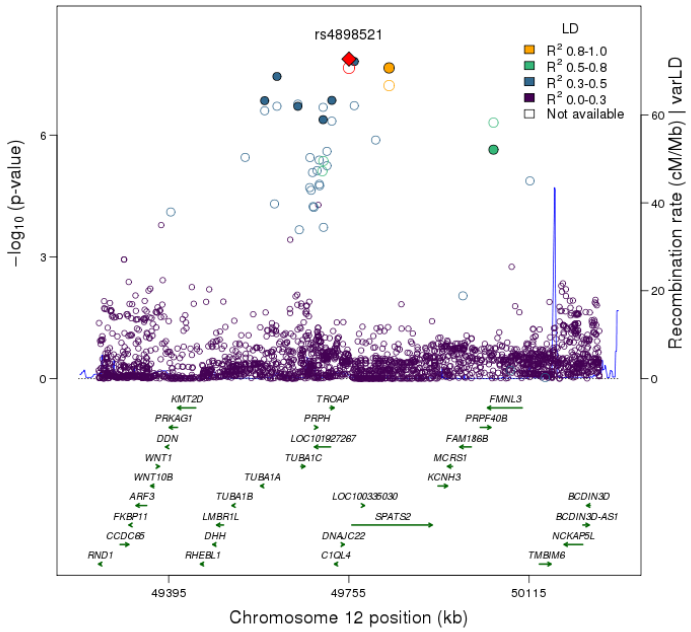
3n. Variant rs7904973 at chromosome 10, position 124693587. LDL-C Current Drinker (META)



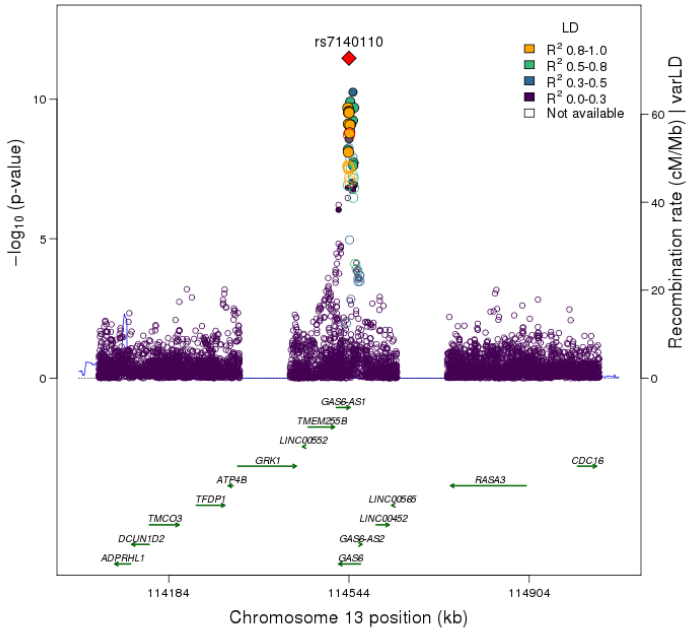
3o. Variant rs190528931 at chromosome 11, position 63911273. HDL-C Current Drinker (META)



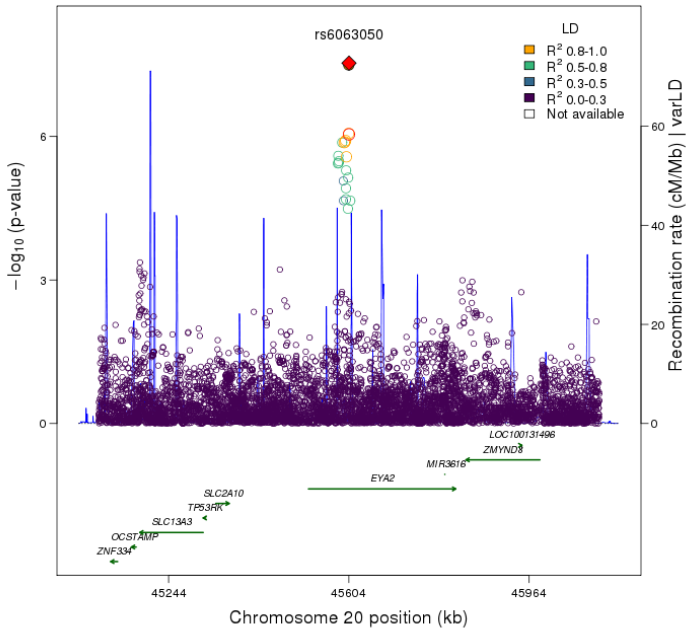
3p. Variant rs4898521 at chromosome 12, position 49755162. HDL-C Regular Drinker (EUR)



3q. Variant rs7140110 at chromosome 13, position 114544024. TG Current Drinker (META)



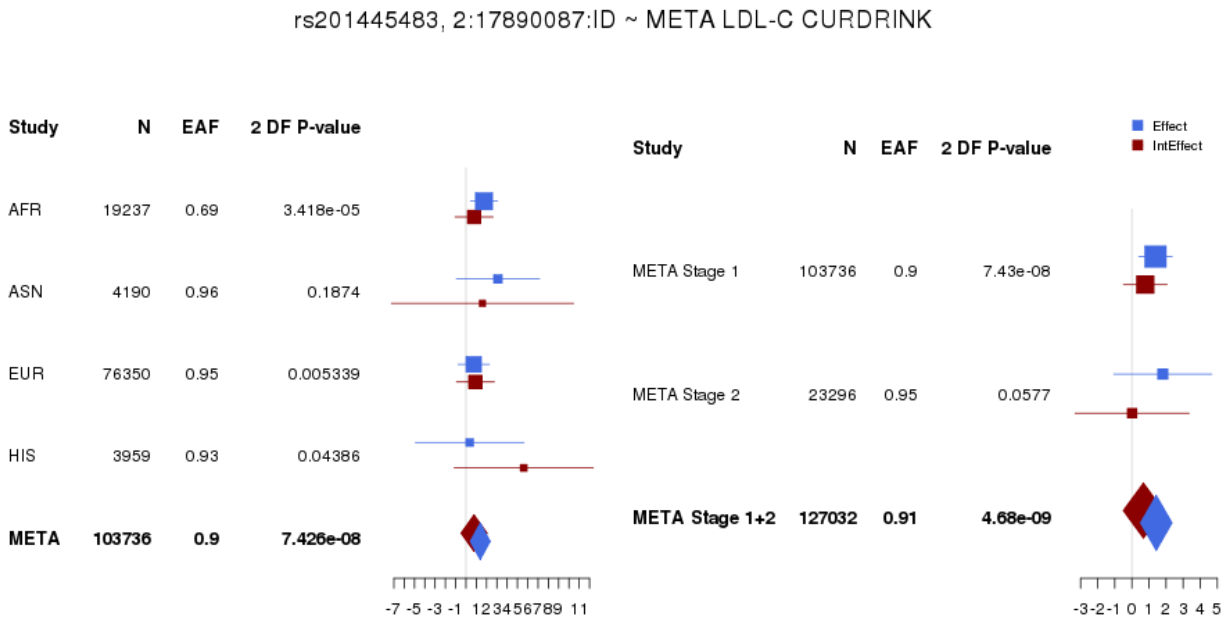
3r. Variant rs6063050 at chromosome 20, position 45604240. TG Current Drinker (META)



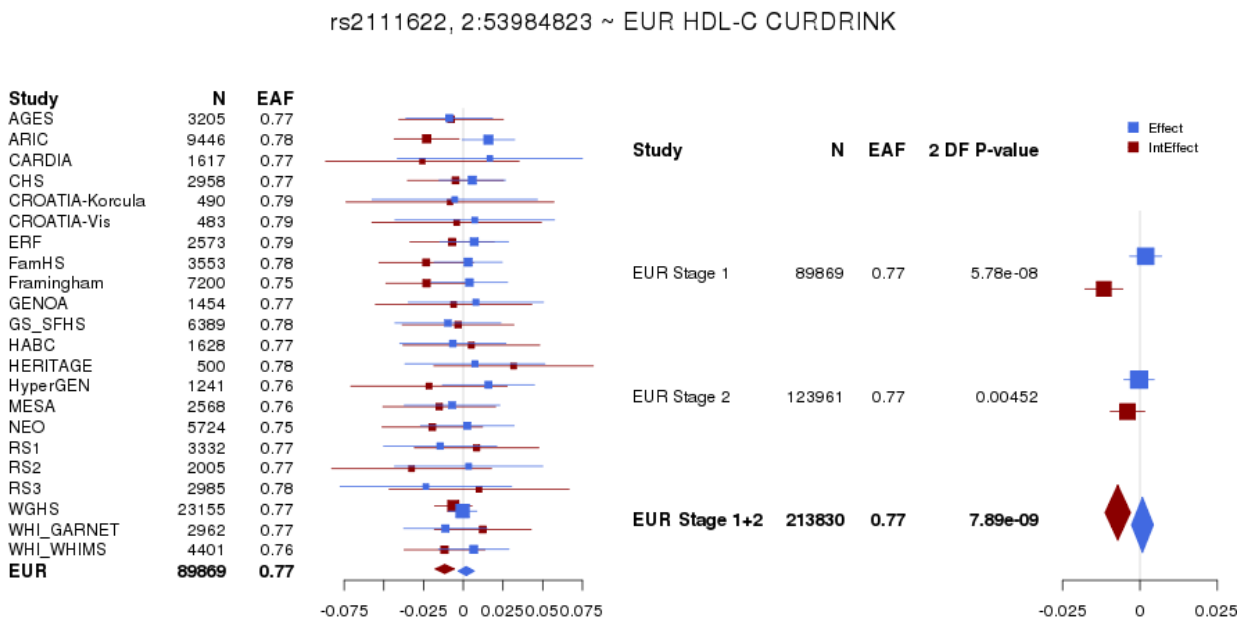
Web Figure 4

Forest plots of the top hits of the 18 novel loci. The left panel shows the studies used in Stage 1, while the right panel compares the effects sizes of the Stage 1 meta-analysis with the Stage 2 meta-analysis, used in the combined Stage 1 + Stage 2 analysis. Point estimates of the main effect are shown in blue with 95% confidence interval bands, and those for the interaction effect are shown in red. For variants identified through trans-ethnic meta-analysis (META), the left panel shows the constituent ancestry-specific meta-analyses instead of individual studies' effects.

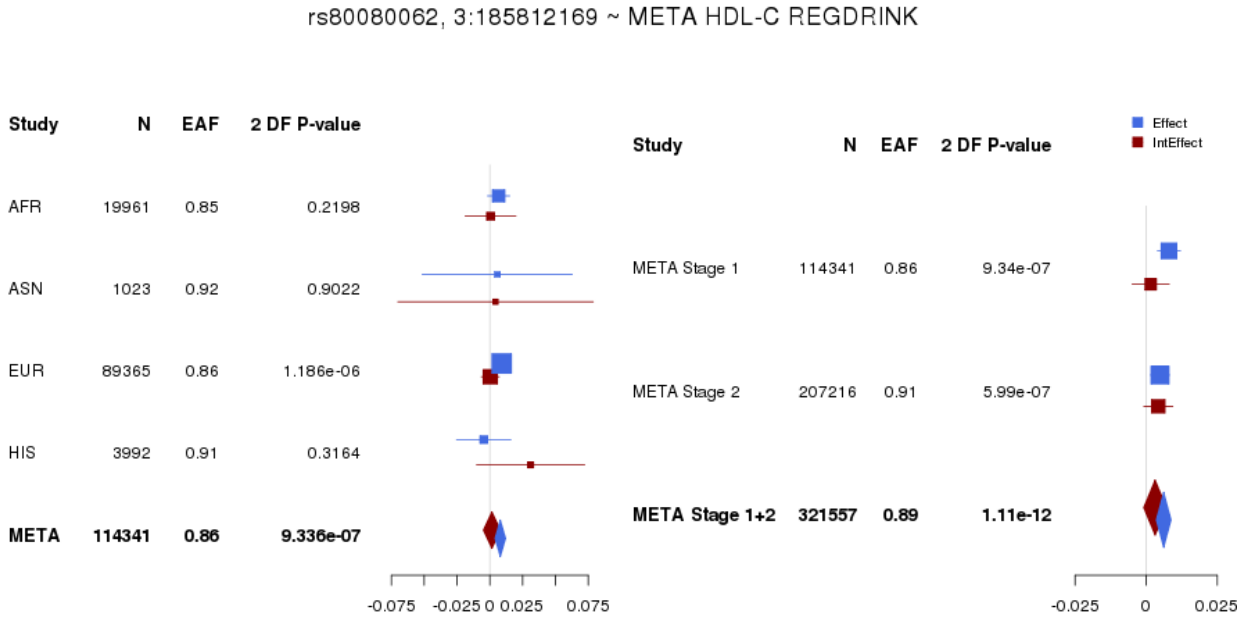
4a. Variant rs201445483



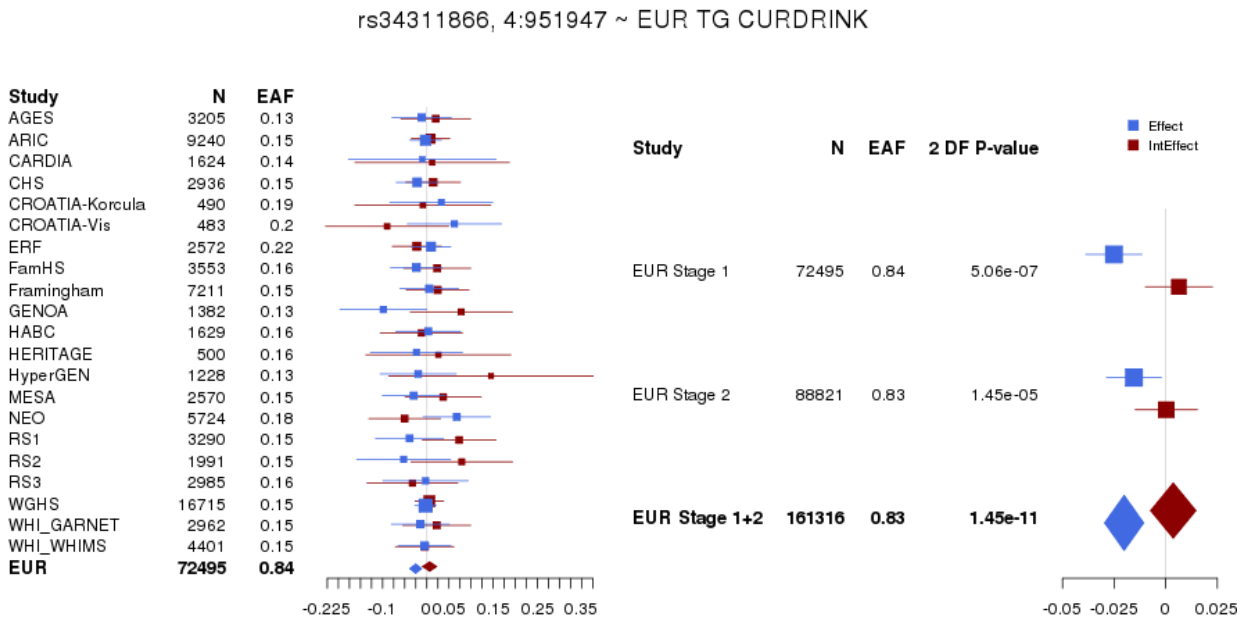
4b. Variant rs2111622



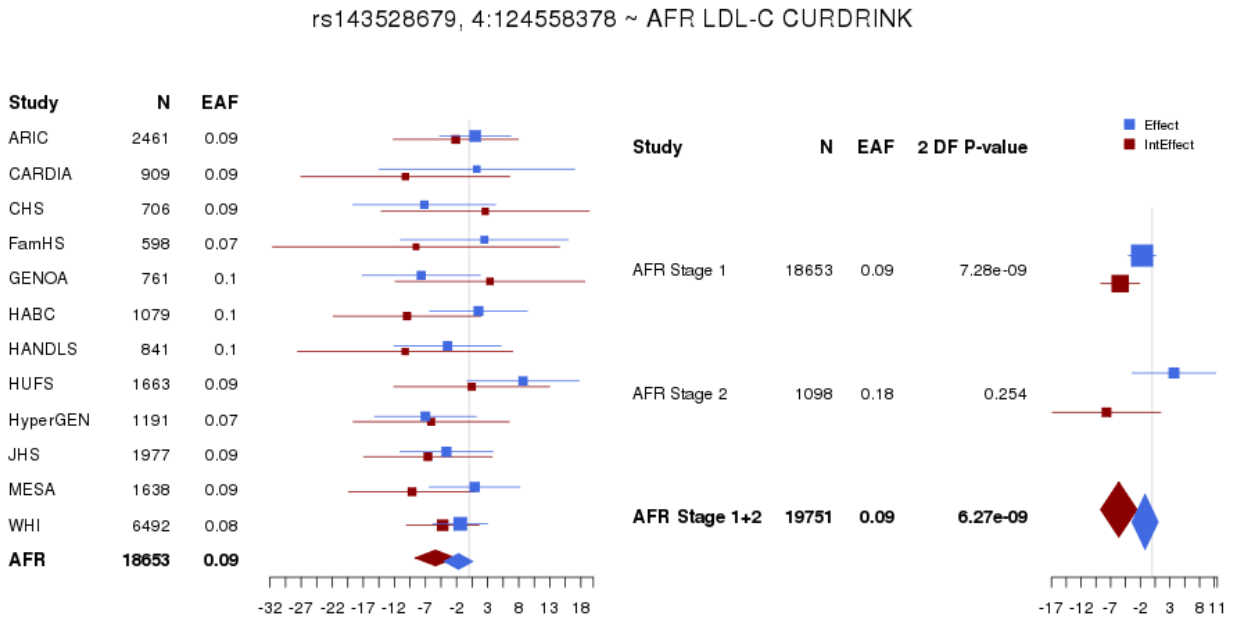
4c. Variant rs80080062



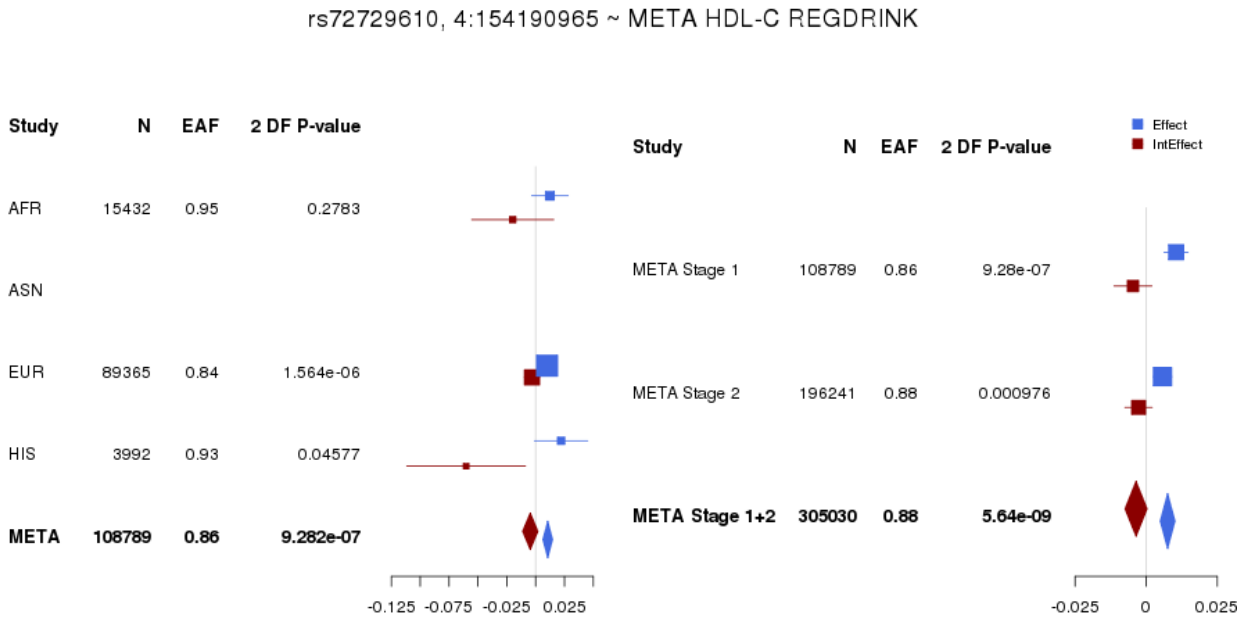
4d. Variant rs34311866



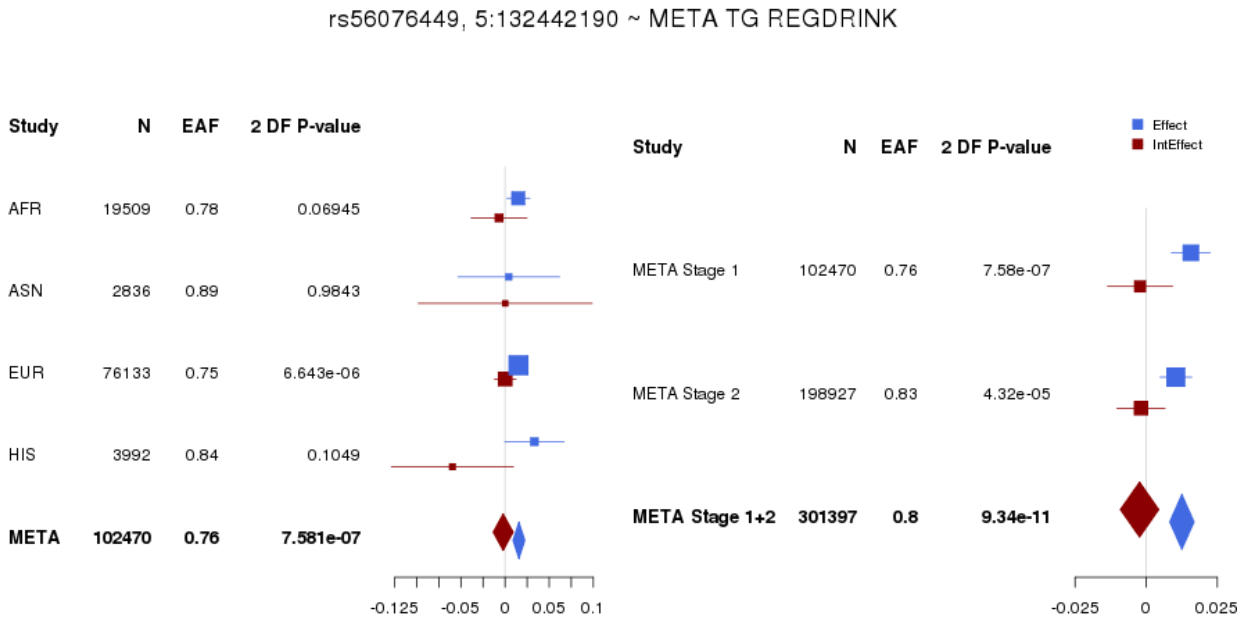
4e. Variant rs143528679



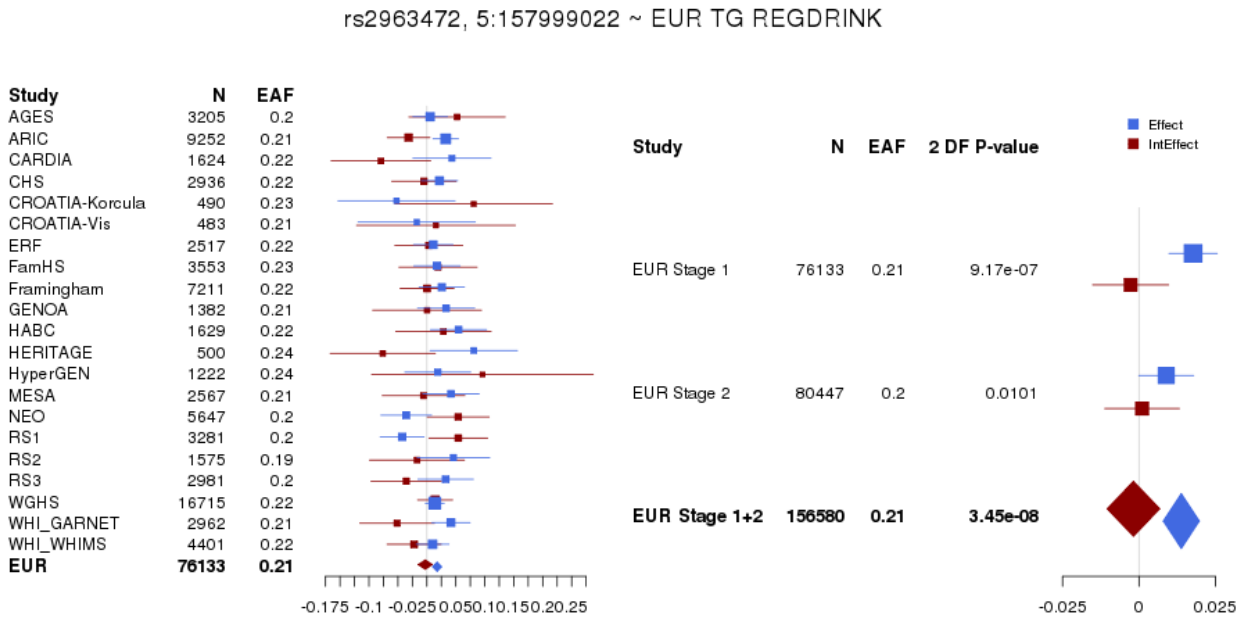
4f. Variant rs72729610



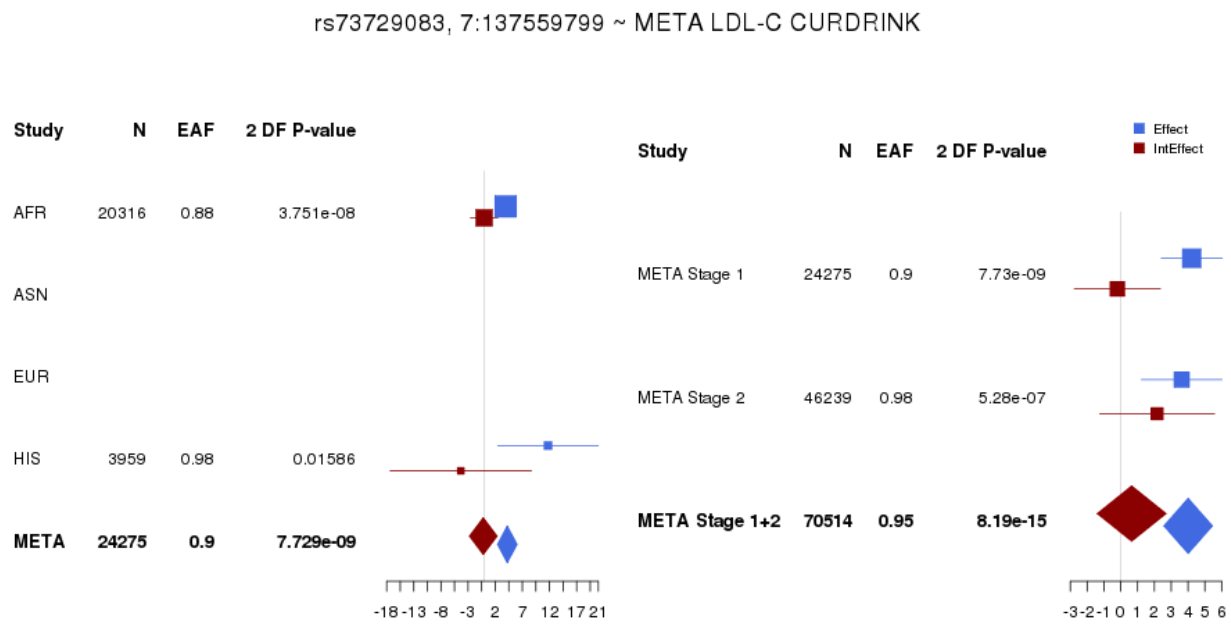
4g. Variant rs56076449



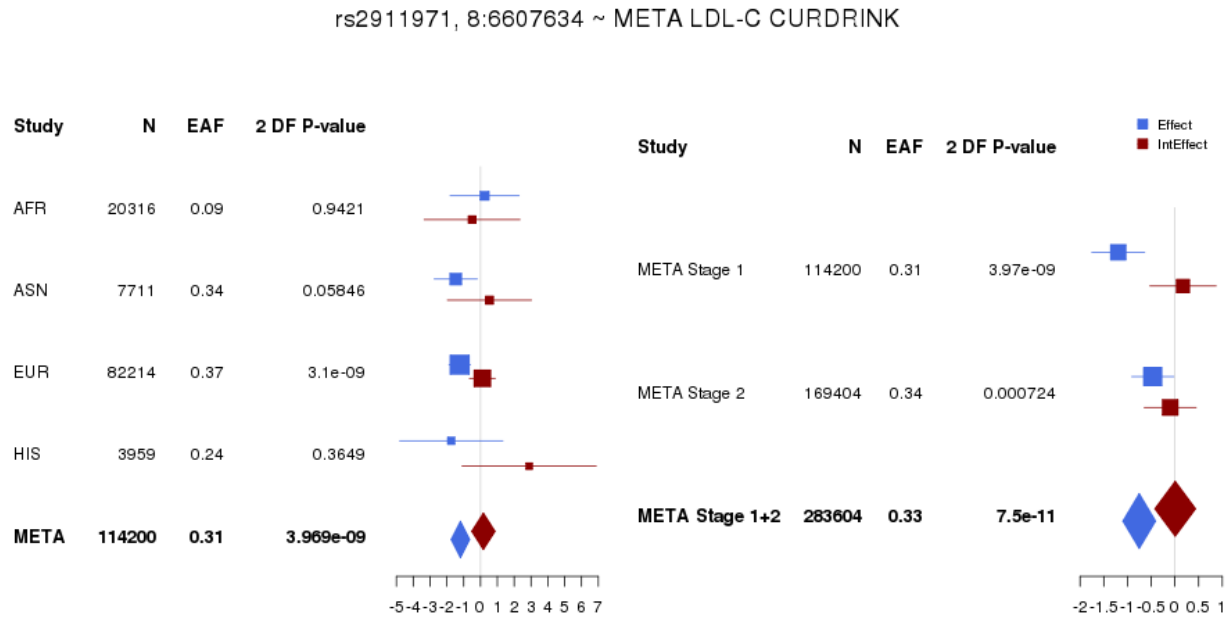
4h. Variant rs2963472



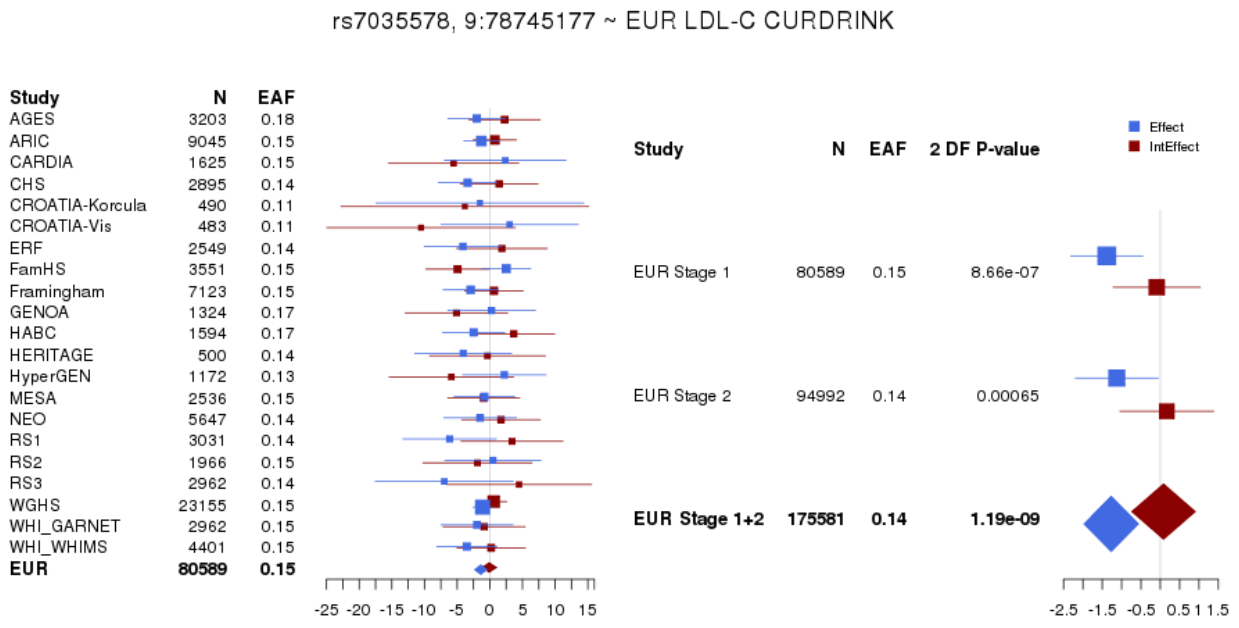
4i. rs73729083



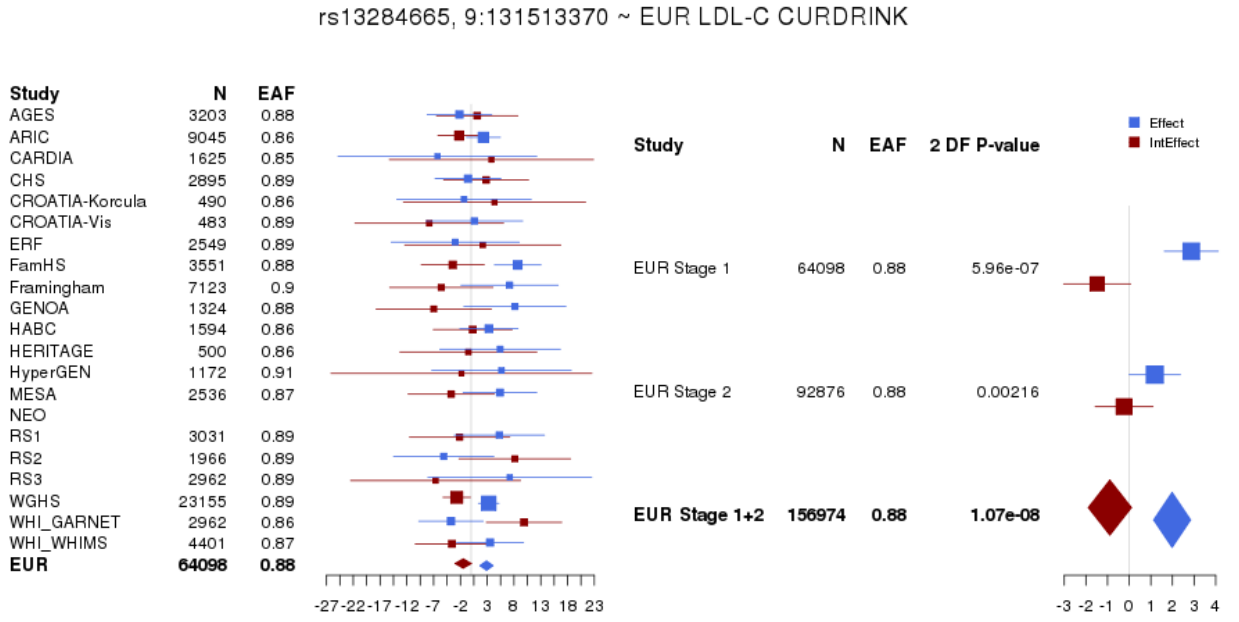
4j. Variant rs2911971



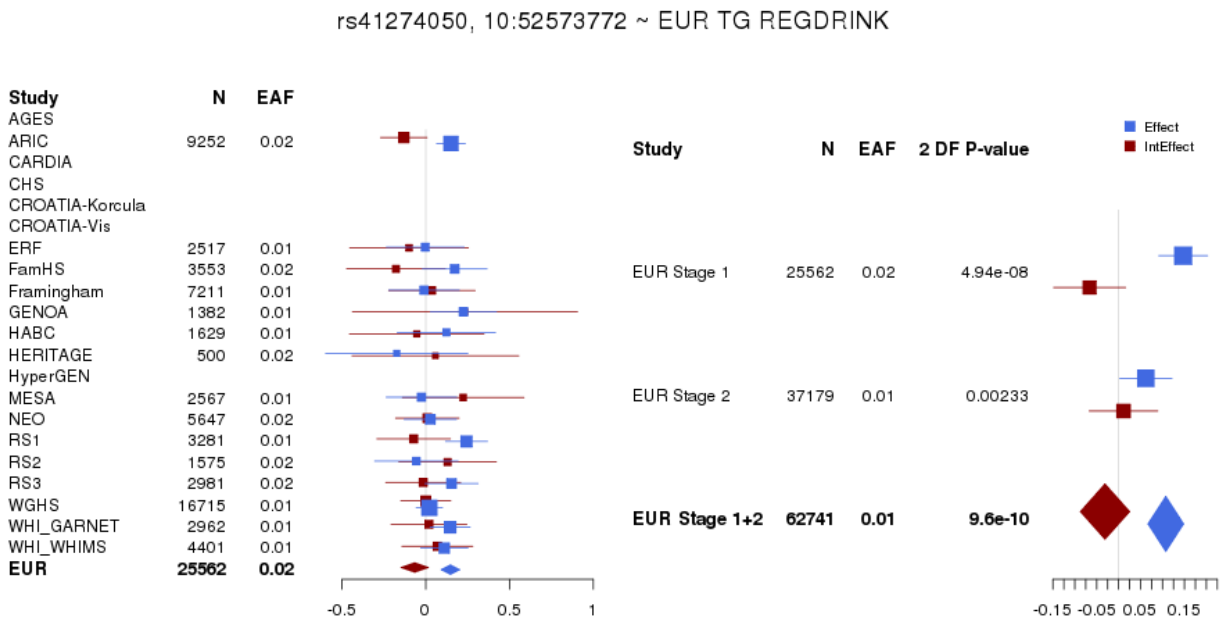
4k. Variant rs7035578



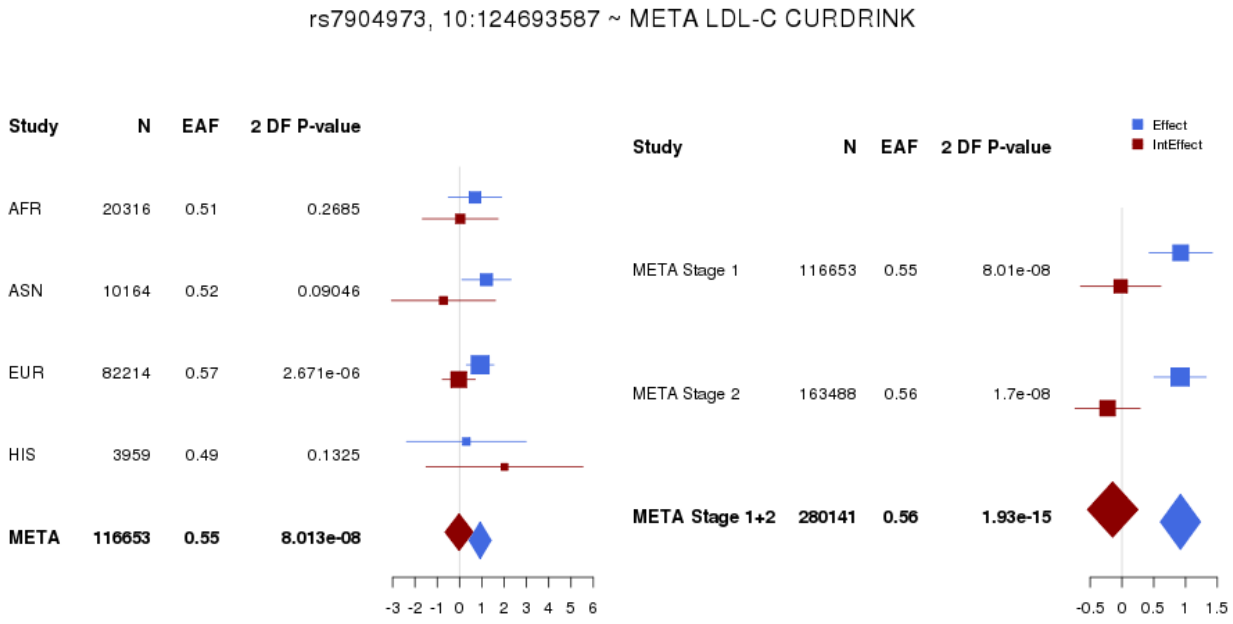
4l. Variant rs13284665



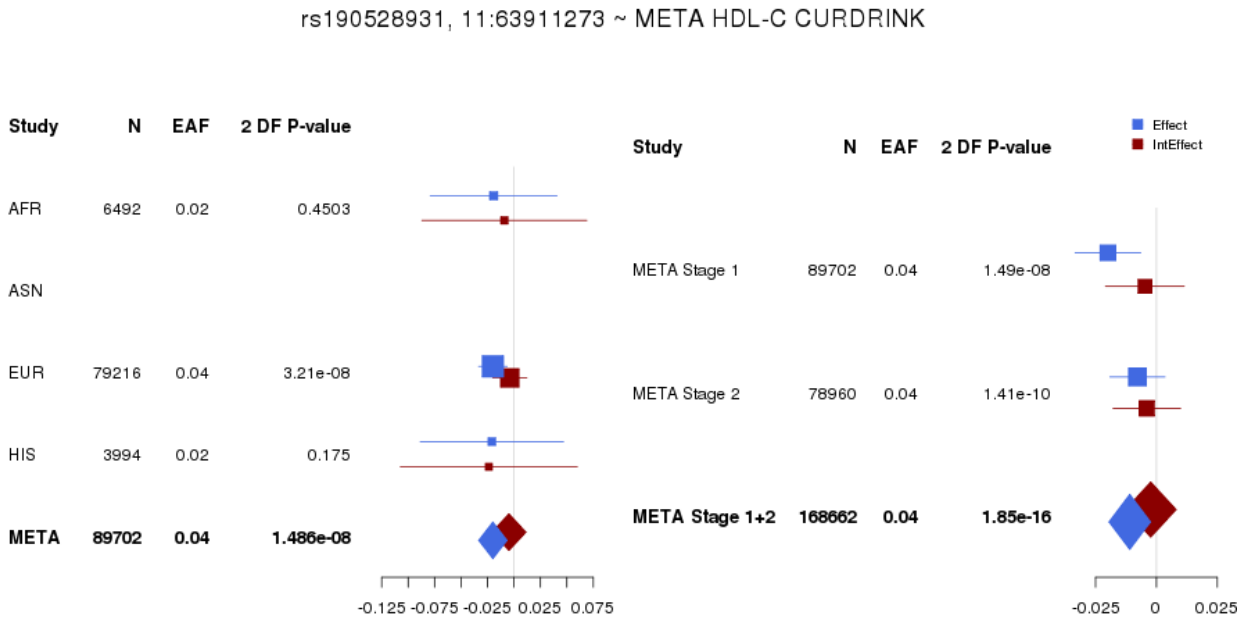
4m. Variant rs41274050



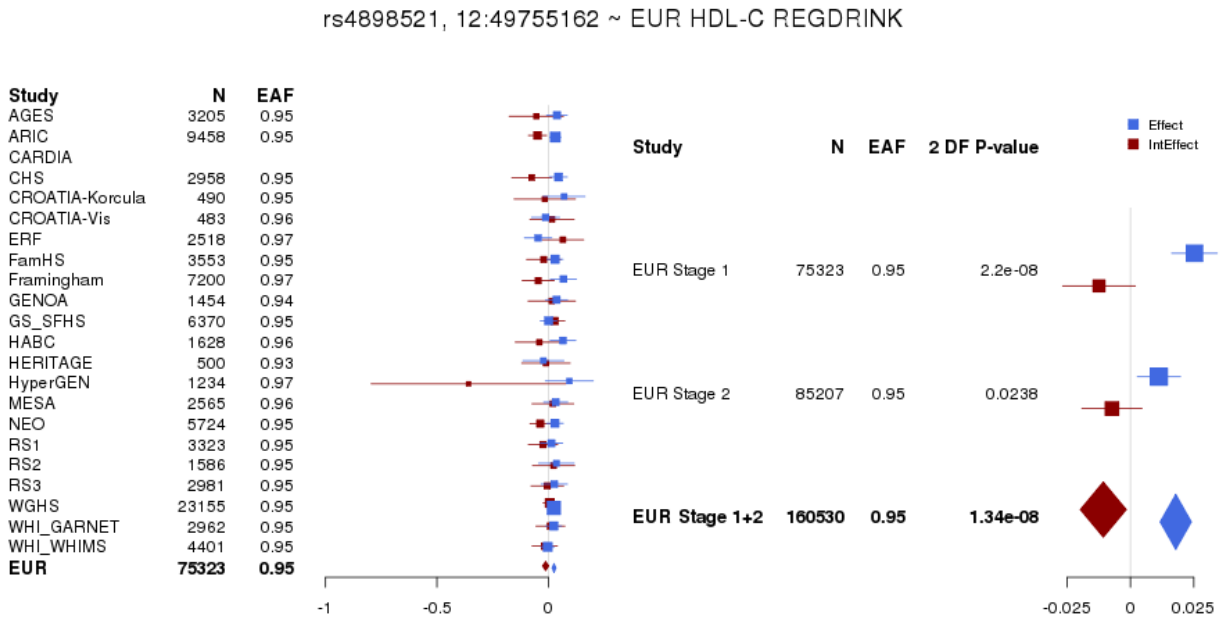
4n. Variant rs7904973



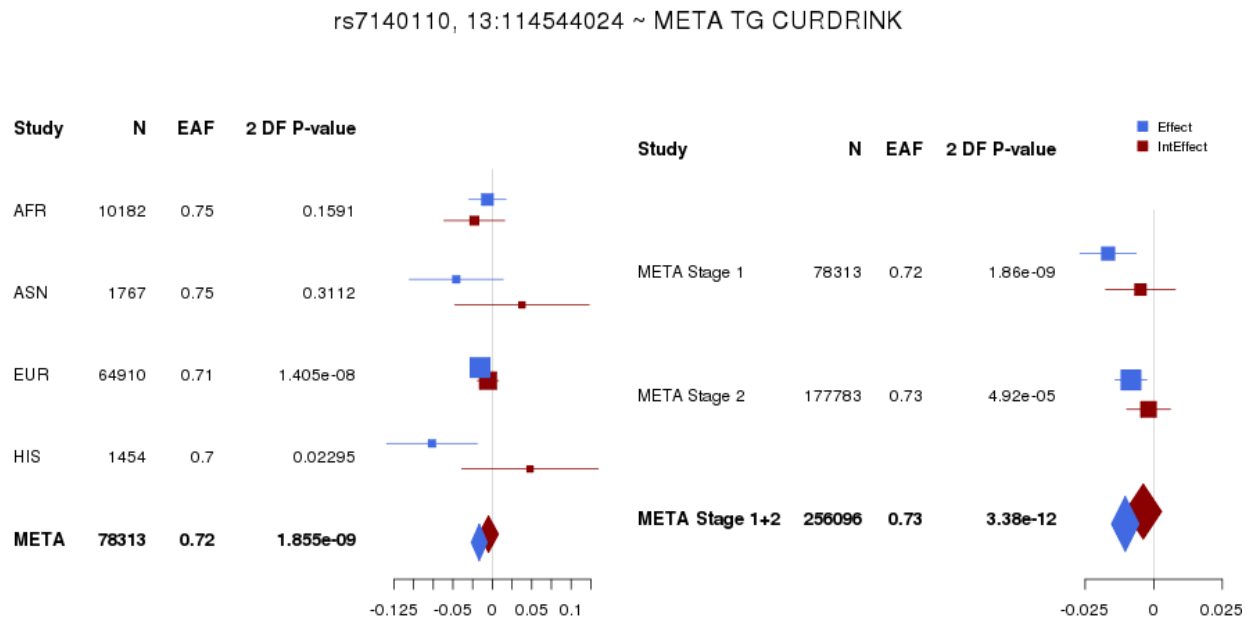
4o. Variant rs190528931



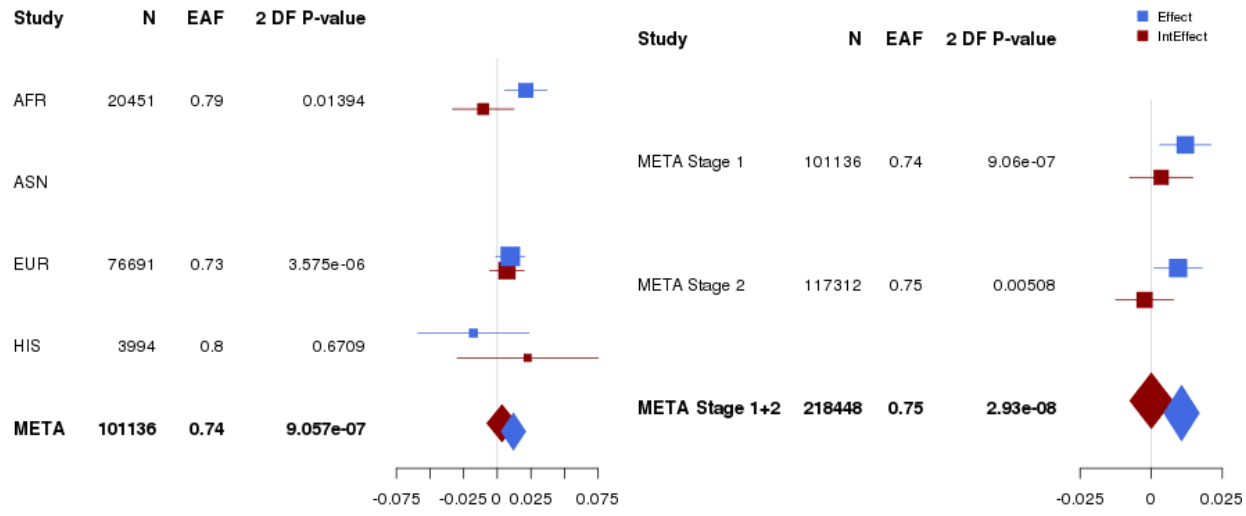
4p. Variant rs4898521



4q. Variant rs7140110

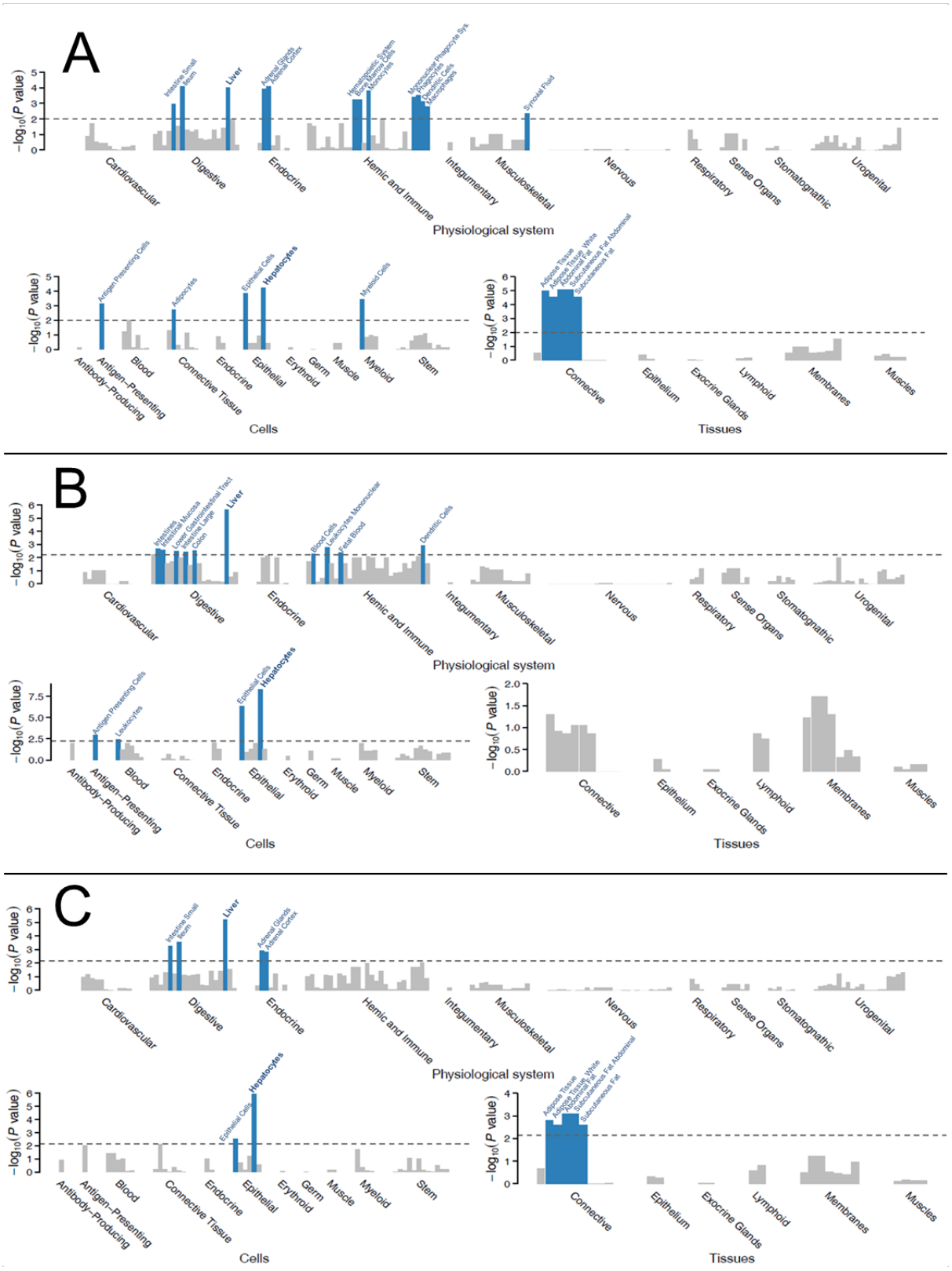


4r. Variant rs6063050



Web Figure 5

Tissue, Cell type and physiological system expression of genes at identified loci associated with A: HDL-C, B: LDL-C, and C: TG.



Web Tables

Multi-ancestry genome-wide association study of lipid levels incorporating gene-alcohol interactions

Paul S. de Vries et al.

Contents

tage 1 and 2 analyses, including 129 index variants in published lipid loci.

significant in the combined Stage 1 + 2 analyses (2 DF Joint P-value).

Web Table 1: Demographic and descriptive statistics of Stage 1 studies.

Ancestry	Cohort	N	% Male	% CurDrinker	% RegDrinker	Mean	SD
European	**AGES**	3,205	42.03	65.30	14.23	76.41	5.46
	ARIC	9,470	46.97	65.53	37.62	54.31	5.70
	CARDIA	1,617	46.55	95.86	63.08	25.56	3.34
	CHS	2,958	37.93	54.39	24.61	71.20	4.03
	CROATIA-Korcula	490	44.58	61.84	58.98	48.21	14.12
	CROATIA-Vis	483	47.62	56.73	55.69	51.77	13.29
	ERF	2,573	46.60	68.01	46.51	38.08	9.32
	FamHS	3,553	44.77	53.42	31.64	55.21	10.61
	Framingham	7,200	52.80	84.19	65.90	73.79	2.85
	GENOA	1,454	48.90	72.42	29.23	35.84	14.56
	GS:SFHS	6,389	49.64	90.77	68.46	49.80	13.83
	HABC	1,628	31.80	58.11	37.29	55.63	13.34
	HERITAGE	500	40.30	35.60	29.20	54.91	14.90
	HyperGEN	1,241	41.40	28.28	18.15	53.68	11.66
	MESA	2,568	47.88	71.88	43.00	62.09	9.66
	NEO	5,724	47.90	86.83	68.97	55.97	5.90
	RS1	3,332	42.68	83.61	57.75	65.20	6.24
	RS2	2,005	46.13	84.59	59.90	63.51	6.38
	RS3	2,985	43.95	90.18	65.18	56.73	6.10
	WGHS	23,155	0.00	29.26	56.70	54.70	7.12
	WHI-GARNET	2,962	0.00	74.54	29.03	65.60	6.94
	WHI-WHIMS	4,401	0.00	78.64	35.22	68.01	5.81
African	**ARIC**	2,756	37.61	32.37	23.51	53.40	5.77
	CARDIA	909	38.72	81.52	42.13	24.45	3.80
	CHS	727	37.55	36.73	15.27	71.55	4.16
	FamHS	607	34.60	44.15	28.86	53.08	10.54
	GENOA	984	29.85	38.11	10.37	55.82	10.71
	HABC	1,089	45.92	38.02	17.17	48.56	9.01
	HANDLS	882	42.66	25.28		73.45	2.90
	HUFS	1,669	37.87	60.64	22.65	42.60	14.10
	HyperGEN	1,230	32.76	30.98	21.54	45.04	13.25
	JHS	1,999	39.60	45.87	19.22	49.10	11.29
	MESA	1,645	45.86	50.03	24.65	61.77	9.62
	WHI	6,492	0.00	54.79	14.43	61.41	6.97
Asian	**GenSalt**	1,813	52.95	30.06	21.51	39.27	8.93
	MESA	744	49.00	35.82	8.87	61.75	9.90
	SCES	1,850	51.41	12.05		58.03	9.04
	SCHS-CHD:Cases	719	64.39	20.72	9.04	66.78	7.82
	SCHS-CHD:Controls	1,282	63.06	23.87	10.76	66.48	7.78
	SiMES	2,528	49.39	1.38		59.07	11.04
	SINDI	2,491	50.84	12.89		57.63	9.59
	SP2-1M	519	63.47	70.13	69.36	46.90	10.28
	SP2-610	504	23.42	55.75	53.37	48.62	11.31

Hispanic	**MESA**	1,454	48.32	55.74	22.18	60.80	9.74
	WHI	2,540	0.00	67.64	19.88	60.11	6.69

Age			Natural log HDL-C		Natural log TG		Medication-ad
Median	Min.	Max.	Mean	SD	Mean	SD	Mean
76.00	66.00	95.00	4.08	0.28	4.56	0.45	135.5
54.00	44.00	66.00	3.87	0.32	4.78	0.51	137.92
26.00	18.00	32.00	3.92	0.24	4.22	0.5	108.55
70.00	65.00	80.00	3.98	0.28	4.85	0.43	131.83
48.61	18.03	80.38	4.02	0.23	4.71	0.48	148.69
53.66	25.22	79.90	3.75	0.17	4.91	0.48	125.45
38.00	18.00	72.00	3.86	0.28	4.65	0.52	150.6
55.67	24.89	79.97	3.86	0.29	4.85	0.57	128.21
74.00	69.00	80.00	3.93	0.29	4.44	0.62	110
31.66	17.00	65.00	3.9	0.3	5.14	0.47	129.58
50.00	18.00	80.00	4.01	0.28			
56.00	18.00	80.00	3.9	0.3	4.9	0.49	126.29
54.00	18.00	80.00	3.67	0.24	4.66	0.49	116.1
55.00	18.00	80.00	3.81	0.27	4.94	0.59	121.51
63.00	44.00	80.00	3.92	0.29	4.74	0.53	125.74
56.00	44.00	66.00	3.97	0.28	4.71	0.54	145.4
64.53	55.00	80.46	3.95	0.27	4.81	0.43	151.5
61.59	55.12	80.46	3.93	0.26	4.84	0.45	150.1
56.69	45.46	80.38	3.97	0.31	4.76	0.48	144.8
52.90	38.71	89.89	3.95	0.28	4.78	0.54	124.34
66.00	50.00	79.00	3.89	0.23	4.92	0.47	159.93
68.00	50.00	79.00	3.98	0.22	4.81	0.45	157.76
53.00	44.00	66.00	3.96	0.3	4.58	0.47	138.5
25.00	18.00	32.00	3.97	0.24	4.08	0.44	111.4
71.00	65.00	80.00	4.02	0.26	4.65	0.43	132.65
52.00	30.00	80.00	3.94	0.28	4.57	0.52	119.08
55.61	20.50	79.60	3.96	0.3	4.84	0.44	122.44
49.00	30.00	64.00	4	0.29	4.68	0.43	129.61
73.00	68.00	80.00	3.96	0.31	4.54	0.48	113.6
44.00	18.00	80.00	3.92	0.31	4.48	0.5	117.4
45.00	18.00	79.00	3.94	0.28	4.52	0.51	121.64
49.00	21.00	79.00	3.88	0.27	4.5	0.54	122.31
62.00	45.00	80.00	3.92	0.28	4.53	0.48	123.88
61.00	50.00	79.00	4.01	0.25	4.6	0.45	151
39.00	18.00	62.00	3.91	0.24	4.67	0.51	96.3
62.00	44.00	80.00	3.87	0.24	4.83	0.52	121.44
56.91	44.44	79.94	3.87	0.3			138.96
66.80	49.78	79.35	3.88	0.22			128.77
66.56	50.07	78.92	3.92	0.23			122.38
58.00	40.00	80.00	3.93	0.24			142.65
56.00	43.00	80.00	3.67	0.29			141.66
46.23	24.62	79.72	3.9	0.26	4.64	0.56	128.21
48.83	23.19	79.99	4	0.25	4.5	0.57	126.54

61.00	44.00	80.00	3.83	0.26	4.93	0.51	126.41
59.00	50.00	79.00	3.95	0.24	4.89	0.45	144.75

ljusted LDL-C SD
40.04
38.2
29.22
36.2
40.15
35.2
38.84
37.67
34.68
37.59
35.34
31.4
35.93
32.1
36.1
35.65
34.9
40.74
34.44
38.7
38.84
42.67
30.84
39.14
39
44.4
40.95
41.28
39.34
39.89
42.96
36.91
44.33
27.83
30.83
35.52
33.69
30.68
40.3
37.7
32.8
35.47

35.77
38.57

Web Table 2: Demographic and descriptive statistics of Stage 2 studies.

Ancestry	Cohort	N	% Male	% CurDrinker	% RegDrinker	Mean
European	ASCOT-SC	2,420	74.59	76.53	64.05	60.98
	ASCOT-UK	3,770	80.32	77.53	71.54	63.79
	BRIGHT	1,726	39.75	71.32	58.97	56.97
	DESIR-1	696	40.23	69.97	47.99	53.50
	DHS	949	46.45	18.55	8.54	61.41
	DR's EXTRA	1,230	47.24	85.93	51.46	66.48
	EGCUT-Human370CNV	683	49.78	94.14	24.89	38.65
	EGCUT-OmniExpress	1,078	52.00	91.00	24.40	49.18
	EPIC	19,977	53.35	86.98	67.86	59.14
	FENLAND-GWAS	1,340	44.00	94.25	41.45	45.05
	FENLAND-OMICS	8,448	47.00	92.67	39.31	48.86
	FUSION Case	702	65.77	68.66	36.18	62.64
	FUSION Control	255	31.82	77.65	33.33	62.97
	GeneSTAR	744	43.41	69.62	28.40	52.42
	GLACIER	3,265	36.52	89.77	32.47	50.18
	GRAPHIC	987	50.10	85.01	81.56	52.90
	HRS	6,903	42.33	59.37	33.46	64.51
	INGI-CARL	374	38.23	38.50	16.84	49.70
	INGI-FVG	935	41.92	66.42	16.04	51.31
	InterAct-CoreExome CASES	4,461	51.11	86.82	60.75	55.70
	InterAct-CoreExome SUBCOHORT	7,715	39.62	86.31	61.41	52.42
	InterAct-GWAS CASES	3,684	46.12	79.07	52.85	54.53
	InterAct-GWAS SUBCOHORT	4,309	35.39	82.39	55.72	51.06
	KORA_S3	3,046	48.50	68.71	58.47	47.32
	KORA_S4	3,750	48.94	72.75	59.65	49.17
	LBC1936	909	50.17	80.09	57.87	69.68
	LifeLines	12,296	41.55	67.75	49.81	48.06
	LOLIPOP-EW610	927	73.14	73.68	66.67	54.38
	LOLIPOP-EWA	582	86.94	74.57	65.98	55.70
	LOLIPOP-EWP	644	100.00	79.50	72.67	61.25
	Long Life Family Study (LLFS)	3,153	44.59	60.93	NA	55.96
	METSIM	8,507	100.00	77.65	67.99	56.93
	NESDA	2,712	33.32	82.93	69.06	42.12
	OBA - French obese cases	668	21.11	61.08	NA	44.22
	PREVEND	3,553	52.00	76.30	61.24	49.67
	PROCARDIS (case)	3,631	83.12	61.50	NA	61.71
	PROCARDIS (control)	1,012	78.56	78.36	NA	57.67
	SHEEP-CASE	1,156	70.59	89.27	65.31	59.25
	SHEEP-CONTROL	1,533	67.51	91.65	70.45	59.87
	SHIP-0	3,752	46.06	83.34	56.74	49.18
	SHIP-Trend	978	43.96	88.96	49.59	50.08
	TWINGENE	5,469	48.29	83.71	48.66	63.51
	YFS	2,057	44.48	71.12	62.47	31.67

African	**AA-DHS**	592	43.10	32.26	NA	56.23
	GeneSTAR	525	36.38	51.43	16.57	50.64
	HRS	1646	36.63	45.81	23.03	61.76
	HyperGEN-AXIOM	418	45.69	31.82	24.64	48.34
	Loyola GxE	603	23.05	72.80	5.97	40.18
	Loyola SPT	691	39.07	34.88	15.34	46.53
Asian	**BBJ**	90922	55.98	38.69	33.56	62.74
	Beijing Eye Study (BES)-610	488	34.02	24.18	19.47	61.79
	BES-omniexpress	388	38.66	14.95	10.31	64.05
	CAGE-Amagasaki	911	62.81	75.30	51.59	53.04
	DF-TJ	1419	77.93	35.02	28.89	63.48
	LOLIPOP-IA317	2059	100.00	47.30	40.26	48.25
	LOLIPOP-IA610-Case	2785	81.82	30.99	23.88	59.31
	LOLIPOP-IA610-Control	3750	86.13	41.15	33.25	52.45
	LOLIPOP-IAP	501	100.00	53.09	46.31	51.08
	LOLIPOP-OmniEE	891	53.56	29.07	23.34	49.64
	Ragama Health Study (RHS)	2169	45.27	30.52	11.57	52.53
	SWHS/SMHS	2148	13.87	6.42	6.05	57.30
Hispanic	**HCHS/SOL**	12731	41.04	47.82	27.01	46.13
	IRASC	183	40.77	48.09	24.04	53.92
	IRAS Family Study	800	38.25	55.75	32.38	40.83
Brazilian	**1982 Pelotas Birth Cohort Study**	2749	48.53	62.53	NA	30.18
	Baependi Heart Study	903	40.20	29.35	NA	48.38

Age				Natural log HDL-C		Natural log TG		Medication-ad
SD	Median	Min.	Max.	Mean	SD	Mean	SD	Mean
8.74	61.00	40.00	80.00	3.90	0.27	4.95	0.48	150.92
8.08	64.00	40.00	80.00	3.87	0.25	4.99	0.48	153.79
10.97	58.00	21.00	80.00	3.90	0.30	5.10	0.54	130.89
5.66	53.00	45.00	65.00	4.19	0.25	4.36	0.47	130.80
9.10	61.61	33.54	79.86	3.73	0.29	5.15	0.56	121.70
5.38	66.27	57.36	78.70	4.15	0.29	4.66	0.44	139.96
15.92	35.00	18.00	80.00	4.04	0.29			133.90
15.98	51.00	18.00	80.00	4.07	0.28	4.65	0.50	135.50
9.28	58.88	39.49	79.08	3.96	0.29	4.93	0.53	154.91
7.25	45.55	29.40	57.60	4.00	0.27	4.50	0.55	131.52
7.35	49.10	30.50	64.00	4.05	0.26	4.47	0.54	132.52
7.22	63.40	40.77	77.99	3.73	0.27	5.16	0.56	155.10
7.61	63.07	42.60	79.88	4.00	0.27	4.69	0.39	154.08
11.98	53.00	25.00	80.00	3.99	0.30	4.67	0.52	123.35
8.45	50.10	29.30	64.20	3.96	0.29	4.70	0.44	165.58
4.41	53.00	40.00	61.00	4.00	0.26	4.98	0.47	127.71
8.82	65.00	33.00	80.00	3.96	0.30			
16.37	52.00	18.00	79.00			4.73	0.49	
15.45	51.78	18.00	79.00	3.96	0.24	4.58	0.48	145.40
6.88	56.21	26.19	75.58	3.84	0.29			
8.82	53.00	20.18	76.90	4.01	0.29			
7.93	54.80	29.51	76.46	3.83	0.27			
9.21	50.85	21.06	74.62	4.02	0.28			
12.96	47.00	24.00	75.00	3.96	0.29	4.70	0.60	141.21
13.86	49.00	24.00	75.00	4.02	0.29	4.77	0.49	140.62
0.76	69.68	67.64	71.30	4.03	0.28			
11.07	47.00	18.00	80.00	3.99	0.27	4.58	0.51	135.25
10.38	55.47	22.68	74.98	3.97	0.25	4.75	0.55	139.34
9.08	58.35	32.38	67.33	3.89	0.23	4.85	0.56	139.37
8.72	61.00	24.00	80.00	3.85	0.23	4.88	0.61	137.41
9.80	56.41	35.09	75.01	4.05	0.30	4.58	0.52	132.32
6.84	56.00	45.00	74.00	3.98	0.27	4.73	0.50	140.51
13.01	43.00	18.00	65.00	4.11	0.27	4.60	0.51	128.39
11.71	44.50	18.00	77.00	3.70	0.29	4.92	0.49	134.44
12.48	49.00	28.00	75.00	3.88	0.30	4.69	0.53	145.83
7.08	62.00	35.00	80.00	3.76	0.27	4.95	0.51	137.18
8.51	58.00	28.00	80.00	3.95	0.26	4.68	0.52	129.79
7.18	60.00	45.00	70.00	3.69	0.28	5.05	0.51	163.57
7.13	61.00	45.00	70.00	3.87	0.28	4.76	0.49	153.62
16.22	49.00	20.00	80.00	3.99	0.29			140.63
13.69	50.00	20.00	80.00	4.02	0.25	5.00	1.00	135.67
7.48	63.00	47.00	80.00	3.95	0.30	4.66	0.49	150.25
4.98	33.00	24.00	39.00	3.88	0.25	4.62	0.47	120.74

9.40	56.00	33.00	79.00	3.83	0.26	4.67	0.52	127.91
11.98	51.00	25.00	77.00	4.02	0.29	4.45	0.51	122.50
8.36	61.00	28.00	80.00	3.98	0.29			
12.26	47.50	18.00	76.00	3.93	0.27	4.54	0.53	121.20
8.29	39.73	24.64	77.53	3.92	0.22	4.32	0.50	135.61
13.84	45.45	24.38	75.76	3.85	0.25	4.39	0.50	123.43
11.78	65.00	20.00	80.00	3.97	0.26	4.79	0.51	134.87
7.81	61.00	50.00	80.00	4.04	0.31	4.78	0.59	136.49
8.76	65.00	50.00	80.00	3.93	0.28	4.87	0.55	138.02
12.94	56.00	21.00	80.00	4.07	0.27	4.60	0.51	125.80
7.70	63.00	35.00	80.00	3.96	0.31	4.66	0.55	121.39
10.46	46.92	35.03	74.86	3.83	0.24	4.89	0.49	134.64
9.69	59.63	26.66	80.18	3.79	0.25	4.92	0.51	129.45
10.23	52.31	22.00	74.99	3.83	0.23	4.94	0.54	133.16
8.35	50.37	31.25	65.95	3.84	0.24	4.98	0.56	138.61
9.91	48.30	23.70	76.40	3.89	0.22	4.85	0.51	127.17
7.86	53.00	30.00	77.00	3.90	0.09	4.75	0.46	136.90
9.27	58.93	40.00	75.00	3.88	0.25	4.92	0.54	105.20
13.86	48.00	18.00	76.00	3.86	0.26	4.77	0.55	128.40
8.20	54.00	40.00	69.00	3.71	0.33	4.89	0.55	144.18
13.29	40.17	18.00	79.90	3.73	0.26	4.60	0.58	109.96
0.34	30.17	29.43	31.14	4.05	0.24			109.67
15.01	48.00	22.00	80.00	3.82	0.24	4.78	0.46	128.20

ljusted LDL-C SD
39.83
39.69
36.04
32.20
35.81
34.54
43.42
39.52
43.21
33.19
35.00
49.90
40.25
35.01
45.24
29.40
43.09
45.46
45.13
41.00
36.15
38.00
37.03
34.84
34.99
44.41
36.17
41.70
38.81
31.79
38.42
37.13
46.44
36.68
37.25
34.73

40.15
40.01

36.39
39.06
39.32
40.97
41.05
41.45
29.71
39.52
36.23
44.00
36.15
38.37
36.49
36.15
32.58
40.06
42.82
30.47
29.32
37.66

Web Table 3: Genotyping, imputation, and statistical analysis for Stage 1 an

Ancestry	Cohort	Genotyping Platform
European	**AGES**	Illumina 370CNV
	ARIC	Affymetrix 6.0
	CARDIA	Affymetrix 6.0
	CHS	Illumina 370CNV/iSELECT
	CROATIA-Korcula	Illumina HumanHap 370 CNV Duochip
	CROATIA-Vis	Illlumina Infinium HumanHap 300 Bead chip
	ERF	Illumina 6K/318K/350K/610K, Affymetrix 250K
	Fam HS	Illumina 550K/610K/1M
	FHS	Affymetrix Nsp, Sty and 50K gene centric
	GENOA	Affymetrix 6.0 / Illumina 1M-Duo
	GS:SFHS	Illumina HumanOmniPlusExome
	Health ABC	Illumina 1M
	HERITAGE	Illumina 370CNV
	HyperGEN	Affymetrix 5.0
	MESA	Affymetrix 6.0
	NEO	Illumina HumanCoreExome-24v1_A Beadchip
	RS1	Illumina 550-Duo, Illumina 610 Quad
	RS2	Illumina 550-Duo
	RS3	Illumina 610-Quad
	WGHS	Illumina HumanHap 300 DuoPlus
	WHI-GARNET	Illumina HumanOmni1-Quad v1-0 B
	WHI-WHIMS	Illumina HumanOmniPlusExome-8v1 B
African	**ARIC**	Affymetrix 6.0
	CARDIA	Affymetrix 6.0
	CHS	Illumina Human Omni1-Quad_v1 BeadChip
	Fam HS	Illumina 1M
	GENOA	Affymetrix 6.0 / Illumina 1M-Duo
	HANDLS	Illumina 1M/1M-Duo/550K/370K/510S/240S
	HABC	Illumina 1M
	HUFS	Affymetrix 6.0
	HyperGEN	Affymetrix 6.0, Affymetrix 5.0
	JHS	Affymetrix 6.0
	MESA	Affymetrix 6.0
	WHI	Affymetrix 6.0
Asian	**GenSalt**	Affymetrix 6.0
	MESA	Affymetrix 6.0
	SCES	Illumina 610K
	SCHS-CHD:Cases	Illumina Omni Zhonghua-8
	SCHS-CHD:Controls	Illumina Omni Zhonghua-8
	SiMES	Illumina 610K
	SINDI	Illumina 610K
	SP2-1M	Illumina 1M
	SP2-610	Illumina 610K
Hispanic	**MESA**	Affymetrix 6.0
	WHI	Affymetrix 6.0

[1] Cohort unrelated (UN), family-based (FB), case-control (CC)

[2] Other than those specified in the analysis plan.

alysis.

Imputation Software	Association Test	Study Design[1]	PCs Used
MaCH/minimac	ProbABEL	UN	1, 2
ShapeIt/IMPUTE2	ProbABEL	UN	1-10
BEAGLE	ProbABEL	UN	1-4
MaCH/minimac	R/sandwich	UN	0
ShapeIt/IMPUTE2	ProbABEL	UN	1-3
ShapeIt/IMPUTE2	ProbABEL	UN	1-3
MaCH/minimac	ProbABEL/GenABEL	FB	0
MaCH/minimac	R/geepack	FB	1
MaCH/minimac	R	FB	0
ShapeIt/IMPUTE2	R/geepack	FB	1-4
ShapeIt/IMPUTE2	ProbABEL	UN	1-4
MaCH/minimac	R/sandwich	UN	1, 2
MaCH/minimac	R/geepack	FB	0
MaCH/minimac	R/geepack	FB	0
IMPUTE2	ProbABEL	UN	1-3
IMPUTE2	ProbABEL	UN	1-4
MaCH/minimac	ProbABEL	UN	0
MaCH/minimac	ProbABEL	UN	0
MaCH/minimac	ProbABEL	UN	0
MaCH/minimac	ProbABEL	UN	1, 2, 5, 6, 10
MaCH/minimac	R/sandwich	CC	1-10
MaCH/minimac	R/sandwich	UN	1-10
ShapeIt/IMPUTE2	ProbABEL	UN	1-10
MaCH/minimac	ProbABEL	UN	1-2
IMPUTE2	R/sandwich	UN	1
MaCH/minimac	R/geepack	FB	1-10
ShapeIt/IMPUTE2	R/geepack	FB	1-4
MaCH/minimac	ProbABEL	UN	1-10
MaCH/minimac	R (lm) + sandwich	UN	1, 2
MaCH-Admix	R/geepack	FB	1
MaCH/minimac	R/geepack	FB	1
MaCH	ProbABEL	UN	1-10
IMPUTE2	SNPTEST2	UN	1-3
MaCH/minimac	ProbABEL	UN	1-10
MaCH-Admix/minimac	R/geepack	FB	0
IMPUTE2	SNPTEST2	UN	1-3
MaCH/minimac	R/sandwich	UN	None
IMPUTE2	ProbABEL/SNPTEST2	CC	1-3
IMPUTE2	ProbABEL/SNPTEST2	CC	1-3
MaCH/minimac	R/sandwich	UN	1-2
MaCH/minimac	R/sandwich	UN	1-3
MaCH/minimac	R/sandwich	UN	None
MaCH/minimac	R/sandwich	UN	None
IMPUTE2	SNPTEST2	UN	1-3
MaCH/minimac	ProbABEL	UN	1-10

Other Covariates[2]
Field center
Field center
Clinic
Familial relationship
Field center, Chip
ID type (to identify different generations)
Field Center
Site
Geographic site of recruitment (region)
Geographic site of recruitment (region)
Field center
Field center
Clinic
Field Center
Site
Geographic site of recruitment (region)
Field center
Site
Site
Geographic site of recruitment (region)

Web Table 4: Genotyping, imputation, and statistical analysis for Stage 2 analysis.

Ancestry	Cohort	Genotyping Platform
European	**ASCOT-SC**	Illumina Human Omni Exome Express v8.1
	ASCOT-UK	Illumina Human Omni Exome Express v8.1
	BRIGHT	Affymetrix GeneChip 500k array
	DESIR-1	Illumina
	DHS	Affymetrix 5.0
	DR's EXTRA	Cardio-Metabo_Chip_11395247_A
	EGCUT-Human370CNV	Illumina HumanCNV370
	EGCUT-OmniExpress	Illumina OmniExpress
	EPIC	Affymetrix BioBank Axiom
	FENLAND-GWAS	Affymetrix SNP5.0
	FENLAND-OMICS	Affymetrix Axiom UKBiobank
	FUSION Case	Illumina HumanHap300
	FUSION Control	Illumina HumanHap300
	GeneSTAR	Illumina 1M_v1C
	GLACIER	Illumina CardioMetaboCHip
	GRAPHIC	HumanOmniExpress-12v1 array
	HRS	Illumina Omni2.5 Beadchip
	INGI-CARL	Illumina 370K
	INGI-FVG	Illumina 370K
	InterAct-CoreExome CASES	Illumina Human CoreExome-12v1 & 24v1
	InterAct-CoreExome SUBCOHORT	Illumina Human CoreExome-12v1 & 24v1
	InterAct-GWAS CASES	Illumina 660w quad chip
	InterAct-GWAS SUBCOHORT	Illumina 660w quad chip
	KORA_S3	Illumina Omni 2.5/Illumina Omni Express
	KORA_S4	Affymetrix Axiom
	LBC1936	Illumina 610-Quadv1
	LifeLines	Illumina Cyto SNP12 v2
	LOLIPOP-EW610	Illumina Human610
	LOLIPOP-EWA	Affymetrix 500K
	LOLIPOP-EWP	Perlegen custom
	Long Life Family Study (LLFS)	Illumina Omni 2.5
	METSIM	Illumina OmniExpress
	NESDA	Perlegen-Affymetrix 5.0; Affymetrix 6.0 907K
	OBA - French obese cases	Illumina Human CNV370-Duo
	PREVEND	Illumina HumanCyto SNP
	PROCARDIS	Illumina 1M+610K
	SHEEP	Illumina Cardiometabochip
	SHIP-0	Affymetrix Genome-wide Human SNP Array 6.0
	SHIP-Trend	Illumina HumanOmni2.5 BeadChip
	TWINGENE	Illumina OmniExpress bead chip
	YFS	Illumina 670k custom
African	**AA-DHS**	Illumina Omni5 array
	GeneSTAR	Illumina 1M_v1C

	HRS	Illumina Omni2.5 Beadchip
	HyperGEN-AXIOM	Affymetrix Axiom
	Loyola GxE	Illumina Metabochip
	Loyola SPT	Illumina Metabochip
Asian	**BBJ**	Illumina HumanOmniExpressExome OR HumanOmniE
	Beijing Eye Study (BES)-610	Illumina Human610-Quad Beadchips
	BES-omniexpress	Illumina OmniExpress
	CAGE-Amagasaki	Illumina 550K / Omni2.5M
	DF-TJ	Affymetrix 6.0
	LOLIPOP-IA317	Illumina Hap300K
	LOLIPOP-IA610-Case	Illumina Human610
	LOLIPOP-IA610-Control	Illumina Human610
	LOLIPOP-IAP	Perlegen custom
	LOLIPOP-OmniEE	Illumina OmniExpressExome Chip
	Ragama Health Study (RHS)	Illumina 550K / Omni2.5M
	SWHS/SMHS	Affymetrix 6.0, Illumina Omni Express, Illumina 550, Illu
Hispanic	**HCHS/SOL**	Omni 2.5M + custom array, Omni 2M Supplemental arı
	IRASC	Illumina OmniExpress+1S
	IRAS Family Study	Illumina OmniExpress+1S
Brazilian	**1982 Pelotas Birth Cohort Study**	Illumina HumanOmni 2.5-8v1
	Baependi Heart Study	Genome-wide SNP Human Array 6.0 (Affymetrix 6.0)

[1] Cohort unrelated (UN), family-based (FB), case-control (CC)

[2] Other than those specified in the analysis plan.

Imputation Software	Association Test	Study Design[1]
MaCH/minimac	ProbABEL	UN
MaCH/minimac	ProbABEL	UN
MaCH/minimac	ProbABEL	UN (hypertensive cases)
ShapeIt / Impute2	R	UN
IMPUTE2	GWAF	FB
MaCH/minimac	ProbABEL	UN
Impute2 converted to MACH format	ProbABEL/R	UN
Impute2 converted to MACH format	ProbABEL/R	UN
IMPUTE	QUICKTEST	UN
IMPUTE2	QUICKTEST	UN
IMPUTE2	QUICKTEST	UN
MaCH/minimac	ProbABEL	CC
MaCH/minimac	ProbABEL	CC
IMPUTE2	MMAP	FB
	QUICKTEST	UN
IMPUTE2	STATA	UN
IMPUTE2	ProbABEL	UN
IMPUTE2	ProbABEL	FB
IMPUTE2	ProbABEL	FB
IMPUTE2	QUICKTEST	case-cohort
IMPUTE2	QUICKTEST	case-cohort
IMPUTE2	QUICKTEST	case-cohort
IMPUTE2	QUICKTEST	case-cohort
IMPUTE v2.3.0	Snptest	UN
IMPUTE v2.3.0	Snptest	UN
Minimac	ProbABEL	UN
Minimac	Quicktest v0.95	UN
IMPUTE2	ProbABEL	UN
IMPUTE2	ProbABEL	UN
IMPUTE2	ProbABEL	UN
MACH and MINIMAC	MMAP	FB
MaCH/minimac	ProbABEL	UN
Minimac	Quicktest v0.95	UN
ShapeIt - Impute2	R	UN
IMPUTE2	R	UN
MaCH/minimac	STATA	CC
	PLINK	CC
IMPUTE v2.2.2	ProbABEL 0.4.3	UN
IMPUTE v2.2.2	ProbABEL 0.4.3	UN
MaCH/minimac	ProbABEL v 0.4.4	FB
IMPUTE2	R, sandwich	UN
IMPUTE2	sas proc reg	CC
IMPUTE2	MMAP	FB

IMPUTE2	ProbABEL	UN
MACH-ADMIX	ProbABEL	FB
MaCH/minimac	ProbABEL	UN
MaCH/minimac	ProbABEL	UN
MaCH/minimac	ProbABEL	UN
MaCH (UM imputation server)	ProbABEL	UN
MaCH (UM imputation server)	ProbABEL	UN
SHAPEIT/minimac3	sandwich package of R	UN
Mach/minimac	ProbABEL	UN
IMPUTE2	ProbABEL	UN
IMPUTE2	ProbABEL	CC
IMPUTE2	ProbABEL	CC
IMPUTE2	ProbABEL	UN
IMPUTE2	ProbABEL	UN
Beagle version 4 (r1399)	sandwich package of R	UN
MaCH/minimac	R	UN
SHAPEIT2 and IMPUTE2	GENESIS	FB
IMPUTE2	GWAF	UN
IMPUTE2	GWAF	FB
IMPUTE2 (version 2.3.0)	R (version 3.2.0)	UN
SHAPEIT and IMPUTE2	MMAP	FB

PCs Used	Other Covariates[2]
1-10	
1-10	
1-10	
5	
None	Diabetes Status
1	
4	
4	
1, 4	
1-4	
1-4	
5	
5	
1, 2	
4	FASTAMISS (GLACIER is a fasted cohort - individuals were asked to fast overnight. Indivic
None	
4	
None	
None	
1-4	
1-4	
1-4	
1-4	
0	
None	
4	
10	
1-5	
1-5	
1-5	
1	Field Center
5	
3	
5	Region (instead of FieldCentre)
1-10	
None	Study, Country of origin
None	
None	
None	
1-4	
4	Center
Admixture estimation instead of PC	
1, 2, 3, 5, 6	

4	
3	
1-3	
1-3	
10	46 (Affection status at registry)
NA	
NA	
None	
None	
1-5	
1-5	Cohort
1-5	Cohort
1-5	
1-5	Batch
10	
None	Genotyping platforms
1-5	Genetic subgroup (6 levels), heterogeneous residual variance by genetic subgroup, kinsh
Admixture estimation instead of PC	
Admixture estimat	Recruiting center
1, 2, 5, 9	
2	

duals who reported <8 hours fasting has been dealt with accordingly to the AP. In some participants, however, w

e did not have information on fasting information. We adjusted with a 0/1 dummy variable for missing fasting in

formation)

Web Table 5: Genomic control lambda values of cohorts used in Stage 1 analyses.

Ancestry	Cohort	HDL-C CurDrink		HDL-C RegDrink		LDL-C
		1 DF Int	2 DF Joint	1 DF Int	2 DF Joint	1 DF Int
European	AGES	1.027	1.07	1.03	1.065	1.03
	ARIC	0.976	0.997	1.039	1.027	1.004
	CARDIA	1.06	1.039	1.015	1.028	1.038
	CHS	1.001	1.024	1.023	1.036	1.006
	CROATIA-Korcula	1.024	1.038	1.03	1.035	1.035
	CROATIA-Vis	1.177	1.118	1.175	1.117	1.061
	ERF	1.006	0.949	0.98	0.941	0.994
	FamHS	1.029	1.055	1.037	1.06	1.016
	Framingham	0.86	0.949	0.95	0.992	0.979
	GENOA	1.022	1.045	1.034	1.042	1.021
	GS:SFHS	1.015	1.03	1.001	1.023	NA
	HABC	0.993	0.999	0.992	1.001	0.996
	HERITAGE	1.053	1.09	1.034	1.08	1.072
	HyperGEN	1.042	1.064	1.07	1.076	1.068
	MESA	1.017	1.027	0.999	1.033	1.013
	NEO	1.023	1.03	1.014	1.023	1.007
	RS1	1.019	1.03	1.004	1.024	1.028
	RS2	1.033	1.035	1.028	1.036	1.027
	RS3	1.02	1.018	1.013	1.022	1.038
	WGHS	1.01	1.035	0.987	1.023	1
	WHI-GARNET	1.019	1.031	1.021	1.032	1.019
	WHI-WHIMS	1.017	1.021	1.003	1.018	1.024
African	ARIC	1.088	1.048	1.125	1.064	0.998
	CARDIA	1.069	1.054	1.051	1.052	1.052
	CHS	1.02	1.037	1.087	1.064	1.045
	FamHS	1.087	1.137	1.06	1.114	1.096
	GENOA	1.057	1.075	1.08	1.076	1.058
	HABC	1.003	1.005	0.994	1.002	0.989
	HANDLS	1.061	1.058	NA	NA	1.046
	HUFS	1.011	1.031	1.028	1.038	1.015
	HyperGEN	1.037	1.051	1.055	1.056	1.038
	JHS	1.003	1.06	1.019	1.066	1.012
	MESA	1.006	1.03	1.008	1.023	1.026
	WHI	1.002	1.016	1.016	1.024	1.007
Asian	GenSalt	1.03	1.042	1.047	1.049	1.039
	MESA	1.029	1.043	1.098	1.072	1.022
	SCES	1.026	1.033	NA	NA	1.02
	SCHS-CHD:Cases	1.039	1.042	1.098	1.064	1.053
	SCHS-CHD:Controls	1.035	1.031	1.044	1.037	1.039
	SiMES	1.192	1.123	NA	NA	1.181
	SINDI	1.022	1.026	NA	NA	1.029
	SP2-1M	1.03	1.036	1.027	1.036	1.031
	SP2-610	1.03	1.043	1.023	1.04	1.041

Hispanic	**MESA**	1.148	1.118	1.066	1.069	0.985
	WHI	1.011	1.036	1.008	1.029	1.017

CurDrink	LDL-C RegDrink		TG CurDrink		TG RegDrink	
2 DF Joint	1 DF Int	2 DF Joint	1 DF Int	2 DF Joint	1 DF Int	2 DF Joint
1.042	1.031	1.039	1.035	1.057	1.038	1.059
1.018	1.001	1.022	0.993	1.016	1.007	1.024
1.028	1.019	1.023	1.066	1.039	1.032	1.033
1.021	1.014	1.021	1.026	1.032	1.011	1.021
1.064	1.039	1.068	1.042	1.041	1.04	1.042
1.057	1.066	1.058	1.03	1.05	1.025	1.047
0.955	1.013	0.96	1.02	0.995	1.023	0.999
1.034	0.999	1.029	1.037	1.055	1.045	1.059
1.004	1.017	1.02	0.993	1.011	0.973	1.001
1.044	1.029	1.049	1.021	1.038	1.036	1.04
NA	NA	NA	NA	NA	NA	NA
0.998	0.994	0.998	1.013	1.011	0.987	1
1.108	1.062	1.097	1.063	1.09	1.055	1.081
1.076	1.065	1.065	1.06	1.064	1.083	1.069
1.019	0.995	1.014	1.023	1.05	1.012	1.045
1.022	1.006	1.028	1.021	1.032	1.003	1.022
1.027	1.012	1.024	1.019	1.029	1.016	1.025
1.025	1.022	1.027	1.031	1.032	1.03	1.03
1.042	1.009	1.028	1.021	1.027	1.023	1.025
1.012	1.006	1.013	1.029	1.042	0.956	1.005
1.019	1.018	1.022	1.023	1.027	1.024	1.024
1.029	0.999	1.018	1.005	1.021	1.008	1.023
1.007	0.989	1.004	1.082	1.042	1.176	1.087
1.042	1.017	1.03	1.061	1.049	1.032	1.041
1.067	1.067	1.077	1.045	1.052	1.093	1.066
1.151	1.098	1.139	1.065	1.141	1.05	1.122
1.068	1.09	1.069	1.069	1.076	1.136	1.091
1.008	0.995	1.01	1.014	1.014	1.029	1.019
1.046	NA	NA	1.052	1.054	NA	NA
1.041	1.038	1.046	1.008	1.025	1.018	1.027
1.053	1.04	1.049	1.04	1.054	1.046	1.054
1.062	1.026	1.066	0.986	1.059	1.03	1.084
1.044	1.031	1.041	1.007	1.026	1.009	1.022
1.03	1.015	1.034	1	1.017	1.051	1.042
1.037	1.037	1.038	1.033	1.045	1.043	1.051
1.035	1.084	1.064	1.016	1.043	1.05	1.059
1.03	NA	NA	NA	NA	NA	NA
1.044	1.096	1.069	NA	NA	NA	NA
1.026	1.049	1.032	NA	NA	NA	NA
1.115	NA	NA	NA	NA	NA	NA
1.024	NA	NA	NA	NA	NA	NA
1.047	1.027	1.046	1.049	1.051	1.049	1.049
1.039	1.042	1.042	1.008	1.032	1.012	1.032

1.039	1.015	1.045	1.122	1.103	1.172	1.12
1.031	1.122	1.077	1.059	1.044	1.025	1.028

Web Table 6: Effect sizes and *P* -values of 147 genome-wide significant index variants f
lipid loci. Brazilian cohorts did not supply REGDRINK analyses. All *P* -value cells less tha
P.min shows the P-value for that model. Cells highlighted in red reflect P.min. For som
model combination may not have met one of the filtering thresholds, but all results ar

SNP	CHR	BP	REF	ALT	rsID	Nearest Gene	Known Locus
2:17890087:ID	2	17,890,087	R	I	rs201445483	*SMC6*	FALSE
2:53984823	2	53,984,823	A	G	rs2111622	*ASB3;GPR75-ASB3*	FALSE
3:185812169	3	185,812,169	C	G	rs80080062	*ETV5*	FALSE
4:951947	4	951,947	T	C	rs34311866	*TMEM175*	FALSE
4:124558378	4	124,558,378	A	G	rs143528679	*SPRY1;LINC01091*	FALSE
4:154190965	4	154,190,965	A	G	rs72729610	*TRIM2*	FALSE
5:132442190	5	132,442,190	T	G	rs56076449	*HSPA4;FSTL4*	FALSE
5:157999022	5	157,999,022	G	A	rs2963472	*LOC101927697;EBF1*	FALSE
7:137559799	7	137,559,799	T	C	rs73729083	*CREB3L2*	FALSE
8:6607634	8	6,607,634	C	G	rs2911971	*AGPAT5*	FALSE
9:78745177	9	78,745,177	G	A	rs7035578	*PCSK5*	FALSE
9:131513370	9	131,513,370	A	G	rs13284665	*ZER1*	FALSE
10:52573772	10	52,573,772	C	T	rs41274050	*A1CF*	FALSE
10:124693587	10	124,693,587	G	T	rs7904973	*C10orf88*	FALSE
11:63911273	11	63,911,273	C	A	rs190528931	*MACROD1*	FALSE
12:49755162	12	49,755,162	T	A	rs4898521	*DNAJC22;SPATS2*	FALSE
13:114544024	13	114,544,024	T	C	rs7140110	*GAS6-AS1*	FALSE
20:45604240	20	45,604,240	T	C	rs6063050	*EYA2*	FALSE
1:25764177	1	25,764,177	A	G	rs9438905	*TMEM57*	TRUE
1:27021913	1	27,021,913	G	C	rs114165349	*ARID1A*	TRUE
1:40060473	1	40,060,473	G	A	rs4660303	*PABPC4;HEYL*	TRUE
1:55505647	1	55,505,647	G	T	rs11591147	*PCSK9*	TRUE
1:63124465	1	63,124,465	T	G	rs4495740	*DOCK7*	TRUE
1:93817946	1	93,817,946	A	G	rs4847240	*DR1*	TRUE
1:109817192	1	109,817,192	A	G	rs7528419	*CELSR2*	TRUE
1:178529898	1	178,529,898	G	A	rs12753251	*C1orf220;MIR4424*	TRUE
1:182144422	1	182,144,422	T	C	rs1689788	*ZNF648;LINC01344*	TRUE
1:220970028	1	220,970,028	A	G	rs2642438	*MARC1*	TRUE
1:230295789	1	230,295,789	A	T	rs10127775	*GALNT2*	TRUE
1:234848609	1	234,848,609	G	A	rs486142	*LOC101927787;LINC01132*	TRUE
2:21289432	2	21,289,432	G	A	rs581411	*APOB;TDRD15*	TRUE
2:27598097	2	27,598,097	T	C	rs4665972	*SNX17*	TRUE
2:28657896	2	28,657,896	A	C	rs1111336	*FOSL2;PLB1*	TRUE
2:44072576	2	44,072,576	G	T	rs4299376	*ABCG8*	TRUE
2:62939397	2	62,939,397	G	A	rs360804	*EHBP1*	TRUE
2:118842801	2	118,842,801	T	A	rs55809639	*CCDC93;INSIG2*	TRUE
2:135837906	2	135,837,906	C	A	rs7570971	*RAB3GAP1*	TRUE
2:165528624	2	165,528,624	G	T	rs1128249	*GRB14;COBLL1*	TRUE

2:169830661	2	169,830,661	G	A	rs10176901	*ABCB11*	TRUE
2:211540507	2	211,540,507	C	A	rs1047891	*CPS1*	TRUE
2:227116365	2	227,116,365	A	G	rs2972143	*LOC646736;MIR5702*	TRUE
3:12266855	3	12,266,855	G	A	rs1584063	*SYN2;PPARG*	TRUE
3:50129399	3	50,129,399	C	T	rs2013208	*RBM5*	TRUE
3:135925191	3	135,925,191	T	A	rs1154988	*MSL2;PCCB*	TRUE
3:156797609	3	156,797,609	T	C	rs17451107	*LEKR1;LINC00880*	TRUE
4:3443931	4	3,443,931	A	G	rs13108218	*HGFAC*	TRUE
4:26050450:ID	4	26,050,450	R	D	rs10713774		TRUE
4:88022709	4	88,022,709	C	T	rs60695258	*AFF1*	TRUE
4:103198082	4	103,198,082	A	G	rs13135092	*SLC39A8*	TRUE
5:55808475	5	55,808,475	C	T	rs465002	*C5orf67*	TRUE
5:74745529:ID	5	74,745,529	R	D	rs200174418	*COL4A3BP*	TRUE
5:156484218	5	156,484,218	C	T	rs10066168	*HAVCR1*	TRUE
6:16131156	6	16,131,156	T	C	rs2235215	*MYLIP*	TRUE
6:26021872	6	26,021,872	C	T	rs41266779	*HIST1H4A;HIST1H3A*	TRUE
6:31840021	6	31,840,021	T	A	rs2763981	*SLC44A4*	TRUE
6:34592090	6	34,592,090	A	G	rs6907508	*C6orf106*	TRUE
6:41988742	6	41,988,742	G	A	rs56144648	*CCND3*	TRUE
6:43760327	6	43,760,327	C	G	rs11967262	*VEGFA;LINC01512*	TRUE
6:52626120	6	52,626,120	C	T	rs2749008	*GSTA2*	TRUE
6:100602753	6	100,602,753	G	A	rs9496567	*MCHR2-AS1;SIM1*	TRUE
6:116389636	6	116,389,636	G	A	rs13210143	*FRK;NT5DC1*	TRUE
6:127437100	6	127,437,100	T	A	rs9491694	*MIR588;RSPO3*	TRUE
6:139835399	6	139,835,399	C	G	rs2908522	*LINC01625;LOC100132735*	TRUE
6:161099503	6	161,099,503	G	A	rs5014650	*LPA;PLG*	TRUE
7:1067762:ID	7	1,067,762	R	D		*C7orf50*	TRUE
7:6479668	7	6,479,668	G	A	rs836546	*DAGLB*	TRUE
7:17914600	7	17,914,600	C	T	rs6461354	*SNX13*	TRUE
7:21611399	7	21,611,399	G	C	rs66476925	*DNAH11*	TRUE
7:25991826	7	25,991,826	T	C	rs4722551	*MIR148A;NFE2L3*	TRUE
7:44606217	7	44,606,217	C	G	rs217381	*DDX56*	TRUE
7:73012785	7	73,012,785	A	G	rs79624003	*MLXIPL*	TRUE
7:80344361	7	80,344,361	A	G	rs4470970	*CD36;SEMA3C*	TRUE
7:130424646	7	130,424,646	G	A	rs11762784	*KLF14;MIR29A*	TRUE
8:9183596	8	9,183,596	A	G	rs4841132	*LOC157273*	TRUE
8:11632528	8	11,632,528	A	G	rs1090107	*NEIL2*	TRUE
8:18273300	8	18,273,300	G	C	rs1495743	*NAT2;PSD3*	TRUE
8:19815556	8	19,815,556	A	G	rs287	*LPL*	TRUE
8:55421769	8	55,421,769	T	C	rs56204645	*SOX17;RP1*	TRUE
8:59336556	8	59,336,556	C	T	rs10957054	*UBXN2B*	TRUE
8:116630079	8	116,630,079	A	T	rs2737216	*TRPS1*	TRUE
8:121872464	8	121,872,464	A	C	rs10955992	*SNTB1;HAS2*	TRUE
8:126482077	8	126,482,077	A	G	rs2954021	*TRIB1;LINC00861*	TRUE
8:144300760	8	144,300,760	G	A	rs56960668	*GPIHBP1;ZFP41*	TRUE
9:15303583	9	15,303,583	G	A	rs1215112	*TTC39B*	TRUE
9:107665739	9	107,665,739	G	A	rs2575876	*ABCA1*	TRUE

9:136154867	9	136,154,867	G	T	rs495828	*ABO;SURF6*	TRUE
10:45952745	10	45,952,745	T	A	rs3802548	*MARCH8*	TRUE
10:64882300	10	64,882,300	C	G	rs10761716	*EGR2;NRBF2*	TRUE
10:94839724	10	94,839,724	G	T	rs4418728	*CYP26A1;MYOF*	TRUE
10:113950418	10	113,950,418	T	C	rs7096937	*GPAM;TECTB*	TRUE
11:13359745	11	13,359,745	T	A	rs2896635	*ARNTL*	TRUE
11:18653957	11	18,653,957	C	G	rs10832961	*SPTY2D1*	TRUE
11:47362465	11	47,362,465	G	C	rs10769254	*MYBPC3*	TRUE
11:49255042	11	49,255,042	C	T	rs658118	*FOLH1;LOC440040*	TRUE
11:51377255	11	51,377,255	C	T	rs11246533	*LOC646813;OR4A5*	TRUE
11:55451313	11	55,451,313	G	A	rs11230661	*OR4C6;OR5D13*	TRUE
11:61592362	11	61,592,362	A	G	rs174566	*FADS2*	TRUE
11:75473715	11	75,473,715	T	C	rs1806895	*LOC283214*	TRUE
11:116533167	11	116,533,167	G	C	rs509728	*LINC00900;BUD13*	TRUE
11:126250680	11	126,250,680	G	A	rs76970536	*ST3GAL4*	TRUE
12:7725904:ID	12	7,725,904	R	D			TRUE
12:20442785	12	20,442,785	G	C	rs78459082	*LOC100506393;PDE3A*	TRUE
12:57807114	12	57,807,114	T	C	rs540730	*R3HDM2;INHBC*	TRUE
12:109965512	12	109,965,512	C	G	rs10744826	*UBE3B*	TRUE
12:111865049	12	111,865,049	C	G	rs7310615	*SH2B3*	TRUE
12:121416988	12	121,416,988	A	G	rs2244608	*HNF1A*	TRUE
12:123830939	12	123,830,939	C	T	rs7298909	*SBNO1*	TRUE
12:125363987	12	125,363,987	C	A	rs57276302	*SCARB1;UBC*	TRUE
13:32976640:ID	13	32,976,640	R	D	rs753833181	*N4BP2L1*	TRUE
14:24872209	14	24,872,209	T	C	rs6573778	*NYNRIN*	TRUE
14:105272678	14	105,272,678	A	T	rs45490496	*ZBTB42;LINC00638*	TRUE
15:42679423	15	42,679,423	C	T	rs28364406	*CAPN3*	TRUE
15:43726625	15	43,726,625	A	C	rs150844304	*TP53BP1*	TRUE
15:44784375	15	44,784,375	T	A	rs28487964	*CTDSPL2*	TRUE
15:58674308	15	58,674,308	G	A	rs2043082	*AQP9;LIPC*	TRUE
15:63391362	15	63,391,362	G	C	rs76127683	*TPM1;LACTB*	TRUE
16:53822169:ID	16	53,822,169	R	D		*FTO*	TRUE
16:56985139	16	56,985,139	A	G	rs9989419	*HERPUD1;CETP*	TRUE
16:66944180	16	66,944,180	C	T	rs34621310	*CDH16*	TRUE
16:68016185	16	68,016,185	G	C	rs255056	*DPEP3;DPEP2*	TRUE
16:72097827	16	72,097,827	C	T	rs3794695	*HPR*	TRUE
16:81534790	16	81,534,790	T	C	rs2925979	*CMIP*	TRUE
17:37810218	17	37,810,218	C	G	rs881844	*STARD3*	TRUE
17:41874745	17	41,874,745	C	A	rs112259268	*C17orf105;MPP3*	TRUE
17:45732605	17	45,732,605	G	A	rs11870935	*KPNB1*	TRUE
17:64224775	17	64,224,775	C	T	rs8178824	*APOH*	TRUE
17:67136325	17	67,136,325	C	G	rs117753190	*ABCA6*	TRUE
17:76398058	17	76,398,058	C	G	rs8071884	*PGS1*	TRUE
18:47181668	18	47,181,668	A	T	rs2156552	*LIPG;ACAA2*	TRUE
18:57849429	18	57,849,429	C	T	rs58084604	*PMAIP1;MC4R*	TRUE
19:7222377	19	7,222,377	G	C	rs4804411	*INSR*	TRUE
19:8429323	19	8,429,323	G	A	rs116843064	*ANGPTL4*	TRUE

19:11187324	19	11,187,324	C	G	rs143020224	*SMARCA4;LDLR*	TRUE
19:19746151	19	19,746,151	G	T	rs2304128	*GMIP*	TRUE
19:33911705	19	33,911,705	T	C	rs57457691	*PEPD*	TRUE
19:45242173	19	45,242,173	G	A	rs1531517	*CEACAM16;BCL3*	TRUE
19:49218060	19	49,218,060	C	T	rs35866622	*MAMSTR*	TRUE
19:52314655	19	52,314,655	G	C	rs28873836	*FPR3*	TRUE
19:54800500	19	54,800,500	A	G	rs367070	*LILRA3*	TRUE
20:17845921	20	17,845,921	A	C	rs2328223	*BANF2;SNX5*	TRUE
20:33780985	20	33,780,985	T	C	rs4911477	*PROCR;MMP24*	TRUE
20:39906988	20	39,906,988	G	A	rs2050058	*ZHX3*	TRUE
20:43042364	20	43,042,364	C	T	rs1800961	*HNF4A*	TRUE
20:44551855	20	44,551,855	T	C	rs6073958	*PLTP;PCIF1*	TRUE
21:46271452	21	46,271,452	C	T	rs235314	*PTTG1IP*	TRUE
22:21977047	22	21,977,047	C	T	rs7445	*UBE2L3*	TRUE
22:38599767	22	38,599,767	C	G	rs4820323	*MAFF*	TRUE

rom combined Stage 1 and 2 analyses, including 129 index variants in published
n 5E-8 are highlighted in yellow. Model.min shows the most significant model, and
e variants, the smallest *P* -value may not be the value in P.min because the specific
e gathered here for this table.

P.min	Model.min	SNPEffect				
		EUR	AFR	ASN	HIS	BRA
4.68E-09	META.LDL.CurDrink.Joint2df	0.003	0.002	-0.009	0.028	0.005
7.89E-09	EUR.HDL.CurDrink.Joint2df	0.001	-0.002	0.000	-0.009	-0.009
1.11E-12	META.HDL.RegDrink.Joint2df	0.009	0.007	0.006	0.008	0.009
1.45E-11	EUR.TG.CurDrink.Joint2df	0.005	-0.022	0.005	0.018	-0.019
6.27E-09	AFR.LDL.CurDrink.Joint2df	-0.011	0.008	-0.015	-0.010	-0.021
5.64E-09	META.HDL.RegDrink.Joint2df	0.008	0.002	0.005	0.014	-0.002
9.34E-11	META.TG.RegDrink.Joint2df	-0.003	-0.002	0.002	-0.013	0.013
3.45E-08	EUR.TG.RegDrink.Joint2df	-0.003	-0.003	-0.002	-0.004	-0.010
8.19E-15	META.LDL.CurDrink.Joint2df	NA	0.010	0.006	0.012	0.035
7.50E-11	META.LDL.CurDrink.Joint2df	-0.005	-0.014	-0.002	-0.004	-0.007
1.19E-09	EUR.LDL.CurDrink.Joint2df	0.003	0.009	0.003	0.001	0.005
1.07E-08	EUR.LDL.CurDrink.Joint2df	0.003	0.040	0.006	0.000	0.029
9.60E-10	EUR.TG.RegDrink.Joint2df	-0.017	NA	NA	NA	-0.051
1.93E-15	META.LDL.CurDrink.Joint2df	0.000	0.002	-0.001	0.003	-0.006
1.85E-16	META.HDL.CurDrink.Joint2df	-0.012	-0.019	-0.005	0.000	-0.043
1.34E-08	EUR.HDL.RegDrink.Joint2df	0.014	-0.056	0.014	0.001	-0.038
3.38E-12	META.TG.CurDrink.Joint2df	0.004	0.006	-0.002	0.010	0.012
2.93E-08	META.TG.CurDrink.Joint2df	-0.003	-0.004	0.003	0.000	-0.010
9.29E-21	META.LDL.RegDrink.Joint2df	-0.001	-0.002	0.001	0.000	0.003
7.22E-156	EUR.HDL.CurDrink.Joint2df	-0.039	NA	-0.010	-0.019	-0.107
4.44E-27	META.HDL.CurDrink.Joint2df	-0.009	-0.007	-0.010	-0.022	-0.026
3.06E-176	EUR.LDL.RegDrink.Joint2df	0.015	NA	NA	NA	0.037
3.02E-130	META.TG.CurDrink.Joint2df	0.006	0.004	0.003	0.003	0.001
4.03E-31	META.HDL.CurDrink.Joint2df	0.007	0.011	0.008	0.005	0.014
0	EUR.LDL.CurDrink.Joint2df	-0.011	-0.007	-0.006	-0.017	0.005
7.06E-14	EUR.HDL.CurDrink.Joint2df	-0.008	0.004	-0.003	-0.009	-0.003
3.10E-22	META.HDL.CurDrink.Joint2df	0.008	0.003	0.007	0.008	0.016
1.54E-22	META.LDL.CurDrink.Joint2df	-0.010	0.002	-0.006	-0.005	-0.016
1.15E-58	META.HDL.RegDrink.Joint2df	-0.009	-0.014	-0.009	-0.006	-0.009
3.78E-36	META.LDL.CurDrink.Joint2df	0.001	0.010	0.003	0.004	0.006
1.60E-249	META.LDL.CurDrink.Joint2df	-0.002	0.001	0.006	0.007	0.000
0	META.TG.CurDrink.Joint2df	0.000	0.012	0.002	0.000	-0.006
3.02E-13	EUR.TG.RegDrink.Joint2df	0.003	-0.005	0.002	-0.001	0.016
2.48E-89	META.LDL.CurDrink.Joint2df	0.000	-0.005	-0.007	-0.003	0.003
5.59E-19	META.LDL.RegDrink.Joint2df	0.000	0.004	-0.002	0.003	-0.004
4.68E-16	META.LDL.CurDrink.Joint2df	0.003	-0.005	0.000	0.003	-0.012
9.56E-14	META.LDL.CurDrink.Joint2df	0.005	0.012	0.004	0.002	-0.002
2.94E-26	EUR.HDL.CurDrink.Joint2df	0.008	0.004	0.003	-0.003	0.002

7.71E-15	META.LDL.CurDrink.Joint2df	-0.005	0.000	-0.001	-0.004	0.004
3.19E-16	META.HDL.CurDrink.Joint2df	-0.007	-0.001	-0.006	-0.008	0.002
4.32E-31	META.HDL.CurDrink.Joint2df	0.006	0.004	0.005	0.004	0.014
7.38E-14	META.LDL.CurDrink.Joint2df	-0.003	0.001	-0.002	-0.001	0.000
2.55E-17	META.HDL.RegDrink.Joint2df	0.006	0.012	0.006	0.010	0.003
8.96E-17	EUR.HDL.RegDrink.Joint2df	-0.008	0.000	-0.001	-0.001	-0.012
9.42E-20	META.HDL.RegDrink.Joint2df	-0.005	-0.002	-0.003	-0.010	0.001
7.76E-29	META.TG.RegDrink.Joint2df	0.000	-0.002	-0.001	0.002	0.002
6.85E-09	META.HDL.CurDrink.Joint2df	-0.010	-0.012	-0.002	-0.004	-0.003
4.68E-36	META.TG.CurDrink.Joint2df	-0.005	-0.007	-0.005	-0.009	-0.004
1.69E-33	META.HDL.RegDrink.Joint2df	0.016	-0.005	0.017	0.017	0.013
1.27E-22	META.HDL.RegDrink.Joint2df	-0.008	-0.005	-0.006	-0.005	-0.001
0	EUR.LDL.CurDrink.Joint2df	0.004	0.000	0.006	-0.009	-0.010
0	EUR.LDL.RegDrink.Joint2df	0.001	0.001	0.000	0.004	-0.015
1.35E-30	EUR.LDL.CurDrink.Joint2df	0.000	0.002	-0.001	-0.003	0.000
7.83E-11	EUR.HDL.CurDrink.Joint2df	-0.012	0.021	NA	-0.023	0.019
2.98E-19	EUR.TG.CurDrink.Joint2df	0.002	0.000	0.003	0.010	-0.006
5.62E-13	META.HDL.CurDrink.Joint2df	0.009	0.021	0.012	0.013	0.019
6.95E-12	EUR.HDL.RegDrink.Joint2df	-0.005	0.001	0.002	-0.008	0.000
5.99E-34	META.TG.CurDrink.Joint2df	0.005	0.005	0.003	0.010	0.008
8.98E-14	META.TG.CurDrink.Joint2df	0.005	0.012	0.002	0.001	-0.002
8.66E-11	EUR.LDL.RegDrink.Joint2df	0.000	0.007	-0.004	0.001	0.002
2.59E-15	META.LDL.CurDrink.Joint2df	-0.004	-0.005	-0.009	-0.005	-0.003
1.33E-14	EUR.HDL.CurDrink.Joint2df	-0.008	-0.002	-0.001	-0.015	-0.005
2.23E-26	META.TG.RegDrink.Joint2df	-0.008	-0.007	-0.003	-0.007	0.006
1.56E-178	META.LDL.CurDrink.Joint2df	0.002	0.007	0.001	0.002	-0.011
1.73E-08	META.HDL.CurDrink.Joint2df	0.009	0.009	-0.004	0.000	0.018
6.87E-16	META.HDL.CurDrink.Joint2df	0.004	0.025	0.005	0.001	-0.003
3.74E-29	META.HDL.CurDrink.Joint2df	-0.009	-0.009	-0.005	-0.005	0.001
5.43E-27	META.LDL.CurDrink.Joint2df	0.000	-0.007	0.001	-0.002	0.006
2.22E-18	META.LDL.CurDrink.Joint2df	-0.004	0.006	-0.003	-0.010	0.000
2.41E-38	META.LDL.CurDrink.Joint2df	-0.005	-0.007	0.002	0.002	-0.006
9.03E-203	META.TG.CurDrink.Joint2df	-0.012	-0.006	-0.009	-0.011	-0.017
6.35E-51	META.HDL.RegDrink.Joint2df	0.000	0.016	NA	-0.075	0.024
5.65E-37	META.HDL.CurDrink.Joint2df	0.011	0.007	0.005	0.009	0.014
6.15E-114	META.HDL.CurDrink.Joint2df	-0.031	-0.034	-0.019	-0.025	-0.026
2.20E-13	EUR.TG.CurDrink.Joint2df	0.001	0.005	-0.002	0.001	0.003
3.08E-29	META.TG.CurDrink.Joint2df	0.001	-0.006	-0.001	-0.006	0.003
0	META.TG.CurDrink.Joint2df	-0.031	-0.023	-0.024	-0.031	-0.020
3.01E-20	EUR.LDL.CurDrink.Joint2df	0.000	0.006	0.003	0.007	-0.026
1.77E-30	META.LDL.CurDrink.Joint2df	0.000	0.003	-0.002	0.005	0.006
3.92E-32	META.HDL.CurDrink.Joint2df	-0.006	-0.004	-0.010	0.001	-0.015
7.38E-16	META.HDL.CurDrink.Joint2df	0.006	0.005	0.006	-0.001	0.005
9.35E-179	META.TG.CurDrink.Joint2df	-0.009	0.000	-0.004	-0.006	-0.004
8.01E-18	META.HDL.CurDrink.Joint2df	0.009	0.010	0.006	0.008	0.011
4.24E-41	META.HDL.RegDrink.Joint2df	0.015	0.004	0.010	0.009	0.001
5.93E-162	META.HDL.CurDrink.Joint2df	-0.017	-0.010	-0.021	-0.015	-0.013

9.84E-115	META.LDL.RegDrink.Joint2df	0.003	-0.011	0.006	0.000	0.005
3.41E-09	EUR.HDL.CurDrink.Joint2df	0.006	0.002	0.005	0.010	0.014
1.93E-29	META.TG.CurDrink.Joint2df	-0.002	-0.008	-0.001	-0.008	-0.003
7.15E-27	META.TG.CurDrink.Joint2df	0.006	0.014	0.005	0.003	-0.004
2.47E-32	META.HDL.CurDrink.Joint2df	0.009	0.006	0.008	0.011	0.019
1.85E-10	EUR.TG.RegDrink.Joint2df	-0.004	-0.005	0.000	-0.006	0.010
1.01E-12	EUR.LDL.CurDrink.Joint2df	0.001	-0.002	-0.002	0.002	0.003
4.81E-69	META.HDL.CurDrink.Joint2df	0.012	0.002	0.010	0.011	0.004
1.24E-49	EUR.HDL.CurDrink.Joint2df	0.015	0.001	0.002	0.010	-0.006
6.79E-11	EUR.HDL.RegDrink.Joint2df	0.012	-0.001	0.002	0.007	-0.009
7.60E-19	EUR.HDL.CurDrink.Joint2df	0.010	-0.008	0.010	0.007	-0.011
4.65E-68	META.TG.RegDrink.Joint2df	0.014	0.010	0.005	0.014	-0.001
1.75E-24	META.HDL.CurDrink.Joint2df	0.013	0.011	0.009	0.012	-0.003
0	EUR.HDL.CurDrink.Joint2df	-0.032	NA	-0.017	-0.024	-0.037
3.79E-26	EUR.LDL.CurDrink.Joint2df	-0.010	0.008	-0.001	-0.012	-0.019
3.97E-09	META.HDL.CurDrink.Joint2df	0.010	0.007	0.017	0.016	-0.008
7.73E-14	META.HDL.CurDrink.Joint2df	0.008	0.009	0.008	0.010	0.008
1.11E-20	META.HDL.CurDrink.Joint2df	0.011	0.003	0.006	0.004	-0.009
1.33E-29	META.HDL.CurDrink.Joint2df	-0.008	-0.009	-0.009	-0.011	-0.011
1.77E-12	META.LDL.CurDrink.Joint2df	-0.004	-0.005	-0.015	-0.008	-0.005
1.86E-28	EUR.LDL.CurDrink.Joint2df	-0.004	-0.003	-0.004	-0.007	-0.014
2.38E-31	META.HDL.CurDrink.Joint2df	-0.008	-0.015	-0.012	-0.007	-0.016
8.08E-49	META.HDL.CurDrink.Joint2df	0.011	0.019	0.016	0.011	0.010
3.99E-14	META.LDL.CurDrink.Joint2df	0.005	-0.001	-0.006	0.006	0.002
6.02E-21	META.LDL.CurDrink.Joint2df	0.003	0.000	0.004	0.002	-0.006
2.99E-20	META.HDL.CurDrink.Joint2df	0.008	0.010	0.005	0.005	0.021
2.10E-12	META.TG.RegDrink.Joint2df	-0.023	NA	0.012	-0.030	-0.017
3.44E-35	META.HDL.CurDrink.Joint2df	0.036	NA	-0.037	0.032	0.019
5.64E-16	EUR.HDL.RegDrink.Joint2df	-0.030	NA	0.002	-0.042	-0.040
0	META.HDL.CurDrink.Joint2df	0.025	0.018	0.024	0.024	0.022
1.50E-11	META.HDL.CurDrink.Joint2df	0.008	0.006	0.003	0.004	0.011
7.82E-10	EUR.HDL.RegDrink.Joint2df	-0.004	-0.002	-0.002	-0.003	0.001
0	EUR.HDL.CurDrink.Joint2df	-0.040	0.003	-0.019	-0.027	-0.015
2.33E-09	AFR.HDL.CurDrink.Joint2df	0.013	0.018	NA	-0.010	-0.037
2.22E-99	META.HDL.CurDrink.Joint2df	0.014	0.019	0.015	0.020	0.045
1.52E-59	META.LDL.CurDrink.Joint2df	-0.001	-0.018	0.002	0.006	0.005
1.00E-44	META.HDL.CurDrink.Joint2df	-0.012	-0.007	-0.009	-0.014	-0.010
6.16E-38	META.HDL.CurDrink.Joint2df	-0.009	-0.003	-0.004	-0.004	-0.013
1.38E-41	META.HDL.CurDrink.Joint2df	-0.035	NA	-0.028	-0.049	-0.045
4.83E-24	META.LDL.CurDrink.Joint2df	-0.007	0.001	-0.003	-0.001	-0.008
1.99E-15	META.LDL.CurDrink.Joint2df	-0.001	NA	0.011	0.009	0.009
3.24E-33	EUR.LDL.CurDrink.Joint2df	0.012	NA	NA	0.032	-0.042
4.49E-31	META.HDL.CurDrink.Joint2df	-0.009	-0.007	-0.005	-0.009	0.006
2.20E-121	META.HDL.CurDrink.Joint2df	-0.024	-0.011	-0.016	-0.020	0.001
4.97E-15	META.HDL.CurDrink.Joint2df	-0.007	-0.009	-0.006	-0.014	-0.015
7.97E-12	EUR.TG.CurDrink.Joint2df	-0.006	0.001	0.000	-0.004	0.010
7.38E-36	EUR.HDL.CurDrink.Joint2df	0.058	NA	-0.013	0.059	-0.014

0	EUR.LDL.CurDrink.Joint2df	-0.006	-0.005	0.003	-0.006	-0.012
0	EUR.LDL.RegDrink.Joint2df	0.000	0.003	-0.001	-0.008	-0.002
1.89E-13	EUR.HDL.CurDrink.Joint2df	-0.007	-0.003	-0.003	-0.002	-0.005
0	EUR.LDL.CurDrink.Joint2df	0.014	0.003	0.001	0.012	0.008
2.69E-30	META.LDL.CurDrink.Joint2df	-0.003	-0.001	0.004	0.002	0.009
1.39E-18	META.HDL.CurDrink.Joint2df	-0.007	-0.005	-0.006	0.001	0.012
1.01E-64	META.HDL.CurDrink.Joint2df	-0.013	-0.023	-0.007	-0.015	-0.014
2.67E-85	EUR.LDL.CurDrink.Joint2df	-0.001	0.002	0.001	0.003	0.000
3.25E-09	EUR.HDL.CurDrink.Joint2df	-0.008	0.009	-0.002	-0.002	-0.005
4.07E-46	META.LDL.CurDrink.Joint2df	0.001	-0.003	0.003	0.004	0.008
1.07E-71	META.HDL.CurDrink.Joint2df	-0.032	NA	-0.023	-0.043	-0.044
1.37E-69	META.HDL.CurDrink.Joint2df	0.012	0.020	0.008	0.013	0.001
1.56E-18	META.HDL.CurDrink.Joint2df	-0.004	-0.007	-0.006	-0.009	-0.011
1.37E-29	META.HDL.CurDrink.Joint2df	-0.006	-0.004	-0.008	-0.009	-0.012
1.49E-11	EUR.HDL.CurDrink.Joint2df	0.005	0.001	0.000	0.008	-0.007

				IntEffect			
META	**EUR**	**AFR**	**ASN**	**HIS**	**BRA**	**META**	**EUR**
0.003	0.002	-0.005	-0.001	-0.027	-0.022	-0.002	3.77E-01
-0.001	-0.007	0.002	-0.001	0.008	0.005	-0.004	7.89E-09
0.007	-0.001	-0.003	0.002	-0.008	-0.003	0.000	2.33E-10
0.005	0.001	0.029	-0.005	-0.007	0.040	0.001	9.59E-08
0.002	0.046	-0.002	-0.003	-0.007	0.017	-0.001	3.83E-01
0.007	-0.002	0.002	0.002	-0.016	0.013	-0.001	3.37E-07
-0.002	-0.002	-0.003	0.004	0.005	-0.011	-0.003	4.14E-07
-0.003	-0.004	-0.001	-0.002	-0.001	0.000	-0.004	1.99E-10
0.009	NA	0.006	0.004	-0.002	-0.053	0.003	NA
-0.003	0.002	0.017	0.002	0.007	0.025	0.002	2.61E-04
0.003	-0.002	-0.009	0.004	0.005	-0.003	-0.002	1.97E-01
0.005	-0.003	-0.043	-0.010	0.003	-0.023	-0.005	6.12E-01
-0.019	0.004	NA	NA	NA	0.062	0.008	1.77E-01
0.000	0.002	0.000	0.003	-0.002	0.011	0.003	1.53E-02
-0.011	0.000	-0.009	-0.014	-0.016	0.008	-0.002	7.22E-16
0.012	-0.002	0.061	-0.019	0.013	0.049	0.000	3.49E-08
0.001	-0.002	-0.002	0.000	-0.005	-0.007	0.000	5.54E-02
-0.001	0.000	0.001	-0.007	-0.004	0.001	-0.002	1.55E-03
0.000	0.000	0.003	-0.003	-0.009	-0.009	-0.002	5.49E-01
-0.035	-0.010	NA	-0.001	0.004	0.083	-0.013	7.22E-156
-0.010	0.001	-0.001	0.002	0.018	0.016	0.002	1.69E-17
0.016	-0.001	NA	NA	NA	-0.065	-0.002	8.39E-04
0.004	-0.002	0.010	-0.004	0.004	-0.004	-0.001	1.83E-05
0.008	0.001	-0.007	-0.001	0.001	0.003	-0.001	3.41E-17
-0.009	0.001	0.002	0.003	0.005	-0.018	-0.001	1.05E-28
-0.004	0.002	-0.006	-0.003	0.007	-0.006	-0.001	7.06E-14
0.008	-0.003	0.002	-0.001	-0.002	0.000	-0.002	4.22E-14
-0.007	0.003	0.002	-0.003	-0.004	0.004	0.000	2.74E-17
-0.009	-0.004	0.007	-0.002	0.000	0.009	-0.003	5.90E-48
0.002	0.002	-0.010	0.002	-0.001	-0.001	0.000	2.12E-02
0.001	-0.001	0.003	-0.005	-0.010	-0.008	-0.004	3.20E-02
0.001	-0.003	-0.007	-0.001	0.004	0.022	-0.003	3.22E-02
0.002	-0.003	0.000	0.002	0.001	-0.010	-0.001	4.38E-01
-0.003	0.000	0.004	0.011	0.002	0.015	0.003	9.88E-01
-0.001	0.003	-0.001	0.000	-0.004	0.007	0.002	2.02E-02
0.002	0.001	-0.024	0.027	0.001	0.017	0.002	6.49E-02
0.005	-0.001	-0.005	0.003	-0.002	0.012	-0.001	4.50E-04
0.005	0.001	0.001	-0.005	0.017	0.001	0.003	2.94E-26

-0.003	0.003	-0.004	0.001	-0.006	-0.007	0.000	1.25E-03
-0.006	0.000	-0.004	0.004	-0.001	0.005	0.000	9.96E-14
0.005	0.003	0.002	0.005	0.006	0.003	0.004	9.00E-26
-0.002	0.001	0.002	0.002	0.012	-0.002	0.001	9.31E-03
0.007	0.000	-0.007	-0.002	-0.011	-0.004	-0.002	4.15E-12
-0.004	-0.001	-0.006	-0.002	-0.007	-0.006	-0.004	9.96E-17
-0.004	-0.002	-0.004	-0.003	0.006	0.002	-0.002	1.57E-13
0.000	-0.001	0.005	0.000	-0.002	-0.001	0.000	8.87E-01
-0.008	0.003	0.005	0.005	0.000	0.008	0.002	3.64E-08
-0.006	0.001	0.010	-0.001	0.009	0.018	0.001	9.65E-09
0.016	0.003	0.027	0.002	-0.005	0.021	0.004	1.24E-29
-0.006	0.002	-0.005	0.000	0.002	0.000	0.000	1.60E-14
0.003	-0.004	0.004	0.001	0.007	0.022	-0.002	4.48E-01
0.001	-0.002	-0.002	-0.012	0.001	0.011	-0.002	7.29E-01
-0.001	0.001	0.002	0.001	0.002	0.009	0.001	9.27E-01
-0.011	0.002	-0.016	NA	0.009	-0.014	0.001	7.83E-11
0.003	-0.001	-0.004	-0.001	-0.009	0.022	-0.001	1.53E-01
0.010	0.000	-0.016	-0.010	-0.021	-0.029	-0.003	1.30E-12
-0.002	-0.002	-0.004	0.001	0.000	-0.005	-0.003	3.37E-10
0.004	0.002	0.008	0.007	0.004	-0.011	0.004	2.11E-16
0.004	0.000	0.001	-0.003	0.011	0.012	0.001	3.52E-07
-0.001	0.001	-0.014	0.007	0.005	-0.007	0.001	8.65E-01
-0.005	0.003	0.001	0.006	0.004	-0.005	0.004	1.11E-02
-0.005	0.002	-0.001	0.001	0.010	-0.014	0.000	1.33E-14
-0.005	0.001	0.000	0.002	0.001	-0.001	0.000	3.51E-15
0.002	0.006	-0.006	0.001	0.008	0.015	0.005	1.27E-09
0.006	-0.003	0.003	-0.006	0.004	-0.032	0.001	1.01E-08
0.005	0.003	-0.010	0.000	0.004	0.008	0.002	8.01E-12
-0.006	0.001	-0.001	-0.003	0.003	-0.008	-0.001	3.12E-22
0.001	0.000	-0.002	0.000	0.003	-0.019	-0.001	9.71E-01
-0.004	0.002	-0.007	0.006	0.012	-0.008	0.003	1.18E-01
-0.002	0.004	0.006	-0.008	-0.006	-0.007	0.001	1.33E-02
-0.010	-0.001	0.006	0.000	-0.004	0.013	-0.001	3.66E-21
0.013	0.016	0.006	NA	0.074	-0.021	0.006	3.00E-02
0.008	-0.002	0.003	-0.002	0.006	0.000	0.000	1.39E-31
-0.027	0.008	0.011	-0.003	-0.019	0.029	0.002	6.53E-79
0.000	-0.001	0.007	0.005	0.007	-0.018	0.001	6.91E-01
-0.001	-0.003	-0.003	0.003	0.006	-0.008	0.000	3.32E-01
-0.027	0.002	0.008	-0.008	0.008	-0.001	-0.002	2.87E-225
0.002	0.001	-0.007	-0.007	-0.008	0.026	-0.003	8.57E-01
-0.001	0.000	-0.003	-0.001	-0.006	-0.009	0.000	8.14E-01
-0.007	-0.002	-0.004	0.002	-0.010	0.010	-0.001	2.29E-20
0.006	-0.001	0.006	-0.001	0.008	0.001	0.000	2.32E-09
-0.006	-0.003	0.001	0.001	0.002	0.007	-0.004	3.14E-45
0.007	-0.003	0.005	-0.004	-0.005	-0.009	-0.002	8.08E-13
0.012	0.000	-0.002	0.001	-0.001	0.013	0.002	2.49E-37
-0.019	-0.001	0.007	-0.004	-0.003	-0.017	0.000	2.43E-81

0.004	0.001	0.008	-0.006	0.007	0.005	0.000	9.70E-04
0.006	-0.001	-0.005	-0.001	-0.003	-0.023	-0.001	3.41E-09
-0.002	-0.002	0.002	-0.001	-0.002	-0.004	-0.001	2.44E-04
0.006	-0.001	0.000	0.002	0.003	0.000	0.000	5.50E-09
0.009	-0.002	0.004	0.000	0.004	0.006	-0.001	1.78E-18
-0.002	0.000	-0.003	0.000	0.006	-0.008	-0.002	4.07E-06
-0.001	-0.003	0.000	-0.001	-0.003	0.008	-0.001	1.74E-01
0.012	0.000	0.003	-0.009	-0.016	-0.012	-0.005	6.01E-31
0.007	0.001	0.004	-0.004	-0.009	0.012	0.006	1.24E-49
0.005	-0.002	0.013	-0.006	-0.004	-0.007	0.001	5.88E-13
0.008	0.001	0.013	-0.009	-0.002	-0.002	0.001	7.60E-19
0.009	-0.003	0.007	-0.003	0.002	0.016	0.001	2.09E-48
0.010	-0.005	-0.001	-0.003	-0.009	-0.001	-0.003	5.00E-12
-0.030	-0.005	NA	-0.014	0.012	0.064	-0.007	0.00E+00
-0.004	0.001	-0.039	-0.003	0.001	0.023	-0.004	1.20E-08
0.012	-0.003	-0.003	0.001	-0.016	0.007	-0.006	1.88E-03
0.008	-0.003	0.007	-0.005	-0.006	-0.017	-0.003	1.82E-09
0.007	-0.003	0.002	-0.003	0.001	0.018	0.000	1.43E-20
-0.009	0.001	-0.002	0.005	0.003	0.012	0.002	6.40E-17
-0.006	0.000	-0.008	0.006	0.008	-0.002	0.001	5.32E-07
-0.005	0.000	0.004	0.002	-0.001	0.016	0.001	3.16E-05
-0.011	-0.004	0.009	0.005	-0.010	0.016	0.001	4.97E-15
0.014	0.001	0.005	-0.001	0.000	0.001	-0.001	6.21E-21
0.000	-0.002	-0.006	0.015	-0.006	0.000	0.003	1.13E-02
0.002	-0.003	-0.011	-0.001	-0.001	0.010	-0.003	2.71E-01
0.006	-0.001	0.001	0.003	0.003	-0.008	0.001	1.34E-13
-0.023	0.005	NA	-0.073	0.010	-0.017	0.004	1.40E-08
0.032	-0.003	NA	0.037	0.006	0.022	0.001	7.74E-33
-0.029	0.005	NA	-0.034	0.005	-0.018	0.003	2.58E-13
0.024	0.002	-0.001	0.003	-0.004	0.006	0.002	1.18E-218
0.006	-0.001	0.001	-0.005	0.003	0.000	0.000	2.12E-10
-0.003	-0.003	0.007	0.001	-0.006	-0.008	-0.002	4.97E-09
-0.026	-0.001	0.000	-0.015	-0.002	-0.002	-0.011	0.00E+00
0.013	-0.014	0.020	NA	0.010	0.061	0.016	8.72E-01
0.016	0.003	0.016	0.004	0.007	-0.014	0.003	2.03E-50
0.001	-0.001	0.021	-0.003	-0.010	-0.002	-0.002	3.82E-01
-0.010	0.004	-0.003	0.000	0.006	0.007	0.002	4.71E-28
-0.006	-0.002	-0.003	-0.001	-0.006	0.000	-0.004	4.38E-35
-0.036	-0.008	NA	-0.048	-0.029	-0.037	-0.009	3.19E-36
-0.004	0.004	-0.004	-0.002	0.000	0.004	0.000	4.54E-08
0.002	-0.003	NA	-0.045	-0.016	-0.050	-0.007	5.40E-01
0.012	-0.008	NA	NA	-0.030	0.050	-0.009	3.64E-02
-0.007	0.002	-0.005	-0.003	0.001	-0.019	-0.001	5.34E-22
-0.019	0.004	-0.027	-0.005	0.006	-0.041	-0.002	5.33E-92
-0.007	0.002	0.005	0.004	0.025	-0.001	0.003	8.28E-11
-0.002	0.002	0.000	-0.001	-0.001	-0.006	-0.001	2.73E-08
0.044	-0.009	NA	0.043	-0.032	0.074	0.003	7.38E-36

-0.004	-0.001	0.013	-0.012	0.002	0.009	-0.002	6.76E-06
-0.001	0.003	0.005	0.005	0.009	0.000	0.004	1.57E-01
-0.004	0.001	-0.004	0.001	-0.001	0.011	-0.001	1.89E-13
0.004	0.001	0.014	-0.002	-0.009	-0.007	0.005	6.20E-16
0.000	0.000	-0.002	-0.005	-0.001	-0.008	-0.002	2.23E-03
-0.006	-0.001	-0.008	0.004	-0.008	-0.020	-0.001	9.12E-16
-0.011	-0.004	0.009	-0.002	0.000	0.002	-0.005	1.58E-55
0.001	0.004	0.000	-0.001	-0.001	0.009	0.002	5.27E-02
-0.004	0.003	-0.011	0.000	0.005	0.005	0.000	3.25E-09
0.002	0.001	0.005	-0.006	0.003	-0.007	-0.001	3.26E-01
-0.031	-0.006	NA	-0.006	-0.026	-0.014	-0.009	2.40E-50
0.011	0.006	-0.001	0.003	-0.009	0.010	0.005	5.83E-57
-0.006	-0.001	0.002	-0.002	0.010	0.009	0.000	1.30E-09
-0.007	-0.002	0.002	-0.001	-0.003	0.011	-0.001	3.85E-15
0.002	0.001	-0.003	0.002	-0.003	0.002	0.003	1.49E-11

		HDL.CurDrink					
		PJoint					PI
AFR	ASN	HIS	BRA	META	EUR	AFR	ASN
7.52E-01	7.72E-01	1.81E-01	4.37E-01	6.44E-01	4.99E-01	3.02E-01	6.01E-01
7.76E-01	8.82E-01	8.51E-02	4.86E-01	1.52E-06	1.32E-02	9.04E-01	8.63E-01
2.13E-01	6.87E-02	4.51E-01	7.17E-01	1.03E-11	7.60E-01	6.17E-01	7.90E-01
1.76E-01	5.42E-02	1.38E-02	3.58E-02	2.07E-08	5.92E-01	1.33E-01	2.16E-01
4.01E-01	7.65E-01	3.62E-01	7.60E-01	9.23E-01	3.24E-01	8.13E-01	9.52E-01
8.87E-01	1.25E-01	1.44E-01	6.10E-01	5.96E-08	7.73E-01	8.06E-01	8.37E-01
5.30E-01	8.00E-02	1.53E-02	4.13E-01	3.87E-05	4.70E-01	5.29E-01	2.33E-01
5.00E-01	9.10E-02	2.21E-01	2.19E-01	6.54E-12	2.70E-02	7.38E-01	8.77E-01
4.29E-03	5.09E-01	4.39E-01	5.35E-01	2.58E-03	NA	5.61E-01	7.74E-01
6.02E-02	4.16E-01	5.39E-01	3.78E-02	5.08E-04	2.57E-01	1.04E-01	7.66E-01
2.76E-01	6.39E-01	5.19E-01	8.94E-01	6.22E-02	8.52E-01	1.90E-01	9.77E-01
4.63E-02	1.08E-01	8.92E-01	1.62E-01	6.44E-02	5.70E-01	1.04E-01	4.58E-02
NA	NA	NA	5.84E-01	1.74E-01	9.91E-01	NA	NA
6.49E-01	3.66E-01	7.86E-01	5.77E-01	6.32E-03	1.24E-01	9.78E-01	4.87E-01
4.45E-01	6.62E-01	4.96E-01	8.00E-02	1.85E-16	4.45E-01	8.19E-01	4.72E-01
5.89E-01	6.53E-01	7.77E-01	3.31E-01	2.17E-07	7.42E-01	4.65E-01	3.24E-01
5.22E-01	5.19E-01	5.32E-02	3.33E-01	1.54E-01	3.26E-01	7.80E-01	7.54E-01
4.78E-01	2.35E-01	6.92E-01	3.36E-01	1.30E-03	4.36E-01	9.62E-01	2.10E-01
8.18E-01	2.93E-01	3.92E-02	6.18E-01	1.50E-01	9.34E-01	5.71E-01	5.85E-01
NA	5.25E-01	7.75E-01	1.10E-02	4.09E-154	8.59E-01	NA	9.63E-01
5.34E-01	2.46E-07	2.67E-04	1.20E-02	4.44E-27	9.93E-01	7.43E-01	3.29E-01
NA	NA	NA	5.35E-01	1.14E-03	7.91E-01	NA	NA
1.57E-04	1.11E-01	1.13E-01	9.43E-01	2.28E-07	2.86E-01	6.61E-02	1.04E-01
2.06E-02	4.14E-12	1.14E-01	1.56E-02	4.03E-31	4.22E-01	4.03E-01	4.11E-01
6.54E-02	1.07E-02	3.72E-05	2.29E-01	2.55E-32	6.42E-01	8.72E-01	4.36E-02
5.20E-01	1.23E-03	7.52E-02	4.69E-01	5.04E-15	2.61E-01	3.10E-01	9.82E-01
3.58E-01	7.44E-07	4.10E-02	2.45E-02	3.10E-22	9.15E-02	9.07E-01	6.05E-01
7.68E-01	1.67E-05	1.39E-01	6.56E-02	1.36E-21	1.35E-01	6.18E-01	5.05E-01
5.06E-03	2.26E-10	8.67E-02	4.63E-01	8.59E-58	5.50E-02	4.31E-01	5.40E-01
1.21E-01	2.09E-02	5.34E-01	5.79E-01	2.62E-04	5.45E-01	3.89E-01	5.02E-01
5.96E-01	2.02E-01	2.18E-01	6.83E-01	4.38E-02	6.69E-01	8.95E-01	8.15E-01
1.20E-01	3.65E-01	5.03E-01	5.09E-02	1.62E-01	3.09E-01	3.09E-01	7.71E-01
3.63E-01	8.47E-02	9.47E-01	2.37E-01	2.56E-01	1.15E-01	8.92E-01	7.97E-01
4.71E-01	3.60E-03	8.31E-01	6.88E-02	7.84E-02	5.80E-01	4.93E-01	1.21E-01
4.54E-01	2.51E-01	7.41E-01	8.16E-01	8.64E-02	2.47E-01	9.85E-01	9.88E-01
1.86E-01	7.74E-02	8.52E-01	6.39E-01	5.27E-02	7.88E-01	2.38E-01	8.28E-02
3.49E-02	3.67E-01	8.79E-01	4.04E-01	4.21E-05	8.16E-01	2.31E-01	6.84E-01
1.83E-01	3.13E-01	5.72E-04	9.12E-01	8.36E-25	7.80E-01	9.51E-01	1.84E-01

4.87E-01	5.51E-01	1.85E-02	8.00E-01	3.91E-04	9.76E-02	2.92E-01	3.69E-01
5.10E-01	2.57E-03	1.26E-02	6.82E-01	3.19E-16	7.59E-01	4.36E-01	1.26E-01
1.96E-01	6.85E-04	5.23E-02	1.81E-02	4.32E-31	1.59E-01	5.93E-01	2.28E-01
7.44E-01	2.08E-01	1.80E-02	9.72E-01	1.66E-02	4.20E-01	5.87E-01	3.76E-01
1.24E-03	1.76E-03	4.32E-02	8.99E-01	4.88E-17	9.15E-01	6.59E-02	4.08E-01
3.98E-01	4.02E-01	2.08E-01	4.23E-02	4.17E-16	9.04E-01	3.60E-01	5.98E-01
1.59E-01	2.70E-03	1.46E-02	9.46E-01	5.46E-17	3.19E-01	3.00E-01	2.83E-01
7.15E-01	4.14E-01	8.99E-01	9.72E-01	7.44E-01	5.65E-01	1.45E-01	7.28E-01
8.83E-03	7.78E-01	5.40E-01	8.68E-01	6.85E-09	9.19E-01	3.72E-01	6.87E-01
1.37E-01	6.65E-05	8.62E-02	1.49E-01	1.10E-12	7.77E-01	7.63E-02	9.55E-01
4.24E-01	8.15E-01	7.41E-02	3.88E-02	2.40E-31	4.15E-01	3.85E-01	9.70E-01
6.47E-03	2.01E-06	3.74E-01	9.90E-01	4.08E-21	6.87E-01	3.67E-01	4.86E-01
8.12E-01	5.44E-01	8.31E-01	5.13E-01	4.78E-01	2.66E-01	6.17E-01	9.86E-01
9.53E-01	1.39E-01	6.30E-01	4.26E-01	5.93E-01	3.22E-01	6.90E-01	1.22E-01
4.38E-01	7.68E-01	7.49E-01	4.29E-01	6.52E-01	9.03E-01	5.91E-01	1.00E+00
3.77E-01	NA	1.49E-01	7.41E-01	6.46E-10	8.04E-01	4.46E-01	NA
8.11E-01	2.89E-01	2.00E-01	2.51E-01	2.96E-02	5.39E-01	7.84E-01	8.01E-01
1.04E-01	2.30E-01	1.76E-01	3.06E-01	5.62E-13	9.17E-01	3.06E-01	3.02E-01
9.43E-01	4.72E-01	1.01E-01	8.27E-01	2.11E-08	3.59E-01	6.90E-01	6.72E-01
6.94E-03	1.04E-06	5.63E-05	5.66E-01	6.95E-26	2.02E-01	1.27E-01	6.81E-02
7.35E-02	3.19E-01	3.54E-02	4.27E-01	5.05E-08	8.17E-01	8.19E-01	4.54E-01
1.12E-01	2.18E-01	4.08E-01	8.11E-01	7.41E-01	4.00E-01	2.99E-02	4.65E-02
2.83E-01	1.35E-03	4.47E-01	5.12E-01	1.34E-05	6.17E-02	7.74E-01	2.26E-01
6.72E-01	6.47E-01	5.06E-04	4.28E-02	6.37E-13	3.33E-01	9.05E-01	9.82E-01
2.55E-02	1.21E-01	4.13E-02	6.34E-01	2.45E-15	3.91E-01	9.78E-01	4.55E-01
2.37E-01	8.86E-01	1.90E-01	3.69E-01	1.06E-09	6.37E-03	3.17E-01	6.75E-01
6.06E-03	5.39E-01	7.20E-01	1.15E-01	1.73E-08	4.62E-01	7.58E-01	4.52E-01
2.00E-04	7.26E-04	6.48E-01	8.41E-01	6.87E-16	2.16E-01	1.60E-01	7.66E-01
5.25E-03	3.06E-07	4.07E-01	6.75E-01	3.74E-29	5.87E-01	4.64E-01	9.78E-01
1.55E-01	6.08E-01	9.19E-01	3.76E-01	8.47E-01	4.37E-01	8.60E-01	8.73E-01
8.12E-01	5.01E-01	1.88E-01	7.17E-01	4.63E-02	2.71E-01	6.96E-01	4.02E-01
1.06E-01	1.42E-01	5.26E-01	1.31E-01	5.22E-02	2.94E-02	5.52E-01	1.21E-01
6.02E-01	4.37E-05	5.07E-02	4.56E-01	2.04E-25	8.40E-01	5.69E-01	8.00E-01
4.80E-08	NA	2.85E-01	5.55E-01	1.79E-08	1.61E-01	4.45E-01	NA
2.40E-02	4.83E-04	1.65E-05	4.45E-02	5.65E-37	2.37E-01	9.72E-01	3.06E-01
2.66E-14	3.56E-08	7.19E-23	1.51E-01	6.15E-114	1.72E-02	1.51E-01	9.42E-01
1.16E-02	2.61E-01	1.26E-01	1.15E-01	5.76E-01	3.53E-01	1.65E-01	5.55E-01
9.93E-03	5.42E-01	3.54E-01	7.56E-01	3.33E-01	1.47E-01	5.81E-01	8.11E-02
3.05E-13	1.68E-79	2.06E-17	2.89E-03	8.10267659	2.59E-01	1.32E-01	9.84E-01
3.81E-01	2.82E-02	4.19E-01	6.19E-02	1.61E-01	4.62E-01	3.96E-01	2.18E-02
8.24E-01	1.62E-01	4.85E-01	7.30E-01	4.71E-01	9.37E-01	5.73E-01	3.99E-01
5.20E-02	4.00E-12	5.98E-02	7.75E-02	3.92E-32	2.72E-01	1.95E-01	2.76E-01
1.28E-02	7.02E-06	1.48E-01	5.47E-01	7.38E-16	7.72E-01	2.65E-01	9.79E-01
9.56E-01	1.52E-03	1.55E-01	8.17E-01	5.28E-39	1.45E-01	8.25E-01	6.45E-01
9.22E-03	1.15E-04	9.57E-02	4.70E-01	8.01E-18	3.12E-01	5.67E-01	3.01E-01
6.98E-01	4.70E-03	1.94E-01	3.65E-01	8.16E-38	9.37E-01	8.78E-01	6.30E-01
3.54E-02	8.88E-80	1.35E-07	2.73E-04	5.93E-162	5.28E-01	5.21E-01	6.29E-01

6.27E-02	8.97E-04	3.94E-01	4.42E-01	4.70E-05	4.10E-01	4.56E-01	4.21E-02
7.42E-01	2.50E-02	1.97E-02	1.40E-01	4.29E-11	9.69E-01	3.29E-01	7.40E-01
2.45E-02	3.57E-01	1.27E-02	6.28E-01	2.41E-06	3.06E-01	5.87E-01	8.38E-01
2.97E-06	1.55E-06	2.89E-01	7.99E-01	5.95E-17	8.42E-01	8.59E-01	9.42E-01
1.59E-02	4.97E-08	4.87E-05	3.36E-04	2.47E-32	2.80E-01	6.65E-01	6.39E-01
1.26E-01	9.97E-01	2.52E-01	5.09E-01	4.69E-05	6.46E-01	6.95E-01	7.51E-01
7.44E-01	1.13E-01	8.34E-01	3.36E-01	7.56E-02	1.67E-01	7.03E-01	4.94E-01
3.90E-01	1.02E-48	1.03E-02	6.66E-01	4.81E-69	8.88E-01	9.08E-01	1.86E-01
3.94E-01	4.96E-01	2.06E-01	8.48E-01	1.42E-39	9.52E-01	3.53E-01	5.12E-01
4.07E-01	1.59E-01	5.65E-01	3.96E-01	1.33E-07	7.17E-01	2.86E-01	1.37E-01
4.87E-01	4.19E-02	4.13E-01	4.64E-01	9.91E-18	6.94E-01	2.84E-01	2.20E-01
1.73E-05	2.27E-03	2.85E-06	1.36E-01	2.92E-50	3.91E-01	2.47E-01	1.75E-01
4.15E-04	3.59E-10	5.44E-02	8.88E-01	1.75E-24	2.51E-01	9.68E-01	2.52E-01
NA	2.63E-02	1.76E-01	3.62E-01	0.00E+00	8.58E-01	NA	5.36E-01
2.56E-01	2.86E-01	1.78E-01	7.10E-01	1.51E-07	6.42E-01	9.07E-02	2.71E-01
1.32E-01	1.28E-05	7.72E-03	8.84E-01	3.97E-09	6.24E-01	9.55E-01	7.57E-01
1.19E-01	3.78E-04	7.98E-02	4.07E-01	7.73E-14	7.22E-01	4.51E-01	1.48E-01
2.02E-01	1.65E-02	3.40E-01	2.50E-01	1.11E-20	1.43E-01	4.29E-01	5.19E-01
1.18E-03	5.57E-09	1.14E-03	2.86E-01	1.33E-29	7.19E-01	6.32E-01	1.49E-01
8.35E-02	5.12E-03	2.08E-01	5.52E-01	2.30E-09	9.06E-01	3.18E-01	5.14E-01
7.99E-01	1.20E-03	4.34E-02	2.50E-01	3.57E-09	9.69E-01	5.64E-01	2.80E-01
2.38E-02	2.70E-15	4.53E-03	3.04E-01	2.38E-31	2.12E-01	2.89E-01	1.37E-02
3.42E-02	2.78E-27	6.11E-02	4.52E-01	8.08E-49	6.52E-01	8.31E-01	7.72E-01
3.96E-01	6.06E-04	3.28E-01	9.21E-01	6.73E-02	7.49E-01	5.65E-01	9.80E-03
5.37E-02	9.74E-02	8.98E-01	6.06E-01	8.59E-02	1.09E-01	8.40E-02	3.83E-01
1.59E-02	3.22E-04	5.05E-02	8.86E-03	2.99E-20	4.84E-01	7.24E-01	5.05E-01
NA	2.46E-01	4.56E-03	1.02E-01	3.17E-11	3.73E-01	NA	1.25E-01
NA	4.85E-01	1.70E-04	5.34E-02	3.44E-35	3.72E-01	NA	4.41E-01
NA	3.38E-01	3.23E-04	6.23E-03	1.46E-17	4.33E-01	NA	1.50E-01
1.73E-09	7.21E-105	5.21E-14	3.38E-05	0.00E+00	2.18E-01	8.28E-01	7.31E-01
6.00E-02	4.33E-01	2.42E-01	2.73E-01	1.50E-11	9.17E-01	8.86E-01	2.96E-01
3.41E-01	6.69E-01	9.08E-02	6.38E-01	3.45E-08	2.19E-01	3.01E-01	9.99E-01
4.16E-01	1.82E-32	5.02E-23	9.19E-03	0.00E+00	4.87E-01	9.46E-01	6.09E-01
2.33E-09	NA	8.43E-01	4.96E-01	3.93E-07	6.63E-01	8.53E-03	NA
5.25E-19	3.73E-24	2.75E-11	1.52E-06	2.22E-99	1.99E-01	3.92E-03	6.98E-01
6.36E-03	2.76E-01	3.25E-01	8.56E-01	2.75E-01	6.34E-01	5.53E-03	4.10E-02
3.88E-03	2.22E-14	3.93E-03	5.40E-01	1.00E-44	1.18E-01	3.78E-01	4.19E-01
2.39E-01	5.16E-04	1.27E-02	5.14E-02	6.16E-38	3.45E-01	9.63E-01	8.81E-01
NA	1.82E-02	6.91E-05	3.13E-02	1.38E-41	2.54E-01	NA	2.87E-01
7.02E-01	2.12E-02	9.32E-01	4.69E-01	7.39E-08	1.30E-01	5.41E-01	6.28E-01
NA	7.08E-01	5.80E-01	1.30E-01	2.95E-01	3.57E-01	NA	4.25E-01
NA	NA	2.55E-01	5.98E-01	2.78E-02	2.36E-01	NA	NA
6.89E-04	2.09E-06	6.22E-03	1.36E-01	4.49E-31	5.79E-01	2.44E-01	1.02E-01
2.60E-04	2.00E-28	2.52E-03	7.27E-04	2.20E-121	1.90E-01	6.36E-02	3.32E-01
4.27E-02	3.22E-04	1.56E-03	9.47E-02	4.97E-15	6.08E-01	3.90E-01	7.79E-02
8.66E-01	6.50E-01	2.55E-01	3.70E-01	6.96E-06	2.32E-01	7.50E-01	4.97E-01
NA	3.77E-01	4.36E-03	2.98E-01	1.54E-34	1.48E-01	NA	1.61E-01

4.78E-01	3.38E-01	5.81E-01	7.13E-01	1.92E-05	9.48E-01	1.78E-01	3.20E-01
2.20E-01	4.37E-01	3.96E-01	9.70E-01	3.51E-02	7.41E-01	6.15E-01	3.18E-01
9.50E-02	5.93E-02	5.25E-01	5.48E-01	3.07E-13	7.03E-01	5.39E-01	3.87E-01
5.80E-04	8.17E-01	2.40E-01	8.58E-01	1.73E-10	7.92E-01	2.10E-02	7.22E-01
8.29E-01	2.03E-01	8.21E-01	5.46E-01	1.59E-02	9.56E-01	8.29E-01	2.54E-01
2.30E-02	1.94E-04	1.82E-01	2.00E-01	1.39E-18	4.60E-01	2.65E-01	8.28E-02
1.43E-05	6.80E-06	1.31E-05	2.27E-01	1.01E-64	1.21E-01	3.50E-01	9.95E-01
8.41E-01	8.62E-01	7.64E-01	6.29E-01	8.51E-02	1.29E-01	8.15E-01	7.25E-01
1.20E-01	4.35E-01	5.81E-01	8.20E-01	4.17E-06	8.34E-02	1.25E-01	6.41E-01
6.64E-01	8.90E-02	1.37E-01	6.09E-01	8.25E-02	7.80E-01	2.76E-01	1.89E-01
NA	4.32E-07	3.68E-17	1.32E-04	1.07E-71	2.85E-01	NA	7.82E-01
1.93E-11	2.71E-07	3.78E-02	4.44E-01	1.37E-69	4.25E-02	8.44E-01	9.94E-01
2.89E-02	2.07E-08	6.36E-02	3.29E-01	1.56E-18	4.86E-01	8.84E-01	9.42E-01
6.38E-01	3.91E-13	8.63E-04	4.26E-01	1.37E-29	1.55E-01	7.27E-01	5.84E-01
8.53E-01	5.60E-01	5.08E-02	5.17E-01	1.81E-09	6.34E-01	8.90E-01	7.76E-01

nt						PMain	
HIS	BRA	META	EUR	AFR	ASN	HIS	BRA
2.65E-01	3.02E-01	4.50E-01	6.55E-01	6.76E-01	5.28E-01	6.50E-02	7.72E-01
1.16E-01	6.15E-01	3.22E-01	4.11E-01	5.24E-01	4.56E-01	2.68E-02	3.57E-01
3.32E-01	5.56E-01	3.99E-01	2.28E-04	1.33E-01	8.44E-02	2.15E-01	5.40E-01
5.80E-01	4.04E-02	9.83E-01	1.60E-02	7.11E-02	2.20E-02	1.03E-02	1.13E-01
6.71E-01	6.53E-01	9.06E-01	7.84E-01	2.56E-01	5.85E-01	4.58E-01	4.70E-01
1.09E-01	4.06E-01	7.39E-01	5.25E-04	7.98E-01	7.20E-02	4.73E-02	8.20E-01
5.68E-01	3.81E-01	8.81E-01	1.08E-01	6.01E-01	3.79E-01	1.13E-02	3.47E-01
9.53E-01	8.92E-01	1.22E-01	8.23E-02	4.42E-01	2.54E-01	2.73E-01	2.32E-01
8.57E-01	2.81E-01	6.95E-01	NA	5.76E-02	4.85E-01	3.14E-01	4.20E-01
2.91E-01	3.28E-02	7.81E-02	2.04E-03	2.01E-02	3.21E-01	3.76E-01	4.47E-01
5.33E-01	4.06E-01	8.64E-01	1.64E-01	1.13E-01	6.59E-01	8.53E-01	6.13E-01
7.44E-01	2.38E-01	8.15E-02	3.38E-01	1.29E-02	7.91E-02	9.84E-01	6.46E-02
NA	3.14E-01	7.74E-01	2.58E-01	NA	NA	NA	3.24E-01
8.19E-01	3.15E-01	1.07E-01	8.70E-01	5.17E-01	9.43E-01	4.70E-01	4.13E-01
6.03E-01	8.18E-01	3.20E-01	3.63E-04	5.33E-01	7.65E-01	9.74E-01	1.19E-01
6.10E-01	1.72E-01	6.26E-01	6.63E-04	3.04E-01	3.68E-01	9.80E-01	1.57E-01
4.51E-01	6.51E-01	3.97E-01	8.43E-02	2.84E-01	2.45E-01	2.66E-02	1.87E-01
4.59E-01	6.94E-01	1.81E-01	6.98E-02	3.39E-01	6.83E-01	9.35E-01	2.33E-01
5.51E-02	5.55E-01	4.23E-01	6.20E-01	5.67E-01	6.70E-01	9.37E-01	8.63E-01
9.92E-01	8.59E-02	7.27E-01	4.72E-07	NA	3.86E-01	5.49E-01	3.64E-03
1.21E-02	1.70E-01	2.34E-01	2.64E-06	4.90E-01	4.92E-07	5.71E-05	3.09E-03
NA	2.65E-01	6.60E-01	1.16E-01	NA	NA	NA	4.18E-01
5.29E-01	9.53E-01	3.81E-01	5.75E-04	2.00E-01	2.04E-01	3.47E-01	9.47E-01
9.33E-01	7.12E-01	9.44E-01	4.95E-05	7.10E-03	5.78E-09	1.43E-01	7.47E-02
4.94E-01	8.00E-02	1.92E-01	1.45E-09	4.46E-02	1.94E-02	1.70E-04	5.61E-01
2.11E-01	3.99E-01	4.57E-01	4.51E-07	3.09E-01	7.85E-03	2.31E-02	7.09E-01
7.01E-01	6.33E-01	1.10E-01	2.90E-07	4.75E-01	3.36E-04	4.41E-02	7.35E-02
4.79E-01	8.63E-01	6.09E-01	3.38E-07	6.55E-01	6.89E-04	3.48E-01	7.16E-02
8.24E-01	2.19E-01	1.23E-01	6.88E-09	4.00E-03	1.81E-07	8.91E-02	2.39E-01
6.68E-01	9.13E-01	6.03E-01	7.52E-01	3.67E-02	7.22E-02	3.10E-01	4.39E-01
9.51E-02	3.55E-01	3.06E-01	3.85E-01	7.92E-01	4.24E-01	1.24E-01	9.00E-01
5.75E-01	2.85E-02	4.93E-01	7.73E-01	5.34E-02	1.91E-01	9.78E-01	4.43E-01
7.92E-01	4.00E-01	3.71E-01	1.97E-01	2.92E-01	1.68E-01	7.73E-01	1.12E-01
8.26E-01	1.75E-01	1.53E-01	1.00E+00	2.44E-01	8.84E-02	5.51E-01	7.49E-01
5.28E-01	4.15E-01	5.47E-01	9.81E-01	3.23E-01	1.92E-01	4.77E-01	7.64E-01
7.46E-01	7.23E-01	5.46E-01	3.22E-01	7.36E-01	9.78E-01	7.22E-01	2.54E-01
7.26E-01	4.88E-01	7.12E-01	4.68E-03	1.91E-02	3.92E-01	6.15E-01	8.28E-01
7.02E-04	4.30E-01	4.03E-01	1.15E-06	2.58E-01	1.88E-01	4.76E-01	8.54E-01

2.49E-01	3.56E-01	3.48E-01	3.95E-03	8.78E-01	1.14E-01	3.11E-01	8.05E-01
7.17E-01	7.32E-01	5.18E-01	4.72E-05	8.40E-01	1.72E-03	5.94E-02	9.00E-01
2.95E-01	7.57E-01	4.72E-02	7.09E-05	3.02E-01	7.29E-02	3.14E-01	1.88E-01
2.90E-02	8.50E-01	7.14E-02	8.26E-02	8.28E-01	1.60E-01	8.02E-01	9.90E-01
5.61E-02	9.84E-01	1.27E-01	1.54E-04	7.01E-04	2.94E-03	1.20E-02	6.59E-01
2.99E-01	8.44E-01	3.20E-01	6.58E-05	8.93E-01	2.92E-01	8.81E-01	1.65E-01
3.53E-01	6.02E-01	1.95E-01	3.71E-03	4.98E-01	5.34E-02	7.32E-03	8.23E-01
8.35E-01	8.67E-01	7.31E-01	7.81E-01	6.49E-01	3.47E-01	6.51E-01	8.02E-01
9.69E-01	6.22E-01	5.31E-01	1.02E-04	6.84E-03	6.23E-01	4.10E-01	7.90E-01
9.39E-02	7.84E-02	3.49E-01	8.01E-04	5.60E-02	2.47E-04	2.77E-02	5.37E-01
6.60E-01	3.88E-01	3.69E-01	1.79E-07	8.32E-01	6.46E-01	5.62E-02	3.21E-01
8.75E-01	7.32E-01	7.53E-01	2.96E-06	1.35E-01	1.18E-04	2.16E-01	9.39E-01
6.65E-01	2.70E-01	6.04E-01	2.16E-01	9.66E-01	3.75E-01	5.43E-01	5.25E-01
9.00E-01	6.32E-01	1.91E-01	5.68E-01	7.72E-01	8.71E-01	5.67E-01	1.36E-01
7.40E-01	8.55E-01	7.36E-01	8.37E-01	6.09E-01	4.23E-01	4.49E-01	8.96E-01
3.63E-01	9.36E-01	7.85E-01	5.73E-05	1.46E-01	NA	1.03E-01	4.06E-01
1.74E-01	1.89E-01	4.04E-01	1.87E-01	9.61E-01	4.55E-01	7.53E-02	6.56E-01
7.68E-02	9.16E-02	3.25E-01	7.32E-05	2.48E-02	8.43E-02	1.23E-01	2.40E-01
8.92E-01	7.63E-01	4.94E-01	7.65E-03	9.41E-01	6.53E-01	1.24E-01	9.42E-01
4.80E-01	3.80E-01	1.27E-02	1.31E-03	2.14E-01	1.33E-02	7.74E-03	2.71E-01
9.64E-02	2.29E-01	7.26E-01	3.65E-03	1.09E-01	3.17E-01	8.56E-01	8.34E-01
3.87E-01	6.70E-01	3.23E-01	8.54E-01	1.56E-01	3.89E-01	8.01E-01	7.94E-01
4.01E-01	9.68E-01	2.27E-02	4.80E-03	1.69E-01	4.70E-04	2.00E-01	7.16E-01
2.92E-02	6.85E-02	2.86E-01	1.68E-06	7.23E-01	4.56E-01	1.48E-04	4.96E-01
7.46E-01	8.62E-01	2.55E-01	1.19E-06	4.53E-02	5.43E-02	4.84E-02	4.67E-01
2.89E-01	2.21E-01	2.16E-02	2.58E-01	9.05E-02	3.60E-01	7.72E-01	4.50E-01
7.68E-01	3.82E-02	3.65E-01	4.52E-03	4.79E-02	2.40E-01	9.72E-01	1.29E-01
6.16E-01	4.07E-01	2.78E-01	2.12E-02	3.01E-04	2.37E-03	9.43E-01	7.19E-01
7.32E-01	7.44E-01	8.30E-01	1.04E-08	2.24E-02	1.57E-06	2.01E-01	8.82E-01
5.55E-01	2.09E-01	4.79E-01	8.96E-01	2.24E-01	2.56E-01	7.47E-01	3.40E-01
1.66E-01	6.19E-01	1.34E-01	9.40E-02	5.33E-01	3.94E-01	7.19E-02	9.65E-01
2.09E-01	5.74E-01	3.33E-01	4.36E-03	3.73E-02	3.86E-01	6.63E-01	4.91E-01
8.94E-01	5.40E-01	8.99E-01	1.18E-06	3.28E-01	1.28E-04	1.23E-01	1.66E-01
2.15E-01	4.77E-01	2.07E-01	9.14E-01	3.73E-04	NA	1.14E-01	2.81E-01
3.12E-01	8.74E-01	2.58E-01	6.64E-13	1.07E-01	2.65E-03	2.07E-02	7.73E-02
2.04E-03	1.07E-01	1.85E-01	1.97E-31	1.46E-11	8.81E-07	3.32E-07	5.71E-02
1.99E-01	5.40E-02	9.32E-01	4.68E-01	2.26E-01	9.69E-01	8.29E-01	6.64E-01
3.28E-01	5.07E-01	9.72E-01	4.40E-01	6.43E-02	5.41E-01	1.50E-01	8.43E-01
3.06E-01	6.23E-01	1.46E-01	1.04E-65	1.06E-10	4.11E-50	1.76E-12	1.70E-02
1.94E-01	7.22E-02	2.57E-01	9.94E-01	1.76E-01	1.49E-01	2.09E-01	1.77E-02
3.89E-01	3.36E-01	4.21E-01	9.42E-01	5.32E-01	2.90E-01	2.36E-01	5.39E-01
8.05E-02	4.87E-01	3.11E-01	1.46E-04	2.53E-01	2.71E-11	8.52E-01	3.63E-02
1.40E-01	9.63E-01	6.26E-01	3.26E-04	2.28E-01	1.81E-03	8.81E-01	4.35E-01
8.69E-01	3.18E-01	2.68E-01	3.82E-09	9.83E-01	1.56E-02	1.10E-01	4.31E-01
3.86E-01	5.95E-01	1.29E-01	1.70E-06	4.67E-02	5.44E-04	4.43E-02	2.24E-01
9.51E-01	2.94E-01	9.69E-01	6.71E-11	5.08E-01	5.10E-03	1.84E-01	9.03E-01
4.22E-01	1.28E-01	6.77E-01	1.44E-21	1.28E-02	3.45E-53	4.45E-04	1.54E-01

2.95E-01	5.54E-01	9.41E-01	1.46E-01	2.18E-02	3.54E-04	9.06E-01	5.79E-01
7.28E-01	1.77E-02	4.00E-01	4.29E-04	6.69E-01	5.42E-02	1.75E-02	2.06E-01
9.31E-01	5.11E-01	3.75E-01	1.79E-01	2.53E-02	3.41E-01	7.21E-02	7.97E-01
6.92E-01	8.87E-01	9.70E-01	1.99E-04	2.41E-04	4.86E-05	4.82E-01	6.09E-01
4.25E-01	3.80E-01	5.04E-01	1.10E-07	1.55E-01	8.77E-07	7.91E-03	1.06E-02
2.86E-01	4.65E-01	9.52E-01	2.19E-02	2.42E-01	6.54E-01	1.12E-01	2.12E-01
4.58E-01	7.49E-01	9.94E-02	4.48E-01	5.31E-01	3.60E-01	7.28E-01	6.91E-01
3.22E-03	7.20E-01	7.71E-02	4.13E-09	6.53E-01	1.62E-07	1.10E-02	6.70E-01
2.64E-01	3.65E-01	7.46E-01	4.93E-05	7.19E-01	3.19E-01	7.72E-02	7.21E-01
6.20E-01	8.00E-01	2.29E-01	5.23E-05	9.83E-01	3.08E-01	3.28E-01	4.97E-01
8.60E-01	9.35E-01	9.03E-01	2.13E-05	3.37E-01	1.08E-02	2.93E-01	4.85E-01
7.34E-01	3.21E-02	4.56E-01	8.29E-18	1.55E-02	1.20E-03	2.38E-04	8.30E-01
2.04E-01	7.03E-01	6.86E-02	5.53E-07	2.49E-03	1.28E-09	1.92E-02	6.24E-01
8.02E-01	1.57E-01	9.04E-01	6.53E-10	NA	1.02E-01	8.43E-02	3.02E-01
9.66E-01	4.44E-01	5.45E-01	5.79E-04	7.09E-01	8.32E-01	1.67E-01	4.28E-01
2.62E-02	7.36E-01	1.59E-01	2.61E-02	7.98E-02	4.46E-06	1.93E-03	6.23E-01
3.32E-01	1.38E-01	1.73E-01	2.47E-05	2.72E-01	5.04E-04	2.88E-02	5.32E-01
8.29E-01	7.31E-03	5.05E-01	2.17E-09	3.71E-01	7.03E-03	3.52E-01	7.49E-01
8.32E-01	8.96E-01	3.03E-01	2.92E-07	1.91E-02	6.73E-09	2.20E-03	1.26E-01
2.59E-01	6.99E-01	7.76E-01	4.74E-03	4.14E-01	3.62E-03	7.35E-02	5.70E-01
7.70E-01	2.30E-01	4.14E-01	1.21E-02	4.89E-01	2.96E-03	7.54E-02	1.02E-01
1.67E-01	2.23E-01	3.11E-01	2.78E-03	8.31E-03	3.27E-14	1.98E-01	1.24E-01
9.84E-01	9.45E-01	9.25E-01	9.97E-06	1.18E-01	3.25E-20	1.06E-01	4.45E-01
2.70E-01	9.71E-01	9.48E-01	4.11E-02	9.29E-01	4.49E-02	1.44E-01	8.24E-01
7.18E-01	3.06E-01	4.52E-02	1.07E-01	9.89E-01	6.32E-03	6.47E-01	3.30E-01
6.05E-01	6.62E-01	9.85E-01	1.43E-05	3.81E-02	1.59E-03	1.95E-01	4.90E-03
4.71E-01	3.86E-01	5.23E-01	1.79E-04	NA	6.87E-01	5.14E-03	2.87E-01
6.73E-01	5.67E-01	6.62E-01	3.74E-11	NA	2.29E-01	5.41E-03	2.85E-01
8.72E-01	5.94E-01	7.83E-01	1.60E-05	NA	9.10E-01	1.72E-03	1.14E-01
4.87E-01	4.20E-01	6.04E-01	1.88E-50	2.28E-06	5.77E-64	2.54E-09	6.41E-03
4.90E-01	6.80E-01	9.09E-01	1.24E-04	1.26E-01	3.37E-01	4.26E-01	2.28E-01
2.80E-01	5.12E-01	2.91E-01	3.82E-02	5.12E-01	7.29E-01	4.75E-01	9.45E-01
9.11E-01	8.04E-01	3.99E-01	5.03E-126	3.81E-01	7.10E-20	4.04E-12	6.41E-02
7.26E-01	2.36E-01	1.20E-02	6.03E-01	4.75E-03	NA	5.52E-01	3.61E-01
3.59E-01	2.34E-01	1.11E-01	4.05E-10	3.88E-06	1.23E-17	4.43E-05	7.67E-05
1.59E-01	6.34E-01	1.75E-01	6.61E-01	2.14E-03	2.78E-02	1.90E-01	6.10E-01
3.09E-01	5.47E-01	9.91E-02	2.80E-13	5.05E-02	4.67E-12	2.80E-03	3.28E-01
1.41E-01	2.71E-01	2.91E-01	9.82E-09	5.15E-01	1.65E-03	2.21E-01	8.13E-02
3.24E-01	4.73E-01	9.92E-02	8.86E-09	NA	2.69E-01	2.01E-02	2.26E-01
9.65E-01	5.02E-01	4.56E-01	2.48E-06	7.91E-01	2.84E-02	8.04E-01	3.47E-01
3.54E-01	1.24E-01	1.14E-01	8.43E-01	NA	7.60E-01	3.92E-01	7.14E-01
2.53E-01	3.85E-01	1.88E-01	2.25E-02	NA	NA	9.94E-02	3.20E-01
9.82E-01	1.17E-01	3.03E-01	7.48E-09	3.26E-02	2.02E-03	1.96E-02	4.77E-01
4.97E-01	4.47E-03	9.76E-01	5.67E-32	2.98E-01	1.38E-17	3.52E-03	9.80E-01
2.02E-04	9.88E-01	1.17E-02	3.76E-05	1.70E-02	1.88E-03	6.45E-03	1.91E-01
8.51E-01	5.33E-01	2.29E-01	1.02E-04	7.62E-01	1.91E-01	2.77E-01	1.56E-01
2.52E-01	1.88E-01	2.88E-01	1.09E-11	NA	4.25E-01	2.12E-03	7.24E-01

7.53E-01	6.27E-01	7.97E-01	2.18E-02	4.67E-01	3.93E-01	3.63E-01	4.32E-01
3.49E-01	9.89E-01	2.29E-01	9.58E-01	6.17E-01	6.84E-01	1.65E-01	8.81E-01
7.73E-01	3.30E-01	4.82E-01	1.10E-05	3.96E-01	5.51E-02	5.22E-01	4.50E-01
1.84E-01	8.21E-01	7.08E-01	4.78E-05	5.16E-01	9.16E-01	9.91E-02	4.86E-01
6.65E-01	3.10E-01	4.80E-01	6.78E-02	8.40E-01	2.41E-01	5.83E-01	2.75E-01
1.66E-01	8.22E-02	6.92E-01	1.87E-04	2.93E-01	1.44E-04	8.84E-01	1.32E-01
8.97E-01	4.67E-01	4.12E-01	1.10E-10	3.18E-05	8.23E-05	6.45E-04	3.25E-01
9.56E-01	5.91E-01	4.24E-01	5.79E-01	6.51E-01	7.58E-01	5.39E-01	9.93E-01
4.23E-01	5.37E-01	1.27E-01	5.70E-06	4.42E-02	2.71E-01	6.46E-01	6.22E-01
6.25E-01	5.98E-01	6.02E-01	7.24E-01	4.04E-01	1.84E-01	3.05E-01	2.98E-01
4.04E-02	5.48E-01	1.17E-01	7.31E-11	NA	1.85E-05	1.86E-06	4.10E-03
1.74E-01	7.76E-01	2.23E-01	5.41E-09	1.15E-07	1.91E-06	1.26E-02	9.31E-01
5.42E-02	9.85E-01	9.62E-01	3.13E-03	3.05E-02	4.31E-06	2.27E-02	2.04E-01
5.52E-01	3.91E-01	5.56E-01	8.52E-04	3.72E-01	3.61E-10	2.29E-02	1.92E-01
5.68E-01	9.42E-01	7.58E-01	3.00E-03	6.80E-01	4.26E-01	4.14E-02	3.33E-01

					SNPEffect		
META	EUR	AFR	ASN	HIS	META	EUR	AFR
4.08E-01	0.004	0.000	0.017	0.011	0.002	-0.001	-0.002
3.60E-01	-0.002	-0.001	0.002	-0.007	-0.001	-0.003	-0.002
9.72E-06	0.007	0.006	0.004	0.004	0.006	0.002	0.003
9.42E-04	0.006	-0.009	0.004	0.017	0.006	-0.001	0.033
7.46E-01	0.004	0.006	-0.019	-0.007	0.002	-0.014	-0.010
4.14E-05	0.007	0.012	0.007	0.011	0.008	-0.003	-0.020
2.69E-01	-0.004	-0.004	0.002	-0.012	-0.003	-0.002	0.011
1.61E-02	-0.005	-0.003	-0.001	-0.001	-0.003	-0.002	-0.001
2.72E-02	NA	0.012	0.006	0.011	0.010	NA	-0.003
1.15E-03	-0.002	-0.011	-0.001	0.003	-0.002	-0.002	0.010
6.82E-02	0.002	0.004	-0.002	0.001	0.002	-0.002	0.008
2.10E-02	0.002	0.017	0.005	0.001	0.003	-0.001	-0.031
1.79E-01	-0.023	NA	NA	NA	-0.022	-0.003	NA
7.00E-01	0.001	0.002	-0.001	0.001	0.000	0.002	0.002
5.79E-04	-0.015	-0.019	0.004	-0.012	-0.014	-0.008	-0.039
2.65E-03	0.018	NA	0.016	0.003	0.017	-0.011	NA
2.71E-01	0.002	0.011	-0.002	0.010	0.001	0.000	-0.010
1.08E-01	-0.003	-0.004	0.000	-0.001	-0.002	-0.002	-0.002
8.69E-01	0.000	-0.002	0.001	-0.003	0.000	-0.001	0.007
2.07E-07	-0.023	NA	-0.006	NA	-0.021	-0.003	NA
5.79E-15	-0.009	-0.002	-0.009	-0.012	-0.009	0.001	0.001
1.06E-01	0.006	NA	NA	NA	0.006	0.005	NA
3.56E-04	0.005	0.005	0.001	0.003	0.004	-0.002	0.013
3.15E-15	0.008	0.009	0.007	0.005	0.007	-0.002	-0.008
8.35E-12	-0.009	-0.005	-0.001	-0.016	-0.007	-0.004	-0.003
9.93E-08	-0.007	0.001	-0.003	-0.006	-0.005	0.001	-0.001
4.62E-11	0.007	0.004	0.006	0.006	0.006	-0.001	0.002
5.23E-09	-0.007	0.003	-0.006	-0.007	-0.006	0.001	0.001
1.12E-16	-0.010	-0.012	-0.009	-0.007	-0.010	-0.005	0.013
3.16E-02	0.001	0.003	0.003	0.003	0.002	0.002	0.005
7.67E-01	-0.003	0.002	0.009	0.003	0.000	0.000	0.005
2.07E-01	-0.002	0.011	0.002	0.004	0.000	0.000	-0.006
9.67E-02	0.000	0.000	0.002	-0.004	0.001	0.000	-0.026
2.26E-01	0.000	-0.005	-0.004	0.000	-0.001	0.000	0.012
5.20E-01	0.002	0.004	-0.003	0.003	0.000	0.000	0.000
4.38E-01	0.001	-0.017	-0.002	0.004	0.001	0.003	-0.055
8.09E-04	0.005	0.010	0.004	0.002	0.005	-0.002	0.000
1.79E-05	0.008	0.004	0.001	0.002	0.006	0.001	0.006

2.53E-03	-0.002	-0.002	-0.001	-0.007	-0.002	-0.001	-0.001
3.56E-07	-0.006	-0.002	-0.006	-0.010	-0.006	0.000	-0.004
5.85E-06	0.008	0.004	0.004	0.007	0.006	0.002	0.005
4.60E-02	-0.002	0.003	-0.002	0.001	-0.002	-0.001	-0.007
2.71E-09	0.005	0.007	0.006	0.008	0.005	0.002	0.001
1.06E-03	-0.008	-0.003	-0.001	-0.001	-0.005	-0.001	-0.004
1.60E-04	-0.004	-0.003	-0.003	-0.010	-0.004	-0.005	-0.011
6.63E-01	0.001	0.000	-0.003	0.001	-0.001	-0.001	0.003
1.37E-05	-0.008	-0.010	-0.004	-0.003	-0.007	0.001	0.008
9.07E-09	-0.004	-0.004	-0.006	-0.005	-0.005	-0.001	0.006
3.93E-08	0.015	0.007	-0.009	0.014	0.014	0.009	0.051
4.70E-09	-0.006	-0.006	-0.006	-0.004	-0.006	-0.003	-0.010
2.71E-01	0.003	0.005	0.005	-0.009	0.003	-0.003	-0.013
5.94E-01	0.000	0.002	-0.003	0.002	0.000	0.000	-0.014
4.30E-01	0.000	0.002	0.000	-0.003	0.000	0.001	0.002
1.79E-04	-0.010	0.017	NA	-0.014	-0.010	0.000	-0.024
8.61E-02	0.003	0.003	0.002	0.003	0.003	-0.001	-0.007
4.34E-07	0.008	0.002	0.012	0.005	0.007	0.001	-0.005
4.26E-02	-0.005	-0.004	0.002	-0.008	-0.004	-0.003	0.005
2.58E-06	0.006	0.007	0.005	0.009	0.006	0.001	0.010
4.18E-03	0.004	0.007	0.001	0.005	0.004	-0.001	0.014
8.51E-01	-0.001	0.002	0.000	0.004	0.000	0.002	-0.016
6.16E-06	-0.002	-0.004	-0.010	-0.003	-0.003	-0.001	-0.001
7.67E-06	-0.008	-0.002	0.000	-0.011	-0.005	0.003	0.009
1.83E-07	-0.007	-0.008	-0.002	-0.008	-0.006	0.000	0.002
7.38E-02	0.003	0.005	0.003	0.004	0.003	0.006	-0.006
1.49E-02	0.005	0.010	-0.008	0.003	0.004	0.000	0.002
3.11E-05	0.004	0.024	0.005	0.002	0.005	0.004	-0.015
1.47E-14	-0.007	-0.011	-0.006	-0.004	-0.007	-0.001	-0.002
4.66E-01	0.000	-0.009	0.001	0.000	0.000	0.001	-0.001
3.15E-02	-0.004	0.006	-0.002	-0.004	-0.004	0.004	-0.038
2.04E-02	-0.001	-0.005	0.000	0.001	-0.001	-0.001	0.007
2.00E-10	-0.013	-0.002	-0.010	-0.013	-0.012	0.002	0.009
1.86E-03	0.014	0.020	NA	-0.076	0.018	0.024	0.001
1.90E-14	0.011	0.009	0.003	0.012	0.008	-0.003	-0.006
4.60E-52	-0.029	-0.031	-0.021	-0.031	-0.028	0.007	0.021
3.59E-01	-0.001	0.008	0.001	0.002	0.000	0.001	0.008
3.55E-01	-0.002	-0.008	-0.001	-0.003	-0.002	0.000	-0.003
4.19E-131	-0.029	-0.019	-0.022	-0.029	-0.025	-0.001	-0.006
1.76E-01	0.001	0.006	0.003	0.003	0.002	0.000	-0.012
7.93E-01	-0.001	0.002	-0.002	0.003	-0.001	0.002	0.006
1.76E-12	-0.008	-0.006	-0.012	-0.001	-0.008	0.000	0.004
2.96E-06	0.005	0.006	0.004	0.003	0.005	0.001	0.005
1.21E-08	-0.010	-0.001	-0.003	-0.005	-0.006	-0.002	-0.002
2.39E-10	0.008	0.010	0.006	0.007	0.007	-0.003	0.001
9.24E-12	0.014	0.002	0.015	0.008	0.013	0.002	0.020
2.04E-75	-0.019	-0.011	-0.021	-0.014	-0.019	0.002	0.006

4.41E-03	0.002	-0.009	0.005	0.000	0.003	0.003	-0.003
6.58E-06	0.007	0.001	0.004	0.008	0.006	-0.002	-0.012
1.62E-02	-0.002	-0.006	-0.001	-0.008	-0.002	-0.002	-0.003
1.56E-09	0.004	0.015	0.005	0.002	0.005	0.002	-0.001
1.33E-16	0.008	0.009	0.008	0.010	0.009	-0.001	0.004
2.80E-02	-0.004	-0.005	-0.002	-0.005	-0.003	0.001	0.000
7.99E-01	-0.002	-0.001	-0.002	0.004	-0.001	0.001	-0.003
9.38E-16	0.013	0.003	0.008	0.006	0.009	-0.001	-0.004
6.62E-04	0.013	0.003	0.002	0.008	0.007	-0.001	-0.001
2.41E-03	0.012	0.004	0.000	0.008	0.006	-0.003	0.006
6.11E-06	0.011	0.000	0.006	0.010	0.010	0.000	0.002
7.51E-19	0.013	0.012	0.005	0.013	0.010	-0.002	0.013
2.72E-17	0.009	0.008	0.010	0.011	0.010	-0.002	0.005
6.55E-11	-0.026	NA	-0.016	-0.022	-0.025	0.000	NA
3.35E-02	-0.009	-0.015	-0.001	-0.013	-0.004	0.001	0.037
1.51E-08	0.012	0.007	0.011	0.009	0.010	-0.005	-0.008
1.33E-09	0.006	0.009	0.008	0.006	0.006	0.001	-0.003
3.44E-09	0.010	0.004	0.005	0.006	0.008	-0.002	0.003
1.39E-18	-0.007	-0.009	-0.008	-0.011	-0.008	0.001	-0.008
4.12E-05	-0.005	-0.011	-0.013	-0.004	-0.005	0.002	-0.007
6.79E-06	-0.004	-0.002	-0.003	-0.008	-0.003	-0.001	-0.002
3.29E-17	-0.013	-0.015	-0.011	-0.011	-0.012	0.002	0.023
2.13E-24	0.011	0.020	0.015	0.010	0.013	0.003	0.011
3.93E-01	0.002	-0.006	-0.006	0.004	0.000	0.000	0.003
7.99E-03	0.000	-0.002	0.006	0.002	0.002	0.000	-0.013
1.79E-09	0.008	0.011	0.005	0.006	0.007	0.000	0.002
5.58E-06	-0.022	NA	NA	-0.027	-0.023	0.004	NA
1.14E-11	0.034	NA	-0.045	0.041	0.033	0.001	NA
2.91E-07	-0.028	NA	0.030	-0.056	-0.030	-0.003	NA
5.39E-124	0.025	0.019	0.024	0.024	0.024	0.001	-0.005
3.10E-05	0.006	0.009	0.003	0.003	0.006	0.000	-0.011
4.02E-02	-0.008	0.003	-0.001	-0.004	-0.005	0.002	-0.005
2.21E-118	-0.038	0.004	-0.014	-0.029	-0.027	-0.003	0.001
2.45E-02	NA	0.027	NA	-0.009	0.023	NA	0.007
2.32E-35	0.016	0.027	0.015	0.022	0.017	-0.002	0.002
2.61E-01	-0.002	-0.015	0.002	0.006	0.000	0.001	0.023
2.02E-25	-0.011	-0.009	-0.009	-0.011	-0.010	0.005	-0.001
2.41E-10	-0.010	-0.005	-0.003	-0.006	-0.007	0.000	0.002
2.28E-10	-0.035	NA	-0.005	-0.063	-0.036	-0.013	NA
1.41E-05	-0.006	-0.001	-0.003	0.001	-0.004	0.005	-0.001
7.24E-01	-0.005	NA	-0.005	0.004	-0.004	0.003	NA
1.50E-02	0.010	NA	NA	0.036	0.011	-0.008	NA
3.46E-11	-0.009	-0.010	-0.004	-0.007	-0.007	0.001	0.000
1.18E-45	-0.021	-0.024	-0.016	-0.018	-0.019	0.000	-0.005
1.43E-09	-0.006	-0.007	-0.005	-0.005	-0.005	-0.001	0.007
1.31E-03	-0.006	-0.002	0.000	-0.005	-0.003	0.004	0.012
4.58E-10	0.045	NA	-0.025	0.053	0.042	0.008	NA

4.44E-02	-0.006	-0.005	0.005	-0.005	-0.004	0.001	0.015
6.18E-01	0.001	0.007	-0.002	-0.005	0.001	0.007	-0.005
1.05E-05	-0.006	-0.004	-0.002	-0.004	-0.004	0.000	-0.012
1.82E-02	0.013	0.005	0.001	0.007	0.005	0.004	0.021
6.20E-01	-0.003	-0.002	0.006	0.001	-0.001	-0.002	-0.009
2.09E-06	-0.006	-0.004	-0.005	0.000	-0.005	-0.002	-0.028
4.86E-17	-0.014	-0.020	-0.007	-0.015	-0.012	-0.003	0.005
8.68E-01	0.001	0.002	0.001	0.002	0.001	0.003	-0.002
1.19E-03	-0.005	0.003	-0.004	0.000	-0.004	0.001	0.001
1.91E-01	0.001	-0.003	0.002	0.004	0.001	0.002	0.012
2.81E-20	-0.033	NA	-0.023	-0.052	-0.033	-0.005	NA
7.61E-20	0.012	0.019	0.007	0.013	0.011	0.006	0.001
4.48E-10	-0.005	-0.006	-0.006	-0.004	-0.005	0.001	-0.001
1.23E-13	-0.007	-0.003	-0.007	-0.011	-0.007	-0.001	0.005
5.29E-03	0.006	0.000	0.002	0.006	0.004	-0.001	-0.002

					HDL.RegDrink		
IntEffect					PJoint		
ASN	HIS	META	EUR	AFR	ASN	HIS	META
0.014	-0.013	0.000	4.18E-01	9.34E-01	3.31E-01	6.39E-01	5.36E-01
-0.003	0.010	-0.003	1.27E-05	7.55E-01	3.12E-01	5.03E-02	3.25E-04
0.005	0.001	0.003	5.91E-12	2.11E-01	1.57E-01	7.16E-01	1.11E-12
-0.005	0.001	-0.001	6.22E-07	4.40E-01	1.09E-01	3.28E-03	7.84E-08
-0.004	-0.022	-0.014	8.73E-01	5.82E-01	6.73E-01	3.01E-01	4.09E-01
-0.004	-0.015	-0.004	2.45E-07	2.79E-01	5.50E-02	1.76E-01	5.64E-09
0.004	0.007	-0.002	2.53E-08	3.26E-01	1.23E-01	1.29E-02	1.12E-05
-0.003	-0.013	-0.004	5.75E-09	5.89E-01	1.18E-01	3.17E-02	7.89E-10
0.000	-0.006	-0.003	NA	2.08E-02	6.93E-01	6.27E-01	1.55E-02
0.000	-0.012	-0.002	3.93E-04	1.15E-01	7.53E-01	2.30E-01	3.50E-04
0.014	0.010	0.000	3.20E-01	2.60E-01	4.34E-01	3.76E-01	2.25E-01
-0.010	0.001	-0.003	6.70E-01	5.56E-01	1.65E-01	9.64E-01	2.86E-01
NA	NA	-0.004	6.59E-04	NA	NA	NA	9.70E-04
0.003	0.000	0.002	3.74E-02	6.37E-01	5.15E-01	9.12E-01	3.55E-02
-0.009	0.009	-0.008	1.47E-12	3.12E-01	9.62E-01	5.72E-01	5.24E-12
-0.018	0.026	-0.010	1.34E-08	NA	5.57E-01	5.61E-01	3.23E-08
0.001	-0.008	0.000	1.68E-01	1.75E-01	4.08E-01	3.91E-02	3.73E-01
-0.002	-0.003	-0.002	3.57E-04	3.56E-01	9.65E-01	7.93E-01	4.15E-04
-0.004	-0.007	-0.002	6.72E-01	6.38E-01	2.60E-01	9.13E-02	2.62E-01
-0.013	NA	-0.005	3.51E-19	NA	4.10E-01	NA	1.69E-18
0.000	0.008	0.001	5.26E-17	9.47E-01	2.93E-07	1.59E-02	3.60E-24
NA	NA	0.005	7.68E-02	NA	NA	NA	8.92E-02
-0.002	0.008	0.000	1.49E-06	2.59E-03	6.55E-01	8.38E-02	3.27E-07
0.001	0.001	-0.001	1.14E-17	2.12E-02	5.10E-10	1.52E-01	4.13E-28
-0.006	0.008	-0.005	2.11E-27	1.86E-01	1.62E-01	3.23E-05	3.95E-28
-0.001	0.006	0.000	2.17E-12	9.80E-01	3.23E-03	2.03E-01	1.51E-13
0.000	0.006	0.000	4.67E-13	3.99E-01	3.18E-05	2.13E-02	1.39E-18
-0.003	0.002	0.000	2.32E-13	7.47E-01	8.75E-06	1.30E-01	7.84E-18
0.000	-0.001	-0.003	4.78E-50	1.24E-02	9.09E-10	5.09E-02	1.15E-58
0.002	0.001	0.002	1.26E-02	5.03E-01	1.80E-02	5.69E-01	1.67E-04
-0.011	-0.005	-0.002	2.11E-02	3.84E-01	1.96E-02	6.37E-01	2.12E-01
0.000	-0.005	-0.001	7.56E-02	1.06E-01	3.31E-01	4.15E-01	4.96E-01
0.002	0.012	0.000	8.47E-01	6.95E-03	7.74E-02	2.79E-01	3.64E-01
0.003	-0.003	0.001	9.76E-01	2.68E-01	3.00E-01	8.79E-01	7.12E-01
0.000	-0.006	0.001	7.58E-02	5.41E-01	1.36E-01	5.49E-01	5.60E-01
0.037	0.010	0.004	7.16E-02	6.98E-02	3.36E-02	4.55E-01	2.75E-02
0.010	-0.003	-0.001	6.56E-05	3.88E-02	8.46E-02	8.96E-01	7.77E-06
0.000	0.014	0.002	9.54E-24	1.45E-01	8.42E-01	1.09E-02	5.17E-22

0.001	0.000	-0.001	1.60E-03	7.55E-01	5.93E-01	5.47E-02	2.28E-04
0.001	0.003	0.000	3.66E-12	4.60E-01	2.48E-03	8.72E-03	5.46E-16
0.004	0.002	0.003	4.40E-25	1.78E-01	4.00E-03	6.31E-02	6.30E-28
0.003	0.015	0.000	1.04E-02	4.73E-01	2.11E-01	1.08E-02	3.19E-02
-0.002	-0.014	0.001	3.13E-13	1.02E-02	1.62E-03	2.63E-02	2.55E-17
-0.002	-0.011	-0.003	8.96E-17	3.68E-01	5.41E-01	1.31E-01	2.54E-14
-0.004	0.010	-0.004	7.82E-15	7.93E-02	2.34E-04	4.40E-03	9.42E-20
0.001	0.001	0.000	9.05E-01	8.99E-01	1.85E-01	9.04E-01	7.96E-01
0.006	-0.002	0.001	1.45E-07	1.53E-02	6.62E-01	5.63E-01	1.67E-08
0.000	0.005	0.000	1.88E-07	4.03E-01	7.61E-05	2.89E-01	1.08E-11
0.054	0.003	0.009	1.58E-32	2.90E-01	6.59E-01	7.00E-02	1.69E-33
0.001	-0.001	-0.002	1.33E-15	3.81E-03	1.40E-06	3.11E-01	1.27E-22
-0.003	0.011	-0.003	4.08E-01	4.56E-01	8.64E-01	7.27E-01	3.27E-01
-0.008	0.006	-0.001	9.35E-01	2.89E-01	2.45E-01	5.97E-01	9.33E-01
-0.001	0.005	0.001	7.04E-01	6.35E-01	8.44E-01	6.01E-01	8.16E-01
NA	-0.021	-0.001	1.22E-10	3.91E-01	NA	6.00E-02	2.26E-10
0.002	0.006	-0.001	5.01E-02	7.41E-01	3.12E-01	3.63E-01	1.27E-02
-0.014	-0.014	0.000	2.23E-10	9.51E-01	2.61E-01	5.44E-01	7.64E-10
0.001	-0.004	-0.003	6.95E-12	8.32E-01	6.14E-01	4.68E-02	6.23E-10
0.002	0.010	0.002	1.30E-13	1.49E-02	1.71E-05	1.49E-05	1.61E-22
-0.004	0.005	0.000	1.42E-05	8.37E-02	5.10E-01	9.33E-02	1.53E-05
0.001	-0.001	0.001	5.18E-01	1.87E-01	9.71E-01	5.55E-01	7.30E-01
0.008	0.003	0.001	1.40E-02	2.25E-01	8.76E-04	6.09E-01	1.57E-04
0.000	0.003	0.001	5.27E-14	3.66E-01	9.68E-01	1.89E-03	1.94E-10
0.001	0.003	0.000	3.51E-15	1.14E-02	2.42E-01	2.49E-02	4.44E-16
-0.001	0.007	0.005	3.85E-08	4.54E-01	7.09E-01	2.37E-01	2.77E-08
-0.023	-0.004	0.000	8.80E-04	1.33E-02	8.51E-02	7.48E-01	8.69E-04
0.002	0.007	0.003	1.09E-10	1.60E-04	4.88E-04	4.03E-01	4.15E-15
0.000	0.004	-0.001	1.76E-19	7.52E-04	4.11E-08	3.77E-01	1.26E-28
0.001	0.009	0.001	8.26E-01	1.64E-01	6.90E-01	6.07E-01	6.63E-01
0.004	0.004	0.003	1.89E-02	8.81E-02	8.31E-01	6.33E-01	2.36E-02
-0.004	-0.010	-0.001	1.92E-01	2.22E-01	6.65E-01	2.40E-01	7.42E-02
0.002	0.000	0.001	3.02E-21	7.99E-01	8.26E-06	5.28E-02	1.24E-25
NA	0.160	0.017	6.19E-45	4.61E-08	NA	3.89E-02	6.35E-51
0.001	0.001	-0.001	2.61E-30	3.31E-02	1.28E-02	4.77E-05	5.77E-32
0.002	-0.014	0.005	9.04E-71	2.44E-12	5.97E-09	8.84E-23	7.54E-106
0.003	0.010	0.001	7.81E-01	1.00E-02	6.69E-01	7.27E-02	5.67E-01
0.002	0.004	0.001	1.93E-01	4.26E-03	7.07E-01	6.63E-01	3.24E-02
-0.009	0.010	-0.004	7.91E-216	6.82E-12	2.74E-69	1.23E-16	6.36E-299
-0.008	-0.005	-0.003	8.40E-01	2.07E-01	1.52E-02	7.76E-01	4.75E-02
-0.002	-0.003	0.001	4.93E-01	5.61E-01	2.32E-01	7.33E-01	6.09E-01
0.006	-0.011	0.001	1.90E-20	1.22E-01	1.93E-13	7.87E-02	1.57E-31
0.004	0.005	0.002	5.46E-09	3.78E-02	2.26E-05	2.92E-01	2.17E-14
-0.002	0.000	-0.004	1.12E-45	7.65E-01	1.24E-02	2.27E-01	4.58E-39
-0.004	-0.007	-0.003	8.85E-12	6.97E-02	3.16E-04	1.02E-01	7.24E-16
-0.004	0.002	0.003	2.18E-38	1.31E-01	2.12E-04	1.75E-01	4.24E-41
-0.004	-0.007	0.000	1.59E-79	8.00E-03	1.84E-74	2.59E-07	8.90E-154

-0.004	0.008	0.001	8.26E-04	3.91E-02	7.04E-03	4.80E-01	3.00E-04
-0.002	-0.002	-0.002	1.74E-08	3.11E-01	8.40E-02	2.58E-02	1.37E-09
-0.001	-0.005	-0.001	6.58E-04	7.56E-02	5.38E-01	8.20E-03	3.38E-05
0.003	0.009	0.002	1.42E-08	3.80E-06	4.29E-06	1.20E-01	9.89E-17
0.000	0.008	-0.001	2.04E-15	4.11E-03	9.64E-08	3.81E-05	2.60E-27
0.004	0.004	0.001	1.19E-04	2.79E-01	2.51E-01	3.44E-01	8.55E-05
-0.001	-0.012	0.000	4.65E-01	7.56E-01	1.49E-01	1.50E-01	1.02E-01
-0.006	-0.013	-0.002	5.22E-28	5.15E-01	2.12E-08	8.04E-02	4.23E-29
-0.003	-0.008	0.001	7.13E-14	7.24E-01	6.79E-01	2.18E-01	3.96E-09
-0.003	-0.012	-0.001	6.79E-11	6.44E-01	6.79E-01	2.74E-01	6.91E-06
-0.004	-0.015	0.000	2.07E-17	9.86E-01	2.86E-01	1.17E-01	1.14E-16
-0.004	0.005	0.000	2.93E-40	4.71E-06	4.02E-03	1.86E-06	6.77E-42
-0.004	-0.014	-0.003	2.41E-08	3.21E-03	6.05E-11	2.81E-02	2.63E-21
-0.017	0.010	-0.001	4.45E-29	NA	2.41E-02	1.63E-01	4.15E-30
-0.001	0.004	-0.002	1.86E-06	5.49E-01	5.53E-01	1.60E-01	5.38E-05
0.009	-0.008	-0.003	1.98E-04	1.33E-01	1.83E-02	1.17E-01	1.15E-06
-0.005	0.002	0.000	6.32E-08	4.09E-01	9.65E-04	1.27E-01	2.74E-11
-0.001	-0.007	0.000	8.37E-19	2.33E-01	4.90E-02	1.68E-01	6.80E-19
0.004	0.005	0.002	1.05E-13	8.58E-04	1.60E-07	6.17E-04	9.97E-25
0.005	0.005	0.002	5.61E-06	3.85E-02	6.28E-02	5.69E-01	2.61E-07
-0.001	0.005	-0.001	3.69E-05	8.58E-01	2.17E-02	3.52E-02	1.29E-07
0.004	-0.002	0.003	1.36E-14	1.13E-02	2.65E-13	1.09E-02	1.52E-29
0.001	0.007	0.001	6.65E-19	4.50E-02	1.10E-24	4.09E-02	7.15E-44
0.012	-0.002	0.003	1.85E-01	2.71E-01	2.57E-02	5.17E-01	3.99E-01
-0.006	-0.003	-0.002	9.66E-01	1.15E-01	6.69E-03	8.08E-01	2.02E-01
0.003	0.002	0.001	6.91E-14	7.50E-03	7.23E-04	4.92E-02	3.34E-19
NA	0.018	0.006	1.57E-09	NA	NA	1.52E-02	7.38E-11
0.065	-0.039	-0.001	6.60E-33	NA	2.65E-01	2.11E-04	3.04E-33
0.016	0.056	0.002	5.64E-16	NA	1.91E-01	4.88E-05	9.67E-17
0.000	-0.005	0.001	3.79E-186	1.43E-08	2.57E-97	5.75E-14	3.40E-294
-0.008	0.007	0.000	3.59E-08	1.22E-02	3.32E-01	2.40E-01	4.71E-09
-0.006	-0.010	-0.002	7.82E-10	6.54E-01	6.63E-01	4.51E-02	5.18E-08
-0.022	0.005	-0.012	0.00E+00	3.75E-01	4.09E-20	3.65E-23	0.00E+00
NA	0.030	0.009	NA	3.68E-08	NA	5.15E-01	7.65E-07
0.003	0.006	-0.001	3.66E-39	1.81E-16	2.79E-23	1.09E-10	4.65E-81
-0.005	-0.019	-0.002	3.52E-01	9.44E-03	1.15E-01	4.87E-02	3.53E-01
0.000	0.004	0.003	1.20E-22	2.81E-03	5.06E-14	7.54E-03	8.41E-39
-0.001	-0.006	-0.002	1.61E-28	2.65E-01	5.19E-03	1.91E-02	8.18E-28
-0.075	-0.005	-0.013	6.50E-31	NA	1.53E-01	9.83E-05	8.77E-34
-0.001	-0.008	0.002	7.34E-08	9.35E-01	1.02E-02	3.84E-01	2.08E-07
-0.007	0.009	0.003	4.72E-01	NA	9.55E-01	7.30E-01	6.44E-01
NA	-0.055	-0.010	4.61E-02	NA	NA	6.20E-02	1.88E-02
-0.004	-0.010	-0.001	2.86E-21	1.02E-03	6.91E-05	1.10E-03	6.01E-28
-0.006	0.007	-0.002	2.22E-79	1.43E-03	1.06E-26	3.22E-03	6.21E-106
0.002	0.016	0.001	1.10E-09	8.35E-02	5.04E-03	1.28E-01	1.74E-11
-0.002	0.002	0.001	9.00E-07	2.23E-01	4.21E-01	2.06E-01	4.02E-05
0.094	-0.032	0.010	6.64E-30	NA	2.03E-01	4.97E-03	7.64E-30

-0.021	0.000	-0.001	2.69E-04	6.31E-01	1.31E-01	5.87E-01	7.82E-04
0.005	0.001	0.006	7.41E-04	1.95E-01	5.31E-01	5.19E-01	2.09E-03
-0.001	0.004	-0.001	5.37E-10	2.40E-02	6.79E-02	3.81E-01	5.43E-11
-0.002	-0.005	0.004	3.63E-16	8.33E-04	7.73E-01	4.76E-01	4.90E-09
-0.013	0.002	-0.004	1.59E-05	4.40E-01	1.48E-02	8.52E-01	3.07E-04
0.003	-0.016	-0.002	1.85E-12	2.53E-04	1.09E-03	2.06E-02	7.95E-16
-0.001	0.001	-0.004	2.88E-48	1.46E-04	2.56E-05	1.09E-05	3.88E-55
-0.002	-0.001	0.001	7.17E-02	8.58E-01	7.52E-01	8.06E-01	1.94E-01
0.004	0.004	0.001	3.79E-07	6.29E-01	9.65E-02	7.24E-01	1.05E-05
-0.004	0.005	0.001	1.81E-01	2.83E-01	3.69E-01	1.26E-01	9.66E-02
-0.006	-0.016	-0.006	4.34E-47	NA	1.27E-06	9.42E-17	5.44E-64
0.004	-0.015	0.005	2.02E-45	9.12E-10	9.52E-07	1.25E-02	7.90E-56
-0.002	0.002	0.000	2.47E-08	4.19E-02	7.71E-08	3.68E-01	3.26E-16
-0.002	0.003	-0.001	1.06E-12	7.27E-01	5.42E-11	1.13E-03	1.32E-24
-0.001	0.001	0.000	4.96E-11	9.42E-01	3.91E-01	3.92E-02	2.16E-09

PInt					PMain		
EUR	AFR	ASN	HIS	META	EUR	AFR	ASN
7.58E-01	8.10E-01	3.25E-01	7.45E-01	8.60E-01	2.85E-01	8.64E-01	3.85E-01
3.78E-01	6.54E-01	8.19E-01	9.09E-02	6.15E-01	7.63E-02	7.04E-01	8.15E-01
3.63E-01	8.08E-01	9.26E-01	9.86E-01	3.75E-01	9.01E-06	1.50E-01	2.13E-01
7.29E-01	2.32E-01	2.02E-01	9.29E-01	3.87E-01	4.28E-05	4.20E-01	3.25E-02
9.03E-01	4.00E-01	9.39E-01	3.43E-01	2.82E-01	8.47E-01	3.20E-01	4.84E-01
2.34E-01	2.53E-01	3.68E-01	1.78E-01	7.69E-02	1.97E-06	1.29E-01	2.29E-02
2.49E-01	2.19E-01	2.95E-01	3.80E-01	9.28E-01	1.67E-03	2.15E-01	2.97E-01
3.98E-01	9.46E-01	5.91E-01	4.64E-02	1.54E-01	7.98E-05	3.81E-01	4.30E-01
NA	4.34E-01	9.72E-01	7.78E-01	5.17E-01	NA	6.91E-03	4.89E-01
3.53E-01	4.80E-01	6.74E-01	8.47E-02	2.08E-01	3.66E-02	4.05E-02	3.59E-01
8.86E-01	4.69E-01	4.76E-01	1.95E-01	6.23E-01	1.53E-01	3.20E-01	5.70E-01
8.26E-01	3.91E-01	8.40E-02	9.76E-01	5.21E-01	4.66E-01	3.13E-01	1.20E-01
8.70E-01	NA	NA	NA	8.67E-01	1.14E-02	NA	NA
2.12E-01	6.55E-01	5.36E-01	1.00E+00	1.56E-01	3.31E-01	4.60E-01	9.63E-01
6.94E-02	4.48E-01	6.96E-01	6.40E-01	8.08E-02	3.23E-05	3.93E-01	8.41E-01
5.97E-02	NA	4.52E-01	4.15E-01	6.70E-02	1.68E-08	NA	2.82E-01
9.33E-01	4.51E-01	6.23E-01	2.76E-01	8.55E-01	1.48E-01	5.83E-02	1.74E-01
1.52E-01	9.88E-01	9.25E-01	7.72E-01	1.88E-01	1.87E-02	2.48E-01	5.29E-01
6.52E-01	3.55E-01	4.38E-01	2.03E-01	3.75E-01	7.57E-01	5.06E-01	6.71E-01
8.41E-01	NA	5.52E-01	NA	7.17E-01	6.12E-09	NA	5.70E-01
3.23E-01	9.62E-01	8.26E-01	3.84E-01	2.51E-01	3.58E-11	7.76E-01	2.35E-06
4.61E-01	NA	NA	NA	4.61E-01	2.38E-01	NA	NA
3.33E-01	1.28E-01	4.00E-01	2.12E-01	5.65E-01	6.65E-06	7.66E-02	6.20E-01
3.05E-01	3.59E-01	9.03E-01	9.04E-01	3.18E-01	8.43E-12	4.89E-03	2.54E-07
5.97E-02	4.91E-01	9.88E-01	2.63E-01	1.48E-01	1.21E-10	1.36E-01	7.06E-01
4.10E-01	6.78E-01	7.55E-01	2.91E-01	3.12E-01	7.06E-09	8.27E-01	4.61E-03
2.74E-01	7.94E-01	7.87E-01	4.03E-01	4.21E-01	8.69E-09	3.00E-01	1.04E-03
3.09E-01	9.12E-01	5.23E-01	7.22E-01	5.46E-01	1.62E-08	5.41E-01	1.63E-04
3.83E-02	1.87E-01	9.89E-01	9.48E-01	1.14E-01	2.57E-17	2.96E-03	1.24E-07
6.58E-01	5.15E-01	4.73E-01	8.12E-01	3.63E-01	3.21E-01	5.14E-01	5.80E-02
6.75E-01	6.51E-01	2.41E-01	4.91E-01	9.84E-01	3.74E-02	4.62E-01	9.37E-02
4.65E-01	5.60E-01	9.16E-01	5.29E-01	7.00E-01	1.30E-01	3.37E-02	2.20E-01
7.21E-01	5.86E-03	8.00E-01	1.29E-01	8.04E-01	7.90E-01	9.36E-01	7.48E-02
8.05E-01	7.47E-02	6.85E-01	6.88E-01	5.75E-01	7.94E-01	1.67E-01	2.22E-01
9.19E-01	8.23E-01	9.65E-01	2.99E-01	7.57E-01	1.24E-01	3.22E-01	1.02E-01
2.98E-01	2.19E-01	3.73E-02	5.38E-01	1.66E-01	4.64E-01	2.15E-01	7.92E-01
6.57E-01	7.50E-01	1.63E-01	6.92E-01	8.08E-01	5.67E-05	1.65E-02	3.67E-01
8.54E-01	5.42E-01	9.78E-01	1.88E-02	3.72E-01	1.57E-13	1.94E-01	6.96E-01

9.14E-01	6.77E-01	5.94E-01	9.63E-01	9.42E-01	4.67E-02	5.50E-01	1.78E-01
6.20E-01	5.51E-01	5.62E-01	7.46E-01	8.35E-01	3.30E-07	4.57E-01	4.16E-03
7.71E-01	5.50E-01	4.94E-01	7.54E-01	5.19E-01	1.40E-10	2.17E-01	4.04E-02
8.62E-01	4.97E-01	2.02E-01	1.04E-02	3.50E-01	5.48E-02	2.84E-01	1.33E-01
3.72E-01	7.16E-01	4.93E-01	1.62E-02	9.81E-01	1.24E-05	6.28E-03	1.17E-03
9.04E-01	4.31E-01	5.93E-01	1.61E-01	5.07E-01	4.10E-09	3.42E-01	4.49E-01
2.42E-02	2.01E-01	2.38E-01	9.97E-02	2.04E-02	1.35E-03	3.83E-01	2.73E-03
5.38E-01	6.39E-01	8.99E-01	9.24E-01	6.66E-01	6.84E-01	9.12E-01	1.43E-01
9.11E-01	2.19E-01	6.86E-01	7.81E-01	6.89E-01	6.38E-06	3.87E-03	4.37E-01
5.91E-01	6.22E-01	6.29E-01	4.29E-01	9.44E-01	2.44E-04	1.79E-01	1.09E-04
2.12E-02	2.36E-01	3.87E-01	7.95E-01	1.54E-02	1.77E-10	7.09E-01	8.03E-01
9.12E-02	1.28E-01	9.72E-01	9.33E-01	1.12E-01	2.13E-06	4.45E-02	7.84E-06
5.13E-01	2.61E-01	6.60E-01	6.20E-01	3.61E-01	1.88E-01	3.55E-01	6.03E-01
7.63E-01	1.44E-01	3.58E-01	5.49E-01	4.67E-01	8.75E-01	5.85E-01	5.14E-01
6.20E-01	6.24E-01	5.80E-01	3.77E-01	6.70E-01	8.03E-01	4.57E-01	8.09E-01
4.80E-01	3.83E-01	NA	4.36E-01	3.66E-01	3.27E-06	1.76E-01	NA
5.14E-01	6.12E-01	8.01E-01	4.53E-01	6.94E-01	4.11E-02	5.51E-01	4.13E-01
4.67E-01	9.41E-01	1.76E-01	2.32E-01	8.35E-01	8.93E-06	7.92E-01	1.01E-01
2.39E-01	8.29E-01	9.92E-01	6.33E-01	2.77E-01	1.90E-04	5.36E-01	4.57E-01
5.36E-01	1.46E-01	5.16E-01	6.23E-02	1.22E-01	2.85E-07	5.78E-02	2.43E-03
7.70E-01	2.71E-01	2.56E-01	4.31E-01	6.88E-01	1.98E-04	2.40E-01	4.16E-01
9.30E-02	6.15E-02	2.99E-01	9.28E-01	1.54E-01	6.21E-01	6.32E-01	7.21E-01
6.03E-01	6.96E-01	1.35E-01	5.17E-01	9.54E-01	8.48E-02	1.40E-01	1.91E-04
1.00E-01	1.10E-01	8.55E-01	6.53E-01	7.81E-02	1.18E-10	4.15E-01	7.95E-01
9.90E-01	8.49E-01	8.72E-01	5.86E-01	7.40E-01	4.50E-09	3.89E-03	1.04E-01
6.99E-03	6.76E-01	6.76E-01	3.72E-01	1.43E-02	7.71E-02	2.08E-01	5.34E-01
9.58E-01	8.57E-01	1.18E-01	6.43E-01	6.93E-01	7.53E-03	9.47E-03	1.42E-01
4.37E-02	2.58E-01	4.66E-01	3.23E-01	3.71E-02	2.33E-03	3.44E-05	2.96E-03
2.89E-01	9.85E-01	8.43E-01	4.58E-01	5.63E-01	1.97E-10	7.29E-04	3.01E-07
9.93E-01	8.97E-01	9.42E-01	3.74E-01	8.52E-01	9.87E-01	1.11E-01	3.78E-01
1.54E-01	3.09E-02	7.13E-01	5.88E-01	2.02E-01	9.40E-03	4.46E-01	5.49E-01
6.46E-01	3.96E-01	4.92E-01	1.22E-01	4.67E-01	3.31E-01	8.47E-02	8.74E-01
4.93E-01	7.73E-01	7.76E-01	9.32E-01	4.28E-01	1.01E-13	6.78E-01	6.43E-06
6.82E-01	8.69E-01	NA	1.58E-02	5.38E-01	5.67E-01	2.04E-07	NA
5.03E-02	5.06E-01	9.07E-01	6.66E-01	1.24E-01	2.41E-22	9.23E-03	3.31E-02
1.56E-02	6.14E-02	6.04E-01	7.21E-02	3.62E-02	7.19E-48	2.80E-13	6.29E-08
5.39E-01	2.94E-01	7.33E-01	7.42E-02	1.94E-01	4.31E-01	2.68E-02	5.33E-01
8.51E-01	8.09E-01	3.28E-01	4.16E-01	6.27E-01	2.36E-01	5.94E-03	3.04E-01
6.62E-01	5.97E-01	9.41E-01	1.31E-01	5.89E-01	3.89E-105	8.36E-10	5.28E-46
9.40E-01	1.13E-01	3.53E-02	5.73E-01	1.10E-01	5.89E-01	1.06E-01	1.74E-01
6.42E-02	4.10E-01	2.83E-01	5.74E-01	3.16E-01	3.15E-01	6.27E-01	5.74E-01
4.91E-01	5.07E-01	4.64E-02	7.21E-02	9.43E-01	1.85E-11	3.93E-02	1.12E-12
8.44E-01	4.41E-01	2.39E-01	4.09E-01	2.57E-01	5.09E-05	4.55E-02	7.02E-03
3.24E-01	8.06E-01	2.80E-01	9.26E-01	1.60E-01	4.63E-20	5.88E-01	3.15E-02
3.75E-01	9.87E-01	2.07E-01	2.85E-01	9.53E-02	1.93E-09	3.94E-02	6.23E-04
4.90E-01	1.10E-01	7.17E-01	9.73E-01	4.18E-01	9.91E-19	6.84E-01	2.77E-04
5.37E-01	3.92E-01	6.50E-01	3.29E-01	5.01E-01	1.28E-45	1.52E-03	3.46E-54

1.53E-01	8.14E-01	1.34E-01	2.88E-01	5.60E-01	9.84E-02	3.16E-02	2.13E-03
2.37E-01	1.47E-01	7.83E-01	7.31E-01	1.25E-01	6.13E-07	8.22E-01	1.28E-01
2.39E-01	6.95E-01	6.94E-01	3.99E-01	3.48E-01	3.04E-02	6.40E-02	2.86E-01
5.49E-02	9.30E-01	7.77E-01	1.54E-01	4.40E-02	7.35E-04	4.45E-06	7.77E-05
1.79E-01	4.03E-01	4.84E-01	2.31E-01	3.30E-01	5.37E-11	8.34E-03	3.29E-07
8.46E-01	9.84E-01	2.33E-01	5.21E-01	3.15E-01	6.56E-04	1.37E-01	3.16E-01
2.67E-01	6.73E-01	7.33E-01	6.57E-02	9.89E-01	2.19E-01	6.40E-01	2.14E-01
3.44E-01	8.54E-01	2.14E-01	3.29E-02	4.53E-02	2.15E-17	2.10E-01	5.51E-07
7.34E-01	8.88E-01	6.71E-01	4.22E-01	4.57E-01	5.24E-09	4.08E-01	4.19E-01
3.59E-01	7.92E-01	5.77E-01	2.77E-01	2.19E-01	3.20E-08	5.24E-01	8.31E-01
9.25E-01	9.47E-01	5.36E-01	1.79E-01	5.48E-01	6.90E-10	9.88E-01	1.30E-01
3.48E-01	9.24E-02	1.47E-01	3.99E-01	3.33E-01	2.96E-24	4.08E-04	4.10E-03
2.79E-01	4.69E-01	1.97E-01	8.62E-02	7.58E-02	4.39E-06	6.26E-03	4.01E-10
8.56E-01	NA	4.36E-01	6.53E-01	9.43E-01	1.54E-16	NA	9.63E-02
7.50E-01	3.25E-01	5.82E-01	7.63E-01	9.58E-01	1.65E-04	3.92E-01	7.16E-01
3.25E-01	3.19E-01	9.98E-01	3.43E-01	1.25E-01	2.83E-04	4.70E-02	2.89E-02
2.56E-01	9.22E-01	1.22E-01	8.13E-01	7.39E-01	1.06E-04	2.05E-01	6.20E-04
4.23E-01	6.54E-01	8.55E-01	2.34E-01	3.21E-01	1.96E-12	2.06E-01	2.52E-02
9.21E-01	2.55E-01	2.03E-01	3.76E-01	4.98E-01	1.41E-09	6.26E-03	6.90E-08
3.05E-01	4.31E-01	7.41E-01	3.89E-01	2.44E-01	3.82E-05	5.03E-02	2.86E-02
4.77E-01	7.68E-01	8.37E-01	3.39E-01	8.15E-01	2.39E-03	6.86E-01	1.79E-02
2.55E-01	4.60E-02	5.18E-02	8.76E-01	1.83E-02	1.82E-10	3.36E-03	1.51E-11
1.56E-01	8.58E-01	9.34E-01	5.17E-01	2.35E-01	3.58E-09	6.27E-02	5.39E-17
8.92E-01	6.13E-01	1.03E-01	6.73E-01	7.91E-01	1.31E-01	1.13E-01	6.75E-02
7.00E-01	8.85E-02	1.73E-01	5.90E-01	5.23E-01	8.36E-01	5.42E-01	3.21E-03
4.66E-01	8.42E-01	6.52E-01	6.71E-01	8.45E-01	6.41E-09	5.28E-03	3.27E-03
3.59E-01	NA	NA	3.38E-01	2.37E-01	3.72E-07	NA	NA
8.63E-01	NA	1.94E-01	4.57E-02	5.56E-01	6.55E-19	NA	1.22E-01
8.86E-01	NA	7.80E-01	2.21E-02	5.78E-01	7.57E-09	NA	2.31E-01
6.85E-01	6.80E-01	1.81E-01	4.23E-01	1.89E-01	1.01E-94	7.30E-09	2.19E-66
5.86E-01	1.43E-01	1.62E-01	3.40E-01	9.19E-01	5.28E-05	2.92E-03	3.53E-01
4.21E-01	5.27E-01	3.88E-01	1.31E-01	8.81E-01	1.44E-07	3.65E-01	9.78E-01
8.78E-01	9.69E-01	3.27E-01	5.15E-01	8.09E-01	4.77E-207	2.15E-01	2.18E-12
NA	3.89E-01	NA	2.49E-01	2.10E-01	NA	4.57E-07	NA
3.37E-01	9.63E-01	4.87E-01	4.45E-01	3.78E-01	3.08E-23	3.10E-14	4.71E-17
9.11E-01	3.77E-02	1.22E-02	1.43E-02	1.04E-01	1.79E-01	3.37E-03	3.36E-02
3.54E-02	9.10E-01	6.03E-01	5.86E-01	3.66E-02	4.31E-18	2.13E-03	4.09E-12
7.00E-01	6.90E-01	9.32E-01	3.90E-01	9.04E-01	2.15E-17	1.21E-01	1.24E-02
7.45E-02	NA	1.34E-01	8.74E-01	5.03E-02	3.57E-12	NA	8.58E-01
9.91E-03	8.87E-01	6.98E-01	1.93E-01	1.36E-01	1.54E-08	8.25E-01	2.09E-02
8.91E-01	NA	9.00E-01	6.47E-01	7.98E-01	2.83E-01	NA	8.79E-01
2.66E-01	NA	NA	4.71E-02	1.32E-01	1.44E-02	NA	NA
3.23E-01	8.62E-01	2.77E-01	1.19E-01	8.13E-01	2.38E-14	5.84E-04	3.18E-03
5.87E-01	4.54E-01	3.34E-01	5.08E-01	9.76E-01	2.36E-43	2.22E-03	1.23E-17
7.42E-01	3.70E-01	2.47E-01	4.84E-02	3.30E-01	1.34E-05	2.76E-02	4.46E-03
3.69E-02	8.69E-02	7.66E-01	6.54E-01	5.73E-02	6.92E-07	4.74E-01	3.86E-01
4.88E-01	NA	8.90E-02	3.14E-01	5.16E-01	2.26E-14	NA	2.44E-01

4.00E-01	3.63E-01	2.08E-01	9.70E-01	5.26E-01	2.10E-03	5.27E-01	3.28E-01
1.12E-01	7.18E-01	4.27E-01	8.29E-01	1.14E-01	5.78E-01	8.05E-02	5.59E-01
8.24E-01	9.82E-02	9.74E-01	4.85E-01	9.85E-01	1.94E-06	2.02E-01	9.16E-02
2.13E-01	1.13E-02	6.81E-01	6.69E-01	2.72E-01	9.85E-08	1.63E-01	8.13E-01
3.00E-01	4.71E-01	2.55E-02	7.69E-01	1.16E-01	8.18E-03	6.07E-01	4.55E-02
3.25E-01	2.97E-03	2.22E-01	1.32E-02	2.43E-01	3.83E-06	2.80E-01	2.87E-04
2.64E-01	8.68E-01	8.02E-01	9.79E-01	4.46E-01	4.30E-22	6.86E-05	1.78E-04
1.29E-01	6.93E-01	3.78E-01	9.32E-01	5.88E-01	8.40E-01	5.51E-01	7.57E-01
4.80E-01	8.35E-01	1.64E-01	4.31E-01	1.49E-01	2.28E-05	4.10E-01	3.33E-02
8.32E-01	2.32E-01	2.86E-01	4.50E-01	9.11E-01	6.24E-01	3.60E-01	3.89E-01
6.78E-01	NA	7.90E-01	3.04E-01	5.72E-01	4.85E-23	NA	1.65E-05
1.75E-02	9.06E-01	8.15E-01	7.81E-02	1.05E-01	1.23E-15	2.52E-09	1.00E-05
9.26E-01	7.62E-01	8.79E-01	8.04E-01	9.91E-01	2.81E-06	2.88E-02	2.93E-06
5.20E-01	4.48E-01	6.82E-01	6.57E-01	9.57E-01	3.56E-07	4.58E-01	2.12E-09
4.76E-01	7.29E-01	5.52E-01	8.40E-01	3.74E-01	1.27E-07	9.33E-01	1.35E-01

					SNPEffect		
HIS	META	EUR	AFR	ASN	HIS	BRA	META
3.47E-01	3.94E-01	0.847	1.753	2.342	1.498	2.156	1.427
2.12E-02	5.08E-02	-0.261	0.519	0.565	0.100	1.215	0.244
5.25E-01	6.67E-06	-0.146	1.113	-0.194	0.264	3.596	0.108
4.62E-03	1.21E-06	-0.327	1.935	-0.141	0.263	-0.848	-0.221
5.50E-01	6.28E-01	5.968	-1.201	2.315	0.458	-3.547	-0.659
6.99E-02	3.30E-08	1.578	3.847	0.302	0.087	2.841	1.375
4.06E-03	5.14E-03	-0.220	-0.190	0.347	-0.209	-1.532	-0.078
6.55E-01	8.39E-04	0.320	-0.597	0.166	0.001	-2.056	0.090
3.39E-01	5.15E-03	NA	4.197	3.647	4.370	-5.669	4.009
4.64E-01	2.56E-02	-0.913	-0.117	-0.607	-0.727	-0.933	-0.752
8.49E-01	1.85E-01	-1.269	-1.003	-0.470	0.117	-0.209	-0.974
8.43E-01	1.29E-01	1.985	0.890	1.528	-0.192	4.059	1.679
NA	1.74E-02	4.100	NA	NA	NA	-5.277	2.372
7.05E-01	3.42E-01	1.105	0.793	0.758	0.888	0.494	0.920
3.11E-01	4.07E-05	0.441	-13.320	-1.601	2.275	-2.919	0.122
8.55E-01	4.09E-08	0.109	8.745	3.298	-3.591	-2.095	0.189
1.20E-02	2.93E-01	-0.483	-0.981	-0.943	0.083	-1.611	-0.675
7.30E-01	1.61E-02	0.622	-1.129	0.044	-0.601	-1.818	0.177
3.76E-01	7.06E-01	-1.222	-1.666	-0.549	-0.745	-0.372	-0.964
NA	4.37E-08	2.541	NA	2.113	8.095	-3.695	2.438
4.78E-03	5.28E-17	0.290	-0.375	-0.720	0.087	-1.077	-0.040
NA	2.73E-01	-16.480	NA	NA	NA	-7.397	-16.100
2.99E-01	2.61E-05	2.053	1.727	1.190	1.672	0.822	1.723
1.04E-01	2.79E-19	0.252	-0.002	0.809	0.319	1.322	0.481
1.14E-05	1.16E-10	5.981	5.228	5.363	7.336	7.046	5.885
7.79E-02	1.71E-09	0.009	-0.039	0.068	-0.019	0.135	0.027
8.81E-02	3.60E-12	-0.605	-0.328	-0.380	-0.448	-0.668	-0.509
6.13E-02	6.12E-11	-1.141	-0.538	-0.931	-2.034	-1.450	-1.113
3.61E-02	1.76E-25	0.563	0.265	-0.596	-0.671	-0.975	0.047
4.06E-01	3.04E-02	1.103	-0.134	1.235	0.053	1.844	1.016
3.68E-01	6.28E-01	4.753	2.740	5.049	5.300	2.594	4.453
1.93E-01	8.35E-01	0.728	1.293	0.182	1.131	-0.528	0.597
2.71E-01	3.03E-01	0.000	-0.689	0.428	-1.726	-0.115	-0.027
9.86E-01	5.29E-01	-2.367	-3.353	-2.394	-4.322	-1.565	-2.636
3.82E-01	5.47E-01	-0.558	-1.065	-1.279	-1.843	-0.079	-0.944
6.01E-01	5.67E-01	-2.508	-1.820	-1.049	-2.163	0.887	-2.230
6.93E-01	1.69E-05	1.147	0.890	2.373	1.452	1.466	1.301
5.90E-01	1.12E-10	-0.770	0.474	0.247	-0.698	-2.026	-0.479

3.41E-02	3.27E-03	-0.623	-0.311	-0.680	-0.968	-1.674	-0.671
3.61E-03	9.31E-10	-0.207	-1.112	-0.217	-0.295	2.649	-0.234
5.78E-02	3.31E-11	0.007	0.316	0.075	0.376	0.211	0.077
7.65E-01	6.20E-02	-1.116	-1.381	-0.877	-1.332	-0.558	-1.056
1.78E-02	4.59E-10	0.298	0.842	-0.593	-0.911	-0.845	-0.004
7.42E-01	1.95E-06	0.532	0.833	-0.389	-0.139	-0.376	0.224
1.14E-03	3.00E-07	-0.198	-0.303	-0.122	0.179	0.411	-0.117
7.30E-01	6.42E-01	1.027	-0.406	0.436	0.016	1.693	0.619
4.43E-01	7.61E-07	0.238	-0.834	-2.058	0.472	-0.492	-0.057
1.05E-01	2.97E-08	0.565	-0.368	-0.016	0.697	-0.336	0.301
6.31E-02	7.36E-11	1.112	1.294	-5.742	1.510	1.829	1.148
1.99E-01	7.94E-12	-0.013	-0.114	-0.440	0.023	0.377	-0.183
4.28E-01	1.48E-01	2.072	3.029	1.862	5.101	-2.273	2.594
6.74E-01	7.42E-01	0.435	1.239	1.502	1.072	-2.378	0.595
3.70E-01	9.91E-01	1.624	0.924	0.250	1.393	-0.062	1.073
2.49E-01	1.22E-05	0.099	-0.890	NA	1.821	-1.108	0.117
5.06E-01	1.88E-02	1.055	0.408	0.418	1.743	3.122	0.934
4.29E-01	6.17E-06	1.002	0.526	1.554	4.041	2.676	1.271
6.27E-02	7.59E-04	0.340	0.679	0.392	1.374	2.069	0.469
3.14E-03	5.57E-11	-0.095	-1.163	-0.574	-0.096	0.797	-0.359
1.53E-01	1.25E-04	-0.388	-0.971	0.089	-1.035	-2.363	-0.393
3.15E-01	9.46E-01	-1.209	-0.682	0.071	-1.358	0.353	-0.947
3.22E-01	7.82E-04	-0.885	-0.342	-0.858	-0.399	-3.024	-0.830
8.72E-04	7.70E-08	0.072	-0.452	-0.114	-0.525	0.190	-0.097
1.10E-02	2.75E-10	0.178	0.081	0.511	0.128	0.608	0.298
4.11E-01	2.79E-02	2.070	-0.175	0.077	2.256	0.672	1.583
4.54E-01	6.55E-03	0.088	0.508	-0.087	1.071	1.058	0.325
7.22E-01	1.28E-06	0.186	0.115	0.331	0.438	1.767	0.292
1.68E-01	7.59E-18	-0.037	-1.117	-0.191	0.017	0.793	-0.131
9.54E-01	7.78E-01	0.887	0.900	0.984	0.245	0.738	0.910
3.23E-01	1.14E-02	-1.212	-1.922	-1.970	-1.138	-5.254	-1.435
7.37E-01	1.85E-01	1.101	1.332	1.073	0.311	2.372	1.094
3.31E-02	1.86E-18	0.191	0.164	-1.598	0.229	1.392	-0.354
4.84E-02	5.21E-06	3.680	0.311	NA	1.674	-3.870	0.464
1.87E-04	1.63E-22	-0.405	0.707	-0.500	0.384	-1.801	-0.353
2.28E-14	3.74E-74	-2.305	-3.495	-3.708	-0.971	-0.032	-2.376
5.44E-01	6.59E-01	-0.198	-0.901	-0.892	-1.364	-0.523	-0.500
3.80E-01	1.01E-02	-0.797	-0.025	-0.446	-0.290	-1.347	-0.565
8.14E-16	4.25E-166	-0.099	-0.805	0.242	0.531	-0.179	0.014
5.14E-01	9.01E-02	-1.910	-1.127	-0.140	-0.412	-4.107	-1.117
4.24E-01	4.79E-01	-1.460	0.493	-1.109	-0.904	-0.173	-1.174
7.68E-01	5.88E-21	0.623	-0.264	0.853	0.428	-0.896	0.564
4.25E-01	1.67E-07	-0.105	0.423	0.193	0.316	1.565	0.108
1.42E-01	2.03E-16	2.079	0.198	1.903	1.555	0.252	1.824
3.12E-02	1.25E-12	-0.149	0.088	-0.634	-0.285	0.318	-0.342
1.28E-01	6.13E-21	-0.018	1.098	-0.092	-0.455	-2.896	-0.089
3.52E-05	7.63E-93	-1.086	-0.594	-0.382	-2.400	-0.795	-0.851

9.73E-01	1.31E-02	2.471	1.954	1.668	3.400	2.085	2.222
1.39E-02	1.13E-07	0.230	1.208	0.347	-0.608	-0.251	0.234
2.82E-02	1.68E-03	-0.595	-1.271	-0.166	-0.352	0.182	-0.433
6.16E-01	8.73E-09	-0.355	-1.993	-0.560	-0.367	-1.428	-0.578
1.54E-03	2.26E-19	0.814	0.470	0.909	1.282	1.414	0.874
1.51E-01	3.30E-04	-0.317	-0.742	0.077	0.056	0.388	-0.138
2.80E-01	1.15E-01	-1.057	-0.447	-0.306	-1.006	-0.491	-0.685
8.17E-02	4.38E-22	0.050	-0.364	0.266	-1.114	-0.771	-0.022
8.23E-02	1.46E-06	0.589	-0.555	-0.096	0.295	-0.305	0.112
1.29E-01	6.10E-05	-0.012	-1.069	0.732	0.896	-1.002	0.359
4.83E-02	2.02E-10	0.141	0.109	0.790	0.641	0.341	0.333
4.61E-05	2.20E-26	2.117	-0.257	1.249	3.211	1.265	1.736
8.87E-03	2.48E-18	-0.009	0.447	0.586	0.251	-0.003	0.359
6.64E-02	9.42E-17	1.951	NA	0.995	4.904	2.614	2.122
7.19E-02	5.45E-03	2.791	5.399	1.010	1.092	-0.625	1.663
4.19E-02	1.07E-06	-1.064	-1.564	-0.150	-0.903	0.773	-0.794
1.04E-01	5.78E-08	-0.347	-0.004	0.539	0.557	1.155	0.036
6.16E-02	1.05E-12	-0.763	-0.163	-0.447	-0.009	-1.871	-0.553
1.71E-04	2.76E-19	-0.253	-1.000	-0.167	-0.077	0.454	-0.252
3.22E-01	2.73E-06	-0.687	-1.966	-0.976	-1.967	0.170	-0.848
1.02E-02	1.88E-05	-1.655	-0.724	-0.393	-1.363	-1.789	-1.079
1.23E-02	8.64E-24	-0.783	-0.915	-0.483	-0.183	-1.661	-0.594
7.11E-02	1.71E-24	0.476	0.189	-0.312	-0.858	1.007	-0.016
2.57E-01	8.47E-01	-0.969	-1.313	-1.741	-0.654	0.504	-1.081
5.86E-01	1.18E-01	1.086	0.752	1.499	1.982	2.254	1.253
5.44E-02	1.96E-12	-0.149	-0.359	-0.244	0.158	0.716	-0.137
4.36E-03	1.52E-08	-0.588	NA	-6.016	-3.139	5.880	-0.837
3.81E-05	1.70E-20	0.450	NA	-2.273	1.045	2.166	0.600
8.96E-06	4.91E-11	-1.153	NA	-0.105	-3.560	-3.975	-1.661
9.14E-13	2.83E-163	0.396	-0.666	-1.260	-0.718	0.685	-0.381
4.14E-01	1.25E-06	-0.014	-0.232	-0.541	-1.403	1.679	-0.213
2.78E-01	1.07E-04	-0.371	0.798	1.272	0.905	1.938	0.230
1.57E-20	1.27E-172	1.408	-0.181	-0.162	0.757	2.517	0.868
5.47E-01	1.37E-05	1.346	-0.288	NA	3.464	3.346	0.314
6.31E-08	6.90E-54	-0.238	-0.577	-0.332	-0.730	-0.267	-0.360
1.18E-01	5.85E-01	1.943	-1.082	1.831	2.948	3.293	1.874
3.54E-03	7.63E-32	0.242	0.212	-0.411	-1.478	-1.525	-0.161
6.88E-02	8.10E-17	-0.296	0.766	0.825	0.886	0.275	0.340
3.88E-04	1.60E-13	-2.739	NA	-2.506	-1.502	6.102	-2.239
6.87E-01	4.08E-07	-0.880	-1.747	-0.637	-1.250	-1.039	-0.894
7.37E-01	4.01E-01	4.202	NA	4.362	4.542	4.072	4.281
2.90E-02	5.36E-03	-4.473	NA	NA	-1.280	3.259	-4.017
3.81E-02	1.61E-17	-0.377	-1.362	0.897	-1.372	-2.161	0.046
1.39E-03	1.87E-58	-0.548	0.593	-1.187	0.005	-3.348	-0.790
2.09E-01	2.54E-08	0.254	0.111	-0.483	0.164	3.751	0.012
8.90E-02	7.56E-06	0.149	0.554	0.160	0.224	-0.029	0.227
1.47E-03	1.92E-14	1.356	NA	-3.225	3.441	13.400	1.562

3.94E-01	1.01E-02	7.846	5.684	7.289	6.898	5.246	7.479
2.84E-01	7.06E-01	-2.956	-0.275	-0.817	-2.531	-2.036	-1.928
1.65E-01	2.08E-06	0.103	0.700	-0.004	-0.669	0.771	0.059
2.28E-01	3.77E-04	-8.125	-1.260	0.417	-1.927	-4.631	-2.618
7.95E-01	1.68E-01	1.165	1.988	2.061	2.339	0.506	1.449
9.56E-01	1.06E-08	-0.117	-0.862	-0.035	-0.021	-0.348	-0.120
3.18E-05	7.41E-29	-0.511	-0.581	-0.142	0.868	-3.318	-0.279
5.59E-01	5.55E-01	-1.891	-0.748	-0.459	-1.080	-1.000	-1.253
9.97E-01	6.12E-05	-0.761	-1.530	0.021	0.404	0.363	-0.416
1.91E-01	3.49E-01	0.957	0.655	3.094	1.957	2.806	2.301
1.95E-12	4.06E-34	-2.121	NA	-4.262	-0.745	-4.958	-2.501
3.43E-03	8.56E-27	0.021	0.203	-0.127	0.066	0.335	-0.004
1.69E-01	9.51E-12	0.418	0.867	0.042	-0.199	0.083	0.265
6.15E-04	3.02E-16	-0.741	-0.243	-0.851	-0.712	-0.353	-0.798
3.72E-02	5.17E-07	-0.131	-0.953	0.021	-0.454	0.081	-0.159

IntEffect							
EUR	AFR	ASN	HIS	BRA	META	EUR	AFR
0.982	0.792	2.553	2.601	-1.694	0.676	4.04E-04	3.42E-05
0.186	-0.967	-1.024	0.139	-2.278	-0.417	5.74E-01	4.75E-01
0.099	-2.425	0.563	0.841	-3.168	-0.166	8.97E-01	8.64E-02
0.233	-0.816	0.015	-0.579	2.715	0.167	5.59E-01	5.90E-01
-3.276	-5.634	-7.894	-2.167	4.181	-4.070	3.80E-01	6.27E-09
-1.027	-1.616	1.495	0.291	-0.749	-0.722	1.95E-07	1.20E-02
0.489	1.214	-0.906	-0.607	1.143	0.259	2.10E-01	3.55E-01
-0.103	0.376	-0.106	0.943	3.999	0.162	2.44E-01	5.37E-01
NA	0.001	1.780	2.648	8.920	0.647	NA	3.17E-10
0.166	0.032	-0.210	-0.280	0.223	0.007	3.71E-09	9.90E-01
0.084	1.266	-0.708	-0.698	-0.988	-0.095	1.19E-09	4.88E-01
-0.893	-3.234	-0.210	2.679	-4.633	-0.555	1.07E-08	8.11E-01
-0.493	NA	NA	NA	16.150	2.222	1.65E-02	NA
-0.361	0.196	-0.156	0.875	-0.551	-0.146	3.29E-11	8.45E-02
0.043	19.600	4.328	-4.686	1.685	0.221	5.03E-01	2.35E-03
-0.785	0.089	-8.442	2.330	3.943	-0.841	2.58E-01	2.58E-01
-0.128	-1.872	0.640	-2.434	2.031	-0.025	2.35E-03	2.79E-02
-0.372	2.084	0.327	0.659	0.570	0.071	2.44E-02	8.55E-02
0.248	1.121	-0.817	-1.079	2.940	-0.013	2.50E-16	1.97E-02
1.295	NA	-2.563	-16.190	9.365	1.200	7.19E-14	NA
-0.213	2.194	0.357	-1.818	0.263	0.022	5.20E-01	3.92E-01
-0.898	NA	NA	NA	2.090	-0.918	1.54E-175	NA
0.036	-0.153	-0.849	-0.197	1.283	0.175	8.67E-58	1.67E-04
0.080	-0.177	-0.607	0.638	-1.060	-0.161	4.54E-02	9.63E-01
0.056	0.452	0.522	0.274	-1.508	0.194	0.00E+00	6.47E-34
0.112	-0.501	0.316	-0.241	0.527	0.096	6.95E-01	7.13E-01
-0.055	0.119	0.579	0.957	0.710	0.025	3.86E-06	8.44E-01
0.048	-0.796	-1.172	-0.121	-0.357	-0.125	6.67E-15	3.39E-01
-0.450	1.370	0.024	0.526	0.616	0.037	5.23E-02	1.11E-01
0.451	2.963	0.109	1.739	-2.768	0.521	1.18E-29	9.30E-04
0.193	0.219	-0.453	-0.044	1.272	0.310	5.24E-213	5.56E-11
0.367	0.250	1.175	0.538	2.415	0.571	7.73E-14	1.42E-01
-0.628	-0.324	0.066	2.445	1.337	-0.347	4.15E-03	2.81E-01
-0.238	0.832	1.779	2.189	0.476	0.152	7.84E-76	2.73E-07
-0.515	-0.037	0.865	-0.018	-0.160	-0.090	1.47E-12	9.25E-02
1.108	2.352	0.261	-0.778	-5.880	0.730	5.78E-15	7.45E-01
-0.297	0.823	-1.469	-0.313	-0.788	-0.416	9.36E-10	7.54E-02
0.331	0.120	-0.371	-1.048	1.879	0.044	4.79E-05	4.73E-01

-0.342	-0.358	-0.181	0.535	0.156	-0.246	6.68E-12	4.03E-01
0.276	0.971	0.099	-0.188	-3.200	0.242	6.72E-01	1.97E-01
-0.389	-0.581	0.118	-0.668	0.407	-0.396	3.07E-02	7.82E-01
0.474	1.665	0.540	-0.199	0.305	0.453	8.07E-10	4.66E-02
-0.665	-0.027	0.557	1.110	0.158	-0.254	1.42E-02	1.01E-01
0.249	-1.282	0.490	1.307	-0.877	0.389	5.79E-06	2.73E-01
0.168	1.261	-0.452	-0.319	-1.460	0.047	7.03E-01	2.20E-01
-0.252	0.243	0.382	1.411	-1.518	0.154	3.79E-09	7.98E-01
0.246	0.723	3.115	-0.441	2.822	0.515	9.34E-02	4.99E-01
-0.156	0.796	-0.830	0.417	0.520	0.012	1.11E-03	6.73E-01
-0.276	3.929	8.362	1.992	-1.777	-0.152	1.75E-03	1.78E-01
-0.146	-0.007	-0.022	0.160	0.878	0.034	6.22E-01	9.57E-01
-0.883	-2.046	-0.178	-5.597	5.015	-0.437	0.00E+00	7.04E-03
0.992	-0.093	-1.286	0.892	3.888	0.792	1.57E-11	8.74E-02
-0.133	-0.588	0.102	-1.128	0.662	0.167	1.35E-30	2.48E-01
0.640	1.981	NA	-0.653	-0.888	0.599	4.07E-02	8.18E-01
-0.037	-0.003	-1.099	-0.021	-2.924	-0.038	4.05E-12	8.01E-01
0.051	-0.312	0.296	-3.364	-1.450	-0.210	2.37E-07	9.55E-01
-0.030	1.831	0.009	-1.222	-0.919	-0.134	6.37E-02	2.17E-01
-0.430	0.968	0.965	-1.053	-1.209	-0.080	2.66E-03	2.44E-01
-0.422	0.129	0.388	0.773	2.067	-0.292	1.71E-07	5.74E-01
0.326	2.031	-1.396	0.554	0.080	0.178	6.06E-10	1.48E-01
-0.066	-0.674	0.114	-0.734	3.360	-0.107	4.52E-13	1.88E-01
0.389	0.600	-0.255	1.316	-1.134	0.420	1.58E-02	7.04E-01
0.168	0.468	-0.664	0.243	0.073	0.012	4.79E-02	6.36E-01
0.249	3.025	2.997	-0.838	1.899	0.828	2.59E-175	5.77E-04
0.931	-0.883	1.319	-1.891	0.105	0.467	6.82E-05	6.94E-01
0.184	-1.001	0.184	0.174	-0.707	0.094	9.41E-02	7.20E-01
-0.199	0.699	-0.404	0.224	-0.256	-0.116	2.63E-01	1.68E-01
0.916	1.637	-0.597	1.708	-0.156	0.712	1.82E-25	2.83E-02
-0.086	0.142	0.308	-1.295	1.641	0.023	7.30E-13	2.55E-01
0.546	-0.405	-0.110	1.173	-2.398	0.467	1.06E-35	1.53E-02
-0.228	-0.070	1.245	0.784	-2.698	0.299	8.64E-01	9.84E-01
-5.248	-0.002	NA	-2.005	3.243	-0.723	1.36E-01	8.48E-01
-0.076	-1.263	0.460	-0.951	0.900	-0.099	1.09E-03	4.54E-01
-0.643	0.620	-0.859	-0.812	-3.175	-0.532	7.18E-36	1.74E-07
0.281	1.181	0.464	0.795	0.485	0.538	5.94E-01	4.00E-01
-0.032	-1.164	0.692	-1.040	1.267	-0.171	8.76E-08	1.07E-01
0.692	0.048	-0.459	-1.191	-0.631	0.335	1.63E-03	2.11E-01
0.671	-0.514	-1.011	-0.056	1.890	-0.118	3.01E-20	2.11E-02
0.158	-1.500	-0.831	-0.142	-1.631	-0.180	3.02E-25	3.55E-01
-0.119	1.097	-0.273	-0.220	1.053	-0.057	8.26E-05	3.37E-01
0.102	-0.974	-0.477	-0.377	0.195	-0.130	9.25E-01	5.80E-01
0.406	0.162	-0.480	1.126	1.716	0.451	1.21E-85	7.69E-01
0.040	-2.130	1.198	0.769	-1.590	0.301	7.52E-01	1.71E-01
-0.238	0.668	-0.489	1.676	4.585	-0.010	4.67E-01	1.17E-01
0.204	0.305	-0.635	1.110	-1.324	-0.069	5.46E-10	6.44E-01

0.235	0.911	-0.090	-0.104	1.029	0.398	4.82E-69	1.36E-04
0.067	-1.382	0.413	1.201	-0.336	0.070	1.39E-01	2.30E-01
0.088	0.477	-0.246	-0.414	-1.520	-0.104	2.99E-05	5.19E-02
-0.452	1.144	0.086	-0.761	1.153	-0.205	5.30E-08	2.31E-03
0.077	-0.113	-0.027	-0.175	0.182	0.014	6.74E-10	6.54E-01
0.233	-0.267	-0.314	-0.254	-0.725	-0.015	3.90E-01	2.12E-01
0.001	0.468	0.167	1.438	-0.939	-0.104	1.01E-12	7.32E-01
0.022	-0.004	0.519	0.792	-0.742	0.117	9.13E-01	6.73E-01
-0.240	1.643	-0.064	-0.034	-2.085	0.208	2.03E-01	2.09E-01
0.460	0.777	-0.747	-1.175	-1.564	-0.093	2.46E-01	7.30E-01
0.137	-0.046	-0.919	-0.346	-0.972	-0.089	4.02E-01	9.96E-01
-0.295	0.774	-1.141	-1.248	-0.181	-0.164	1.54E-48	6.71E-01
0.363	0.128	-0.865	0.201	-0.396	-0.115	3.34E-01	4.69E-01
0.855	NA	-0.709	-6.081	1.210	0.493	9.60E-13	NA
-0.212	-1.622	-0.651	1.932	0.543	0.368	3.79E-26	1.99E-01
0.636	1.055	-1.178	1.028	-4.093	0.251	1.62E-01	5.98E-02
0.342	-0.816	-0.448	-1.096	-2.756	-0.122	5.26E-01	8.32E-01
0.247	-0.143	0.254	-0.672	0.737	0.036	5.73E-05	8.26E-01
-0.106	0.725	0.757	0.243	0.741	0.033	2.16E-02	2.43E-01
-0.101	-0.437	-0.944	0.273	-2.153	-0.043	1.13E-08	1.20E-02
0.251	1.840	-0.224	0.394	1.473	-0.135	1.86E-28	2.67E-01
0.394	-0.778	0.507	-1.259	-1.533	0.111	6.23E-02	1.60E-01
-0.719	-0.813	0.152	3.107	-1.352	-0.145	2.71E-01	9.49E-01
-0.189	0.366	0.714	-0.981	-0.497	-0.056	7.24E-11	9.70E-02
-0.055	0.134	0.645	-1.438	-0.454	-0.183	3.82E-14	2.71E-01
0.091	-1.377	0.636	-0.474	-0.765	0.047	8.23E-01	1.28E-01
0.707	NA	6.649	4.545	-6.498	1.030	8.03E-01	NA
-1.135	NA	-0.156	-3.388	-1.677	-1.330	3.40E-01	NA
1.754	NA	0.269	4.638	4.438	2.228	3.64E-01	NA
-0.192	0.610	0.374	1.208	0.784	0.501	1.20E-01	5.65E-01
-0.232	0.377	1.246	1.177	-1.762	0.022	3.76E-01	9.00E-01
0.573	0.024	-0.430	-0.463	-3.070	-0.007	2.25E-01	1.45E-01
-0.437	-0.014	0.698	-0.588	-1.295	0.010	3.97E-18	9.00E-01
-0.489	1.238	NA	-2.070	5.587	0.967	8.35E-01	6.28E-01
0.180	-0.065	-0.283	1.774	-0.072	0.261	7.48E-01	4.58E-01
0.376	1.368	-0.223	-0.342	-0.957	0.292	2.17E-45	4.91E-01
-0.078	-0.947	0.247	2.162	0.288	0.242	3.81E-01	4.56E-01
-0.182	-1.155	-1.417	-0.646	0.596	-0.778	3.52E-03	4.13E-01
0.879	NA	3.981	-2.018	-8.358	0.369	1.02E-03	NA
-0.238	0.218	-0.365	-0.060	0.327	-0.230	2.71E-17	1.95E-04
-0.753	NA	-12.790	0.193	-2.379	-0.853	6.57E-13	NA
-1.388	NA	NA	-3.069	-5.659	-1.741	3.24E-33	NA
-0.217	1.384	-2.010	1.114	1.187	-0.705	8.45E-05	5.51E-02
-0.212	-2.394	0.689	-3.135	2.556	-0.036	5.46E-05	4.37E-01
-0.475	0.174	0.926	-0.575	-1.926	-0.098	2.69E-01	8.84E-01
-0.044	-0.674	-0.678	0.573	-1.563	-0.213	6.40E-01	6.21E-01
-1.284	NA	-1.019	-1.781	-9.875	-1.403	6.94E-01	NA

0.725	1.655	-1.585	-0.657	0.501	0.833	0.00E+00	3.12E-12
-0.054	0.884	0.665	1.163	1.704	-0.384	5.64E-39	6.82E-01
-0.099	0.344	-0.067	1.051	-1.048	0.001	9.14E-01	1.07E-01
-1.053	-1.004	1.370	0.106	1.050	-4.279	0.00E+00	1.39E-03
0.234	0.230	0.117	-2.191	-0.904	-0.116	4.52E-25	3.12E-03
0.064	0.433	0.321	-0.163	-0.907	0.060	8.67E-01	4.79E-01
0.588	1.844	-0.554	-1.579	1.599	0.233	2.32E-01	3.45E-01
-0.318	-0.192	0.724	-0.196	1.351	-0.763	2.67E-85	3.59E-01
0.481	1.364	0.059	0.185	-0.879	0.219	3.44E-03	1.01E-01
-0.008	0.802	-3.563	-1.414	-1.282	-1.622	9.10E-11	4.22E-02
-0.326	NA	0.580	-1.424	2.076	-0.009	1.00E-08	NA
-0.332	-1.009	0.536	0.197	-1.284	-0.257	2.54E-01	4.20E-01
-0.047	-0.992	0.128	-0.212	1.513	0.048	8.00E-03	2.85E-01
0.451	-0.097	1.554	1.503	0.766	0.750	1.08E-02	8.73E-01
-0.172	0.017	0.018	0.312	-1.114	-0.143	1.14E-01	7.79E-02

LDL.CurDrink							
PJoint						PInt	
ASN	HIS	BRA	META	EUR	AFR	ASN	HIS
1.96E-01	1.18E-01	6.39E-01	4.68E-09	3.33E-01	4.21E-01	3.79E-01	3.83E-01
3.26E-02	9.10E-01	2.99E-01	1.64E-01	7.18E-01	2.75E-01	6.70E-01	9.64E-01
8.66E-01	5.01E-01	1.27E-01	8.84E-01	6.11E-01	3.82E-02	5.24E-01	5.21E-01
9.17E-01	9.27E-01	3.67E-01	6.48E-01	5.44E-01	7.15E-01	9.92E-01	6.49E-01
5.87E-01	7.18E-01	5.01E-01	2.52E-06	6.03E-01	6.37E-04	3.03E-01	7.09E-01
1.49E-01	9.44E-01	1.33E-01	2.01E-08	3.15E-03	2.35E-01	1.75E-01	6.88E-01
4.05E-01	5.58E-01	5.32E-01	4.74E-01	3.02E-01	2.69E-01	2.08E-01	6.76E-01
8.43E-01	3.02E-01	4.20E-02	2.21E-01	9.19E-01	9.15E-01	6.16E-01	3.91E-01
7.64E-03	4.03E-04	3.31E-01	8.19E-15	NA	8.04E-01	5.09E-01	4.10E-01
2.11E-02	2.03E-01	6.00E-01	7.50E-11	8.81E-01	2.97E-01	2.68E-01	7.78E-01
7.00E-01	7.82E-01	6.98E-01	8.96E-09	7.03E-01	3.58E-01	4.52E-01	6.64E-01
2.43E-02	7.21E-02	1.34E-01	3.33E-10	3.50E-01	6.84E-01	8.34E-01	8.39E-02
NA	NA	1.16E-02	3.02E-03	8.60E-01	NA	NA	NA
6.00E-03	3.20E-03	9.01E-01	1.93E-15	1.97E-01	3.70E-01	5.29E-01	2.64E-01
7.02E-01	2.26E-01	6.40E-01	7.51E-01	8.97E-01	1.59E-03	3.24E-01	1.19E-01
1.37E-01	4.75E-01	7.33E-01	2.64E-01	1.48E-01	9.94E-01	4.37E-02	5.98E-01
2.34E-02	3.90E-03	3.88E-01	2.95E-06	8.73E-01	2.00E-01	3.21E-01	1.34E-02
9.20E-01	7.31E-01	1.83E-01	2.09E-01	4.34E-01	6.07E-03	5.75E-01	5.29E-01
8.93E-04	2.62E-03	2.28E-02	9.43E-20	2.64E-01	1.30E-01	2.48E-01	2.32E-01
6.44E-01	2.50E-01	2.87E-01	3.62E-13	4.81E-01	NA	3.36E-01	1.15E-01
2.19E-01	1.02E-01	5.60E-01	9.78E-01	5.90E-01	4.00E-01	8.18E-01	1.49E-01
NA	NA	1.87E-01	6.32E-169	8.46E-01	NA	NA	NA
1.26E-03	1.13E-03	8.45E-02	8.35E-63	8.89E-01	6.30E-01	6.76E-01	7.11E-01
8.55E-03	2.24E-01	5.01E-01	9.39E-04	6.73E-01	5.13E-01	6.22E-01	4.40E-01
6.91E-51	5.43E-50	2.30E-13	0.00E+00	6.20E-01	7.87E-01	1.65E-01	5.91E-01
5.83E-01	9.05E-01	7.77E-01	6.25E-01	6.78E-01	4.03E-01	5.81E-01	7.63E-01
3.98E-01	5.30E-01	8.39E-01	3.53E-05	4.76E-01	8.14E-01	5.49E-01	3.29E-01
7.45E-06	2.29E-04	1.44E-01	1.54E-22	9.76E-01	2.88E-01	3.77E-02	9.34E-01
1.01E-01	5.12E-01	6.01E-01	7.97E-01	1.67E-01	2.07E-01	7.02E-01	5.66E-01
4.61E-06	1.58E-02	1.59E-01	3.78E-36	9.59E-02	1.77E-02	6.99E-01	4.74E-02
1.06E-14	3.30E-23	2.71E-04	1.60E-249	4.53E-01	7.03E-01	8.16E-01	9.51E-01
1.62E-02	6.22E-03	1.11E-01	6.03E-18	9.13E-02	6.65E-01	5.12E-02	4.20E-01
2.27E-01	3.61E-02	5.74E-01	7.87E-02	4.32E-02	9.93E-01	6.08E-01	1.89E-02
6.96E-04	2.33E-10	2.79E-01	2.48E-89	3.64E-01	5.46E-01	2.39E-01	3.36E-02
9.52E-05	1.52E-04	9.71E-01	1.03E-18	2.04E-01	5.90E-01	1.84E-01	8.26E-01
6.58E-01	2.01E-02	2.21E-02	4.68E-16	4.62E-02	4.70E-01	6.01E-01	6.90E-01
3.64E-03	4.48E-02	4.08E-01	9.56E-14	3.47E-01	6.69E-01	1.91E-01	6.13E-01
8.35E-01	1.32E-02	1.81E-01	2.17E-04	5.04E-01	8.16E-01	5.62E-01	1.53E-01

1.08E-02	1.91E-01	1.10E-01	7.71E-15	3.06E-01	7.51E-01	4.94E-01	4.96E-01
8.28E-01	6.68E-01	1.19E-01	4.85E-01	8.64E-01	3.60E-01	5.75E-01	9.75E-01
9.34E-01	7.66E-01	8.13E-01	5.50E-02	2.02E-01	7.71E-01	5.90E-01	4.71E-01
7.07E-03	4.55E-03	8.63E-01	7.38E-14	1.73E-01	1.16E-01	3.14E-01	7.01E-01
2.38E-01	2.94E-01	5.82E-01	1.35E-01	1.45E-02	9.78E-01	2.73E-01	1.47E-01
5.40E-01	2.21E-01	4.53E-01	1.92E-04	4.85E-01	1.38E-01	1.76E-01	3.07E-01
3.04E-01	9.22E-01	4.76E-01	6.76E-01	8.74E-01	4.93E-02	6.58E-01	6.80E-01
4.34E-02	5.24E-02	3.85E-01	7.82E-10	5.98E-01	6.12E-01	4.58E-01	9.61E-02
2.34E-01	8.47E-01	1.77E-01	9.72E-02	5.86E-01	5.89E-01	3.51E-01	6.18E-01
1.20E-01	8.79E-02	9.46E-01	1.22E-02	8.64E-01	3.65E-01	3.44E-01	7.06E-01
6.53E-01	1.71E-02	6.46E-01	1.40E-04	9.70E-01	3.24E-01	4.10E-01	3.71E-01
1.46E-01	9.59E-01	4.25E-01	3.38E-01	9.88E-01	8.14E-01	8.32E-01	8.32E-01
4.54E-02	5.57E-02	1.85E-01	2.17E-18	6.03E-01	6.73E-02	6.79E-01	2.77E-02
2.65E-01	8.47E-02	1.90E-01	7.26E-13	4.08E-02	9.92E-01	5.67E-01	6.79E-01
5.60E-01	5.83E-02	7.90E-01	3.47E-26	9.30E-01	5.78E-01	7.04E-01	1.69E-01
NA	6.18E-01	6.97E-01	4.71E-02	2.65E-01	3.90E-01	NA	8.33E-01
2.86E-01	1.95E-02	2.16E-01	6.72E-12	9.56E-01	7.41E-01	1.73E-01	9.57E-01
2.12E-01	5.60E-03	3.38E-01	3.06E-09	7.90E-01	8.36E-01	9.26E-01	6.40E-02
6.23E-01	2.48E-01	2.31E-01	9.55E-03	8.64E-01	5.17E-01	6.41E-01	3.07E-01
5.69E-02	1.25E-01	7.10E-01	8.34E-04	1.83E-01	2.70E-01	1.15E-01	2.35E-01
6.54E-01	3.21E-01	1.03E-01	1.34E-06	1.93E-01	8.88E-01	3.61E-01	4.39E-01
4.09E-01	1.10E-01	8.95E-01	8.24E-09	3.92E-01	3.97E-02	2.64E-01	5.54E-01
1.29E-01	1.12E-01	1.70E-02	2.59E-15	9.45E-01	3.71E-01	8.81E-01	3.67E-01
5.95E-01	2.61E-01	6.40E-01	5.87E-02	1.14E-01	9.46E-01	3.40E-01	7.38E-02
2.05E-01	7.96E-01	6.82E-01	1.52E-02	6.59E-01	6.49E-01	5.14E-01	1.00E+00
3.35E-02	7.84E-03	1.14E-01	1.56E-178	7.57E-01	4.39E-03	7.17E-02	4.96E-01
8.68E-01	2.67E-01	5.49E-01	7.19E-04	5.05E-02	8.34E-01	9.85E-01	1.00E-01
3.45E-01	6.22E-01	3.26E-01	2.22E-02	4.28E-01	6.94E-01	5.56E-01	9.22E-01
2.45E-01	9.12E-01	6.76E-01	1.22E-01	3.93E-01	3.47E-01	3.97E-01	6.70E-01
8.22E-03	1.09E-01	8.22E-01	5.43E-27	9.62E-03	2.18E-01	4.52E-01	1.43E-01
1.00E-02	4.98E-03	3.19E-04	2.22E-18	6.53E-01	9.80E-01	9.67E-01	2.79E-01
6.94E-02	4.80E-02	1.16E-01	2.41E-38	3.82E-01	8.71E-01	6.46E-01	1.42E-01
3.49E-03	6.49E-01	5.29E-01	4.21E-01	5.63E-01	5.15E-01	9.83E-02	9.88E-01
NA	9.52E-01	5.32E-01	7.38E-01	3.55E-01	9.15E-01	NA	7.76E-01
2.48E-01	4.88E-01	2.15E-01	4.54E-04	7.05E-01	3.23E-01	6.43E-01	3.59E-01
1.64E-08	2.32E-02	1.26E-01	1.58E-48	3.75E-01	5.36E-01	6.35E-01	4.81E-01
1.39E-01	5.51E-02	9.09E-01	3.13E-02	2.86E-01	2.51E-01	4.75E-01	3.63E-01
2.26E-01	8.09E-02	5.61E-01	2.57E-08	8.40E-01	2.01E-01	9.30E-01	2.43E-01
6.82E-01	4.45E-01	7.40E-01	6.53E-02	4.70E-02	8.31E-01	7.96E-01	1.44E-01
4.49E-02	7.61E-01	2.33E-02	8.40E-20	1.87E-02	8.72E-01	9.17E-02	9.17E-01
1.42E-06	1.50E-01	2.25E-01	1.77E-30	5.59E-01	2.56E-01	1.19E-02	8.71E-01
1.62E-02	7.39E-01	7.31E-01	4.03E-06	9.27E-01	1.45E-01	3.50E-01	8.95E-01
6.21E-01	8.73E-01	8.22E-02	8.25E-01	9.80E-01	1.79E-01	4.44E-01	6.98E-01
4.78E-15	4.68E-07	1.12E-01	1.30E-98	4.16E-01	8.86E-02	6.87E-01	1.28E-01
5.42E-02	6.65E-01	4.51E-01	2.41E-01	8.81E-01	8.90E-02	4.33E-03	4.49E-01
8.47E-01	4.13E-01	9.45E-02	8.41E-01	8.50E-01	4.46E-01	9.53E-01	1.72E-01
2.35E-02	1.71E-04	1.29E-01	1.67E-13	3.74E-01	8.42E-01	1.75E-01	2.35E-01

2.34E-08	8.26E-09	1.27E-02	4.14E-86	6.97E-01	1.88E-01	7.01E-01	9.27E-01
4.23E-01	3.80E-01	8.41E-01	7.51E-02	9.13E-01	7.47E-02	4.18E-01	1.44E-01
4.86E-01	4.29E-01	3.86E-01	2.34E-06	8.06E-01	9.27E-01	9.77E-01	6.96E-01
9.50E-02	1.30E-01	3.87E-01	6.29E-11	1.22E-01	4.64E-01	7.17E-01	3.75E-01
6.11E-03	2.73E-02	1.59E-01	7.23E-14	5.72E-01	6.21E-01	6.01E-01	7.34E-01
7.92E-01	9.40E-01	8.98E-01	3.89E-01	2.41E-01	6.16E-01	8.33E-01	7.28E-01
4.82E-01	1.94E-01	3.19E-01	1.73E-10	8.83E-01	9.92E-01	8.31E-01	1.07E-01
1.15E-01	1.93E-01	3.86E-01	8.25E-01	8.74E-01	8.54E-01	2.97E-01	3.54E-01
9.52E-01	9.10E-01	4.36E-01	3.56E-01	4.10E-01	7.34E-02	9.71E-01	9.48E-01
2.43E-01	6.25E-01	3.26E-01	2.62E-01	4.91E-01	5.77E-01	5.52E-01	4.05E-01
4.07E-01	7.67E-01	9.20E-01	2.49E-01	9.62E-01	7.31E-01	5.85E-01	8.14E-01
1.05E-04	1.51E-08	3.06E-01	3.98E-51	1.69E-01	4.19E-01	1.25E-01	8.46E-02
1.41E-01	8.17E-01	9.60E-01	1.25E-01	4.34E-01	8.72E-01	2.84E-01	8.76E-01
8.73E-01	6.88E-02	3.53E-01	1.32E-12	1.99E-01	NA	9.89E-01	5.52E-02
1.78E-02	5.81E-02	9.69E-01	6.27E-23	5.09E-01	7.30E-01	6.61E-01	2.57E-01
3.85E-01	5.14E-01	1.53E-01	1.54E-02	8.11E-01	7.35E-01	2.07E-01	2.72E-01
5.16E-01	5.15E-01	2.67E-01	8.70E-01	2.01E-01	7.88E-01	5.62E-01	1.54E-01
5.83E-01	5.15E-01	2.01E-01	2.60E-05	3.86E-01	8.68E-01	9.12E-01	4.91E-01
3.10E-01	9.48E-01	3.94E-01	7.78E-02	7.43E-01	5.45E-01	2.03E-01	8.16E-01
2.01E-01	8.57E-04	1.39E-01	1.77E-12	5.83E-01	6.55E-01	5.88E-01	7.98E-01
1.20E-01	2.68E-02	3.00E-01	1.07E-25	6.71E-01	1.77E-01	3.27E-01	4.91E-01
3.16E-01	2.22E-01	4.75E-02	3.50E-03	2.95E-01	9.63E-01	7.92E-01	2.55E-01
6.23E-01	7.38E-02	8.21E-01	7.24E-01	3.13E-01	6.52E-01	7.71E-01	4.13E-02
6.46E-03	1.78E-02	9.42E-01	3.99E-14	4.27E-01	5.68E-01	4.33E-01	2.22E-01
1.70E-05	6.70E-03	2.59E-02	6.02E-21	9.40E-01	9.80E-01	2.88E-01	7.65E-02
5.59E-01	8.35E-01	8.29E-01	6.78E-01	5.86E-01	1.89E-01	3.62E-01	6.28E-01
4.13E-01	1.35E-01	1.44E-01	5.37E-01	4.52E-01	NA	4.11E-01	8.44E-02
8.39E-01	4.00E-01	7.25E-01	2.27E-01	1.67E-01	NA	9.85E-01	2.14E-01
9.98E-01	2.22E-01	5.48E-01	1.22E-01	8.14E-02	NA	5.66E-01	1.48E-01
3.75E-06	3.64E-01	2.56E-01	5.36E-02	3.00E-01	8.46E-01	7.10E-01	1.64E-01
5.11E-01	2.07E-01	5.03E-01	3.41E-01	8.34E-01	5.47E-01	3.11E-01	2.41E-01
1.39E-01	3.18E-01	1.83E-01	2.37E-01	1.18E-01	5.05E-01	3.78E-01	5.74E-01
5.89E-01	4.39E-01	4.37E-02	6.46E-15	6.49E-02	4.14E-01	8.71E-01	6.20E-01
NA	4.59E-01	1.40E-01	3.47E-01	8.94E-01	6.27E-01	NA	6.04E-01
3.68E-01	2.36E-01	9.50E-01	2.46E-01	3.98E-01	8.54E-01	8.73E-01	1.11E-01
1.94E-12	1.21E-06	8.28E-03	1.52E-59	3.58E-01	1.91E-01	2.53E-01	8.03E-01
2.94E-01	6.21E-02	3.00E-01	5.44E-01	5.57E-01	5.19E-01	8.47E-01	1.47E-02
6.79E-04	2.85E-01	6.45E-01	4.17E-04	8.18E-01	4.27E-01	5.48E-01	4.48E-01
8.59E-01	5.23E-01	4.42E-01	1.32E-03	3.45E-01	NA	5.98E-01	6.65E-01
2.88E-03	1.00E-02	4.62E-01	4.83E-24	3.99E-01	9.28E-01	4.35E-01	9.94E-01
3.59E-01	8.76E-04	4.53E-01	1.99E-15	4.19E-01	NA	1.56E-01	9.14E-01
NA	3.07E-01	6.85E-01	5.30E-32	3.60E-01	NA	NA	4.64E-01
2.94E-07	7.00E-02	8.59E-02	1.84E-06	3.73E-01	1.71E-01	6.52E-01	2.57E-01
5.78E-03	7.57E-03	9.58E-02	4.52E-08	4.36E-01	3.84E-01	1.93E-01	1.86E-02
1.57E-01	8.45E-01	1.12E-02	8.44E-01	1.50E-01	8.97E-01	7.73E-02	6.17E-01
1.72E-01	3.58E-01	2.14E-01	3.22E-01	4.68E-01	3.78E-01	5.96E-01	3.89E-01
3.86E-01	4.62E-01	4.81E-02	4.62E-01	4.11E-01	NA	8.60E-01	6.85E-01

4.06E-13	4.99E-19	1.96E-06	0.00E+00	7.40E-01	8.72E-01	6.72E-01	6.71E-01
3.28E-01	8.61E-03	6.52E-01	3.56E-31	3.40E-01	2.66E-01	5.19E-01	4.20E-01
9.83E-01	4.03E-01	7.65E-01	8.40E-01	6.58E-01	6.00E-01	5.86E-01	2.43E-01
1.46E-03	7.25E-02	2.72E-02	1.67E-273	9.35E-01	5.31E-01	1.60E-01	7.60E-01
2.37E-04	1.24E-03	8.28E-01	2.69E-30	7.02E-01	8.94E-01	8.15E-01	1.29E-02
8.05E-01	9.57E-01	4.88E-01	7.60E-01	6.43E-01	6.75E-01	5.19E-01	8.43E-01
4.06E-01	2.10E-01	5.07E-02	4.22E-01	7.10E-02	1.42E-01	2.19E-01	6.94E-02
2.63E-01	5.45E-02	7.09E-01	7.02E-77	6.04E-01	7.58E-01	1.08E-01	9.14E-01
9.82E-01	4.96E-01	8.28E-01	3.54E-02	6.38E-02	1.38E-01	9.92E-01	7.21E-01
4.16E-46	6.77E-03	2.24E-02	4.07E-46	9.08E-01	4.92E-01	8.84E-01	1.47E-01
2.63E-04	2.99E-01	8.44E-02	1.94E-12	6.43E-01	NA	7.76E-01	3.21E-01
7.01E-01	9.51E-01	6.93E-01	2.99E-01	2.04E-01	2.19E-01	2.01E-01	1.00E+00
8.99E-01	7.52E-01	2.47E-01	1.53E-02	5.54E-01	4.37E-01	7.62E-01	5.39E-01
2.44E-04	1.71E-01	9.06E-01	4.14E-05	1.94E-01	7.22E-01	3.94E-01	9.85E-02
9.93E-01	7.14E-01	5.20E-01	5.02E-02	4.17E-01	8.82E-01	5.84E-01	6.49E-01

						PMain	
BRA	**META**	**EUR**	**AFR**	**ASN**	**HIS**	**BRA**	**META**
5.55E-01	1.72E-01	2.57E-01	9.23E-03	2.52E-01	4.87E-01	3.57E-01	2.57E-03
1.09E-01	5.81E-01	4.04E-01	3.69E-01	8.25E-01	8.68E-01	3.65E-01	9.32E-01
2.59E-01	9.83E-01	6.31E-01	1.59E-01	8.19E-01	8.07E-01	5.80E-02	7.10E-01
1.41E-01	5.57E-01	3.49E-01	3.74E-01	8.10E-01	7.78E-01	7.96E-01	4.61E-01
3.42E-01	3.70E-03	2.15E-01	2.80E-01	5.90E-01	8.04E-01	2.47E-01	4.83E-01
6.39E-01	1.63E-02	1.61E-06	9.84E-03	5.12E-01	8.95E-01	1.29E-01	5.08E-07
3.30E-01	4.91E-01	4.69E-01	8.18E-01	4.95E-01	8.06E-01	2.71E-01	6.32E-01
1.62E-02	6.03E-01	2.65E-01	2.93E-01	5.19E-01	9.90E-01	9.51E-02	6.10E-01
1.85E-01	5.69E-01	NA	1.77E-06	6.87E-02	2.11E-02	3.57E-01	8.91E-08
9.10E-01	5.30E-01	2.38E-04	9.56E-01	4.38E-02	2.65E-01	4.65E-01	2.90E-05
7.18E-01	8.05E-01	3.18E-04	2.23E-01	6.03E-01	8.97E-01	9.82E-01	7.80E-04
7.14E-02	4.86E-01	5.12E-06	7.78E-01	2.50E-02	8.60E-01	4.91E-02	9.99E-07
1.96E-02	2.59E-01	1.46E-01	NA	NA	NA	3.60E-01	3.65E-01
3.89E-01	3.83E-01	4.12E-06	1.52E-01	9.45E-04	1.32E-01	6.49E-01	2.78E-09
7.08E-01	9.64E-01	5.06E-01	1.64E-03	6.02E-01	2.30E-01	3.98E-01	8.08E-01
4.85E-01	1.21E-01	8.85E-01	2.35E-01	1.89E-01	2.44E-01	6.69E-01	7.81E-01
2.52E-01	8.30E-01	1.31E-01	2.83E-01	1.67E-02	9.04E-01	1.99E-01	4.09E-03
7.53E-01	6.33E-01	2.43E-02	1.02E-01	8.48E-01	4.31E-01	1.62E-01	4.67E-01
7.56E-02	5.05E-01	3.14E-07	6.80E-03	2.37E-02	2.12E-01	8.29E-01	3.14E-09
1.64E-01	6.54E-01	2.33E-03	NA	3.56E-01	3.31E-01	4.96E-01	1.93E-03
9.01E-01	5.28E-01	3.06E-01	7.50E-01	2.21E-01	8.91E-01	4.18E-01	9.99E-01
7.67E-01	8.88E-01	7.02E-52	NA	NA	NA	1.93E-01	8.60E-50
3.98E-01	8.65E-01	2.40E-16	2.29E-03	3.93E-04	5.49E-03	5.56E-01	3.45E-21
4.93E-01	9.56E-01	2.75E-01	9.81E-01	1.06E-02	6.32E-01	1.87E-01	9.91E-03
5.82E-01	2.87E-01	1.34E-98	1.29E-17	1.13E-33	1.77E-25	6.26E-09	1.94E-170
9.67E-01	7.54E-01	9.90E-01	9.43E-01	6.76E-01	9.91E-01	8.86E-01	7.91E-01
9.65E-01	2.93E-01	1.63E-02	5.78E-01	5.26E-01	4.51E-01	5.32E-01	1.37E-02
8.01E-01	2.65E-01	4.02E-05	5.69E-01	1.17E-02	4.27E-03	2.63E-01	4.69E-08
9.64E-01	4.15E-01	2.27E-02	7.58E-01	1.03E-01	2.39E-01	3.51E-01	7.67E-01
4.32E-02	2.42E-02	8.28E-06	8.70E-01	8.60E-05	9.52E-01	8.63E-02	1.69E-08
3.42E-01	3.96E-01	9.43E-57	1.44E-06	7.45E-10	5.24E-14	2.69E-02	1.37E-78
8.66E-02	8.37E-03	4.58E-03	2.33E-01	6.06E-01	6.65E-02	6.26E-01	2.12E-03
3.60E-01	3.44E-01	9.92E-01	3.33E-01	4.28E-02	1.85E-02	9.11E-01	7.33E-01
7.52E-01	7.46E-01	2.97E-19	1.13E-05	1.47E-03	1.44E-09	3.50E-01	5.26E-31
8.83E-01	8.45E-01	2.44E-02	1.29E-01	2.57E-05	3.45E-03	9.72E-01	1.88E-07
3.78E-02	1.14E-01	1.36E-09	4.56E-01	4.17E-01	1.07E-01	6.79E-01	2.34E-09
8.95E-01	2.23E-01	2.70E-05	2.88E-01	9.27E-04	4.77E-02	1.93E-01	1.61E-08
3.77E-01	8.77E-01	1.07E-03	4.37E-01	5.32E-01	2.55E-01	6.31E-02	8.96E-03

9.93E-01	3.30E-01	9.31E-03	5.34E-01	1.56E-02	9.68E-02	3.05E-01	7.25E-05
4.40E-02	8.80E-01	4.19E-01	6.57E-02	9.23E-01	6.27E-01	6.07E-02	3.04E-01
8.80E-01	2.41E-01	9.84E-01	5.61E-01	9.35E-01	6.11E-01	7.97E-01	6.87E-01
6.56E-01	5.79E-02	1.71E-06	1.37E-02	5.62E-03	2.59E-02	6.86E-01	4.86E-10
4.46E-01	2.91E-01	2.11E-01	1.15E-01	8.80E-02	1.41E-01	4.80E-01	9.81E-01
4.29E-01	4.24E-01	6.72E-02	1.49E-01	2.11E-01	8.29E-01	6.44E-01	3.38E-01
2.18E-01	9.02E-01	4.10E-01	5.96E-01	4.58E-01	7.76E-01	7.23E-01	3.29E-01
4.91E-01	6.32E-01	8.93E-05	5.53E-01	1.07E-01	9.95E-01	1.70E-01	3.32E-04
1.79E-01	3.97E-01	5.37E-01	2.62E-01	2.29E-01	5.83E-01	7.68E-01	9.42E-01
4.47E-01	9.03E-01	1.89E-02	5.51E-01	5.56E-01	2.45E-01	7.81E-01	1.56E-01
5.90E-01	7.63E-01	2.10E-02	6.54E-01	3.91E-01	2.67E-01	5.14E-01	1.09E-02
5.07E-01	9.99E-01	9.83E-01	8.68E-01	1.70E-01	9.70E-01	7.36E-01	4.06E-01
9.09E-02	2.93E-01	2.54E-08	3.17E-03	3.29E-02	1.65E-02	3.43E-01	8.66E-11
2.22E-01	5.33E-02	3.45E-01	9.70E-02	1.21E-01	2.80E-01	1.71E-01	6.63E-02
6.46E-01	7.74E-01	1.37E-10	1.08E-01	6.59E-01	1.36E-02	8.49E-01	6.29E-09
7.81E-01	2.58E-01	6.58E-01	6.47E-01	NA	4.10E-01	5.45E-01	6.69E-01
1.90E-01	4.19E-01	5.40E-05	6.73E-01	2.62E-01	4.40E-02	8.10E-02	7.50E-06
4.92E-01	4.36E-01	4.35E-03	8.26E-01	2.01E-01	1.48E-03	2.15E-01	9.34E-05
5.43E-01	9.66E-01	2.27E-01	5.82E-01	7.44E-01	8.52E-02	1.70E-01	6.28E-02
4.80E-01	6.33E-01	7.14E-01	8.65E-02	4.91E-02	8.74E-01	4.87E-01	6.46E-02
6.43E-01	6.27E-01	1.15E-01	3.71E-01	8.92E-01	1.42E-01	4.13E-02	4.19E-02
9.23E-01	2.40E-01	3.08E-05	3.60E-01	7.80E-01	6.57E-02	8.07E-01	6.41E-05
1.10E-02	8.94E-01	2.60E-04	5.34E-01	8.71E-02	5.14E-01	4.49E-03	1.59E-05
4.42E-01	2.65E-01	8.37E-01	4.23E-01	8.08E-01	3.83E-01	8.70E-01	6.10E-01
7.39E-01	8.25E-01	4.60E-01	8.93E-01	4.12E-01	8.46E-01	6.20E-01	2.42E-01
2.45E-01	2.89E-01	3.17E-04	7.70E-01	8.19E-01	8.84E-03	6.02E-01	2.16E-04
9.61E-01	3.27E-01	8.43E-01	4.76E-01	9.76E-01	2.21E-01	5.32E-01	3.06E-01
5.96E-01	4.32E-01	5.18E-01	9.20E-01	4.16E-01	5.74E-01	2.76E-01	2.00E-01
6.58E-01	4.32E-01	9.37E-01	6.90E-02	4.92E-01	9.49E-01	4.84E-01	4.34E-01
5.92E-01	3.15E-02	3.15E-03	3.44E-01	6.18E-03	8.14E-01	7.49E-01	4.93E-05
3.81E-01	5.69E-01	2.82E-04	3.19E-01	4.74E-03	1.77E-01	2.40E-03	2.80E-07
1.90E-01	3.01E-01	7.33E-05	1.79E-02	1.20E-01	6.15E-01	5.68E-02	1.01E-06
5.13E-01	7.43E-01	5.79E-01	8.58E-01	2.71E-03	8.34E-01	4.23E-01	2.93E-01
4.39E-01	9.06E-01	2.21E-01	6.77E-01	NA	7.66E-01	2.68E-01	5.61E-01
8.55E-01	5.45E-01	9.53E-02	3.45E-01	1.76E-01	5.00E-01	1.01E-01	7.19E-02
3.79E-01	2.94E-01	2.65E-08	1.47E-05	7.28E-06	2.03E-01	9.85E-01	1.23E-14
7.55E-01	8.16E-02	4.32E-01	1.89E-01	2.82E-02	1.95E-02	6.70E-01	7.02E-03
5.62E-01	3.94E-01	4.72E-03	9.56E-01	7.58E-01	6.51E-01	2.43E-01	2.22E-02
4.98E-01	3.89E-01	6.88E-01	1.73E-01	8.20E-01	4.45E-01	8.83E-01	7.41E-01
3.93E-01	2.43E-01	5.96E-11	1.18E-01	4.95E-01	6.12E-01	3.20E-02	1.23E-08
2.76E-01	3.02E-01	6.61E-09	5.07E-01	3.23E-03	2.00E-01	9.68E-01	1.29E-09
5.29E-01	8.99E-01	8.76E-03	7.12E-01	6.05E-03	4.71E-01	2.37E-01	1.14E-03
7.68E-01	4.50E-01	6.78E-01	5.15E-01	5.54E-01	6.11E-01	1.80E-01	5.99E-01
8.23E-02	1.12E-01	6.88E-19	6.83E-01	1.00E-10	6.34E-03	8.17E-01	6.74E-27
6.76E-01	2.46E-01	6.28E-01	9.79E-01	4.63E-02	6.86E-01	7.60E-01	1.09E-01
4.80E-02	7.34E-01	9.92E-01	3.11E-01	9.83E-01	6.78E-01	8.00E-02	8.23E-01
5.36E-01	8.37E-01	1.17E-04	4.29E-01	1.23E-01	2.67E-04	5.54E-01	1.77E-06

9.64E-01	6.89E-01	3.87E-18	1.57E-02	9.69E-08	1.05E-05	1.79E-01	7.45E-29
6.76E-01	7.79E-01	4.08E-01	1.09E-01	8.79E-01	3.92E-01	8.50E-01	3.81E-01
3.08E-01	9.72E-01	5.98E-03	3.75E-02	3.82E-01	5.83E-01	8.84E-01	2.80E-03
3.76E-01	1.90E-01	1.39E-01	1.39E-03	1.44E-01	4.94E-01	2.02E-01	1.88E-03
7.86E-01	9.82E-01	2.92E-03	4.80E-01	8.30E-03	4.35E-02	2.50E-01	6.45E-06
3.18E-01	6.57E-01	1.98E-01	2.73E-01	7.56E-01	9.07E-01	6.59E-01	2.20E-01
4.44E-01	8.88E-01	2.06E-04	4.33E-01	2.33E-01	1.03E-01	6.73E-01	1.26E-04
8.70E-01	4.51E-01	9.01E-01	5.18E-01	4.93E-01	7.52E-02	6.70E-01	7.84E-01
6.84E-01	9.32E-01	2.03E-01	4.35E-01	7.57E-01	7.21E-01	9.84E-01	7.16E-01
4.46E-01	9.29E-01	9.95E-01	4.64E-01	1.34E-01	3.52E-01	6.69E-01	2.83E-01
7.28E-01	8.58E-01	6.83E-01	9.43E-01	1.89E-01	4.89E-01	8.79E-01	2.41E-01
8.54E-01	3.84E-02	1.33E-17	6.98E-01	1.55E-04	9.64E-08	2.43E-01	4.73E-22
8.33E-01	9.62E-01	9.70E-01	4.39E-01	2.32E-01	7.75E-01	8.85E-01	2.45E-01
8.10E-01	4.53E-01	3.33E-03	NA	6.13E-01	2.27E-02	5.22E-01	5.04E-04
8.67E-01	6.02E-01	4.57E-10	1.60E-01	5.48E-03	4.00E-01	8.06E-01	1.66E-09
1.55E-01	9.73E-01	1.37E-01	2.02E-02	6.70E-01	2.55E-01	7.41E-01	1.30E-02
1.96E-01	9.14E-01	2.75E-01	9.91E-01	2.98E-01	4.10E-01	4.55E-01	9.23E-01
8.01E-01	6.94E-01	1.07E-02	8.08E-01	2.66E-01	9.74E-01	1.60E-01	9.75E-03
7.06E-01	5.88E-01	2.86E-01	8.99E-02	5.11E-01	8.95E-01	6.66E-01	1.29E-01
1.92E-01	4.15E-01	5.74E-03	5.74E-02	3.25E-01	3.43E-03	8.86E-01	9.94E-05
2.62E-01	1.52E-01	2.99E-11	3.81E-01	1.91E-02	2.85E-02	1.16E-01	4.10E-12
3.87E-01	7.16E-01	7.37E-02	4.10E-01	1.82E-01	8.22E-01	3.28E-01	1.99E-02
5.13E-01	8.06E-01	1.89E-01	8.97E-01	3.57E-01	4.06E-01	5.99E-01	9.96E-01
7.85E-01	4.41E-01	2.31E-03	6.78E-02	7.56E-03	2.91E-01	7.30E-01	2.89E-05
6.33E-01	7.51E-01	4.96E-05	2.99E-01	4.02E-03	1.99E-03	3.42E-02	2.86E-09
6.66E-01	7.78E-01	6.30E-01	6.78E-01	9.96E-01	7.41E-01	5.22E-01	8.36E-01
3.68E-02	3.73E-01	5.64E-01	NA	1.85E-01	6.70E-02	6.38E-02	2.99E-01
7.85E-01	8.49E-02	4.66E-01	NA	7.00E-01	5.52E-01	4.85E-01	3.37E-01
3.23E-01	3.31E-02	2.90E-01	NA	9.73E-01	9.62E-02	2.79E-01	6.92E-02
7.42E-01	6.23E-01	1.31E-01	2.95E-01	1.76E-03	2.43E-01	5.64E-01	1.69E-01
3.28E-01	4.16E-01	9.73E-01	7.31E-01	2.59E-01	7.82E-02	2.48E-01	3.52E-01
6.52E-02	4.18E-01	2.30E-01	2.23E-01	1.34E-01	1.64E-01	1.46E-01	4.14E-01
5.18E-01	1.36E-01	4.66E-07	7.72E-01	5.88E-01	2.01E-01	3.82E-02	3.63E-06
4.63E-01	7.40E-01	6.40E-01	7.37E-01	NA	2.41E-01	5.82E-01	7.63E-01
7.12E-01	2.97E-01	4.62E-01	3.29E-01	4.54E-01	3.66E-01	8.05E-01	1.13E-01
8.66E-01	7.60E-01	3.88E-11	2.39E-01	1.59E-12	7.38E-05	1.31E-02	7.12E-24
8.11E-01	8.89E-01	3.51E-01	7.62E-01	5.46E-01	3.55E-02	2.55E-01	7.26E-01
7.73E-01	7.94E-01	2.28E-01	2.41E-01	7.50E-01	1.25E-01	8.36E-01	8.07E-01
2.16E-01	5.42E-01	1.72E-02	NA	6.33E-01	6.52E-01	2.46E-01	3.21E-02
7.79E-01	3.47E-01	1.65E-04	1.84E-03	1.33E-02	3.72E-02	3.34E-01	2.30E-08
6.04E-01	3.52E-01	6.01E-06	NA	4.50E-01	6.64E-03	2.78E-01	8.00E-08
4.04E-01	2.33E-01	2.25E-07	NA	NA	6.75E-01	5.68E-01	1.51E-06
4.98E-01	9.25E-01	1.24E-01	1.57E-02	5.41E-01	2.20E-02	5.22E-02	2.77E-03
2.16E-01	6.17E-01	7.89E-02	7.17E-01	7.76E-04	9.93E-01	3.32E-02	3.85E-04
2.91E-01	5.53E-01	3.99E-01	8.55E-01	2.07E-01	8.53E-01	8.05E-03	7.78E-01
2.90E-01	3.35E-01	5.58E-01	3.21E-01	8.97E-01	7.21E-01	9.45E-01	5.13E-01
1.59E-01	2.24E-01	4.09E-01	NA	3.18E-01	2.50E-01	2.22E-02	2.24E-01

8.24E-01	8.81E-01	1.48E-96	3.14E-07	3.13E-11	8.09E-12	3.55E-03	1.38E-119
5.40E-01	8.39E-02	5.93E-12	7.28E-01	1.53E-01	5.70E-03	3.64E-01	1.22E-10
6.11E-01	7.63E-01	7.58E-01	2.41E-01	5.93E-01	2.55E-01	4.68E-01	9.82E-01
7.24E-01	4.22E-01	2.48E-49	7.61E-02	1.23E-01	8.15E-02	4.88E-02	3.20E-14
6.05E-01	5.28E-01	3.85E-06	2.26E-02	4.68E-03	2.41E-04	6.71E-01	4.79E-11
5.55E-01	8.92E-01	6.66E-01	2.90E-01	8.90E-01	9.88E-01	7.91E-01	6.44E-01
5.59E-01	4.87E-01	9.98E-02	5.33E-01	6.29E-01	1.95E-01	4.64E-02	1.65E-01
3.31E-01	2.01E-01	1.56E-05	3.46E-01	3.64E-02	1.24E-01	3.92E-01	1.13E-06
3.72E-01	7.62E-02	3.90E-03	3.35E-02	9.49E-01	4.59E-01	6.46E-01	3.27E-02
3.32E-01	6.71E-01	3.79E-04	2.89E-01	9.42E-04	2.33E-03	2.00E-02	4.70E-09
8.83E-01	5.39E-01	5.57E-03	NA	2.47E-03	5.81E-01	6.61E-02	4.32E-05
4.91E-01	3.63E-01	9.29E-01	7.55E-01	7.01E-01	9.45E-01	8.44E-01	9.94E-01
2.46E-01	6.11E-01	8.27E-02	1.40E-01	7.17E-01	6.87E-01	8.53E-01	9.11E-02
9.47E-01	4.36E-02	1.20E-02	7.40E-01	6.16E-01	2.34E-01	7.96E-01	2.04E-02
8.06E-01	7.98E-01	6.09E-01	1.11E-01	8.31E-01	4.57E-01	8.22E-01	2.94E-01

SNPEffect					IntEffect		
EUR	AFR	ASN	HIS	META	EUR	AFR	ASN
1.796	2.342	1.853	3.279	2.114	-0.552	-0.951	1.901
-0.235	0.246	0.373	0.443	0.063	0.187	-0.831	-0.351
-0.044	-0.187	0.230	0.671	0.017	-0.008	-1.142	0.100
-0.255	2.309	0.048	0.140	-0.130	0.230	-3.779	-0.452
6.189	-3.251	1.770	0.835	-1.551	-9.569	-1.845	-7.569
1.224	2.509	0.348	0.430	1.133	-0.745	-0.994	0.810
0.127	0.053	0.169	-0.483	0.085	0.081	2.014	-0.331
0.158	-0.455	0.231	0.364	0.125	0.028	-0.033	0.180
NA	3.861	2.637	3.430	3.668	NA	-0.524	0.532
-0.897	0.273	-0.485	-0.835	-0.743	0.230	1.182	-0.398
-1.048	-1.137	-0.792	0.097	-0.912	-0.256	2.478	0.797
1.554	-0.905	1.480	0.493	1.400	-0.691	-2.829	-0.305
-0.418	NA	NA	NA	-0.524	2.583	NA	NA
0.862	1.174	0.468	1.127	0.809	-0.075	-1.336	0.254
0.286	-4.904	0.379	-0.125	0.145	0.902	17.370	-2.454
-0.368	NA	1.832	-3.757	-0.365	-0.278	NA	-4.623
-0.561	-1.743	-0.879	-0.444	-0.682	-0.058	-2.643	0.663
0.600	-0.700	-0.041	-0.641	0.321	-0.478	1.080	-0.226
-1.169	-0.737	-0.756	-1.034	-1.029	0.226	-1.348	-0.576
2.728	NA	1.634	NA	2.672	1.589	NA	-1.328
-0.007	-0.084	-0.514	-0.745	-0.153	0.287	1.020	0.070
-16.420	NA	NA	NA	-16.370	1.065	NA	NA
1.936	1.437	0.994	1.495	1.671	0.313	0.829	-0.573
0.243	0.022	0.777	0.505	0.396	0.152	0.307	-0.748
5.767	5.925	5.269	7.630	5.865	0.425	-0.629	1.109
0.280	-0.311	-0.012	-0.119	0.136	-0.355	0.634	0.494
-0.846	-0.456	-0.051	-0.566	-0.618	0.311	-0.360	0.015
-1.100	-1.291	-1.084	-1.916	-1.155	-0.119	2.299	-1.005
0.315	0.710	-0.536	-0.603	0.082	-0.197	0.043	-0.288
1.357	0.760	1.139	0.468	1.198	0.145	2.267	0.164
4.773	3.087	4.970	5.153	4.566	0.092	-0.482	-0.042
0.907	1.177	0.337	1.521	0.859	0.163	0.538	0.997
-0.277	-1.055	0.230	-1.040	-0.265	-0.483	1.417	0.800
-2.556	-2.564	-2.403	-3.575	-2.637	-0.097	-0.436	1.857
-0.866	-1.459	-1.155	-1.784	-1.060	-0.250	0.162	0.881
-1.884	-0.879	-1.272	-2.159	-1.841	0.601	14.220	0.243
0.993	1.359	2.629	1.341	1.148	-0.067	-1.139	-2.442
-0.574	0.850	0.315	-0.843	-0.364	-0.236	-1.353	-0.643

-0.831	-0.456	-0.466	-0.711	-0.706	-0.135	-0.123	-0.421
-0.102	-0.768	0.016	-0.183	-0.142	0.157	0.691	-0.234
0.037	0.017	0.443	0.240	0.101	-0.590	-0.676	-0.330
-0.748	-0.764	-1.178	-1.190	-0.883	-0.095	0.246	1.270
0.083	0.763	-0.331	-0.693	0.015	-0.559	0.456	0.231
0.649	-0.041	-0.450	0.353	0.323	0.186	1.021	0.574
-0.075	0.360	-0.331	0.340	-0.060	-0.036	0.175	-0.024
0.799	-0.398	0.501	0.475	0.600	0.052	0.260	0.312
0.296	-0.284	-2.460	0.737	0.190	0.267	-1.368	8.014
0.503	0.165	0.117	0.980	0.430	-0.139	-0.517	-0.998
0.977	3.922	-10.450	1.236	0.990	-0.265	1.823	23.510
0.063	-0.162	-0.297	-0.027	-0.080	-0.428	0.206	-0.104
2.029	2.956	1.268	2.548	2.090	0.617	-2.660	-2.147
-0.038	1.162	1.473	1.388	0.173	-1.555	0.774	-1.771
1.486	1.204	0.093	0.991	1.126	0.141	-2.098	0.214
0.746	0.896	NA	2.605	0.826	0.161	1.628	NA
1.145	1.336	0.208	1.282	1.010	-0.262	-2.621	-0.631
0.829	1.015	1.396	2.954	0.996	0.404	-0.155	1.054
0.473	1.690	-0.021	1.090	0.464	-0.224	0.245	1.209
-0.169	-0.532	-0.640	-0.571	-0.379	-0.555	-1.258	1.186
-0.436	0.262	-0.073	-0.689	-0.380	-0.475	-1.756	0.650
-1.259	-0.181	-0.183	-0.971	-1.055	0.472	2.995	-0.606
-0.886	-0.965	-0.932	-0.896	-0.897	-0.062	1.032	0.208
0.208	-0.081	-0.111	0.040	0.078	0.374	-0.502	-0.509
0.465	0.294	0.353	0.487	0.435	-0.311	0.226	-0.253
1.019	1.278	0.014	2.312	1.095	-0.020	0.706	4.192
0.570	0.195	0.226	0.470	0.517	0.290	-0.968	-4.111
0.246	-0.539	0.283	0.453	0.246	0.020	0.526	0.329
-0.135	-0.559	-0.521	0.086	-0.242	-0.039	-0.024	0.040
1.288	1.447	0.590	0.915	1.076	0.563	1.831	0.285
-1.378	-2.342	-2.096	-1.301	-1.447	0.182	2.629	0.797
1.078	0.594	0.823	0.284	0.928	0.634	1.311	0.191
0.005	0.590	-0.996	0.003	-0.198	-0.032	-2.366	0.334
-0.719	-0.219	NA	1.119	-0.277	2.162	2.464	NA
-0.356	0.482	-0.683	-0.016	-0.370	-0.233	-0.535	1.146
-2.800	-3.116	-3.815	-1.063	-2.639	0.192	0.600	-0.310
-0.190	-0.318	-0.887	-0.931	-0.347	0.295	1.166	0.760
-0.847	-0.956	-0.318	-0.616	-0.700	0.111	0.701	0.486
0.272	-1.267	0.140	0.241	0.104	0.225	1.449	-0.198
-1.604	-1.416	-0.282	-0.798	-1.197	0.359	-0.863	-0.434
-1.351	-0.347	-0.913	-0.893	-1.179	-0.012	-1.169	-0.946
0.443	0.089	0.644	0.386	0.449	0.052	-0.021	0.093
0.250	0.472	-0.102	0.325	0.171	-0.414	-2.086	-0.062
2.025	-0.042	1.478	2.002	1.728	0.654	0.752	0.116
-0.226	-0.491	-0.568	0.028	-0.308	0.180	-0.132	1.000
0.116	1.803	-0.555	-0.234	0.119	-0.666	2.814	-0.327
-0.994	0.276	-0.642	-1.984	-0.894	0.042	-1.878	-0.358

2.645	2.112	1.684	3.350	2.453	-0.070	0.154	-0.485
0.085	0.611	0.362	-0.215	0.133	0.218	0.191	0.218
-0.540	-1.011	-0.275	-0.340	-0.487	-0.239	-0.725	-0.084
-0.600	-1.710	-0.414	-1.041	-0.677	-0.156	2.077	0.015
0.842	0.728	1.270	1.168	0.958	-0.007	-0.248	-0.620
-0.162	-0.637	-0.200	-0.009	-0.193	-0.051	-1.130	-0.073
-0.861	-0.311	0.027	-0.524	-0.518	-0.293	0.290	-0.106
0.077	-0.389	0.296	-1.024	-0.019	0.000	-0.201	0.493
0.373	0.074	0.225	-0.192	0.233	0.069	1.058	-0.252
0.060	-0.409	0.645	0.144	0.237	0.485	1.984	-0.526
-0.099	0.217	0.779	0.232	0.056	0.454	1.533	-0.990
2.146	-0.048	1.051	2.656	1.774	-0.451	0.122	-0.603
0.146	0.453	0.235	0.748	0.278	0.468	0.147	-0.178
1.932	NA	1.726	1.595	1.921	1.003	NA	-3.327
2.848	4.740	1.088	2.078	2.026	-0.568	1.434	-0.976
-0.886	-0.812	0.405	-0.736	-0.558	0.586	0.135	-1.402
-0.038	-0.193	0.520	0.389	0.102	-0.049	-1.103	-0.842
-0.805	-0.010	-0.692	-0.437	-0.643	0.510	-0.862	0.359
-0.224	-0.376	0.122	-0.029	-0.151	-0.196	-0.621	0.266
-0.546	-1.953	-1.099	-1.703	-0.712	-0.426	-2.171	-0.629
-1.693	-0.181	-0.924	-0.960	-1.355	0.508	2.328	0.845
-0.377	-1.902	-0.620	-0.287	-0.550	-0.297	1.494	0.588
0.309	-0.808	-0.361	0.354	0.036	-0.576	3.831	0.267
-0.899	-0.694	-1.420	-0.791	-0.916	-0.316	-1.452	0.311
1.050	1.639	1.743	1.303	1.197	0.019	-2.324	0.467
-0.430	-0.504	-0.282	0.482	-0.290	0.673	-2.721	0.655
-0.045	NA	NA	-1.526	-0.327	0.668	NA	NA
-0.346	NA	-3.084	-0.128	-0.353	0.269	NA	2.104
0.269	NA	7.774	-3.134	0.125	0.554	NA	-11.510
0.150	-0.555	-0.759	-0.119	-0.148	0.118	0.757	-0.599
-0.104	-0.294	-0.284	-1.269	-0.255	-0.189	2.109	1.441
-0.135	0.320	1.135	0.657	0.090	0.391	1.207	-1.662
0.812	-0.450	-0.106	0.514	0.536	0.154	0.393	0.317
NA	0.860	NA	3.690	1.220	NA	-1.071	NA
-0.173	-0.326	-0.403	-0.713	-0.301	0.168	-0.512	-0.685
2.192	-0.629	1.605	2.885	1.940	0.025	1.116	0.149
0.221	-0.245	-0.441	-0.801	-0.067	-0.045	-0.236	0.342
-0.234	0.054	0.579	0.628	0.075	-0.368	-1.366	-0.842
-2.483	NA	NA	-2.707	-2.516	0.501	NA	NA
-0.980	-1.427	-0.491	-1.217	-0.906	-0.171	-0.702	-0.751
3.588	NA	3.194	4.993	3.789	0.195	NA	-12.050
-5.047	NA	NA	-0.003	-4.717	-0.959	NA	NA
-0.504	-0.822	0.122	-1.305	-0.435	-0.029	0.565	-0.442
-0.888	-0.162	-1.014	-0.975	-0.898	0.416	-1.060	-0.081
-0.170	0.359	-0.208	0.181	-0.105	0.068	-0.677	0.558
-0.067	0.668	0.206	0.666	0.139	0.292	-1.707	-1.068
-0.150	NA	-3.968	2.968	0.080	0.649	NA	13.440

7.842	5.986	7.040	6.784	7.649	0.737	3.608	-1.706
-3.507	-0.688	-1.132	-2.294	-2.804	-1.732	1.932	1.691
-0.102	1.066	0.123	-0.546	0.007	0.188	-0.266	-0.048
-7.511	-1.924	0.720	-1.828	-3.046	-0.664	-0.461	0.979
1.403	2.504	2.478	1.429	1.543	-0.270	-2.110	-0.613
-0.195	-0.837	-0.104	-0.308	-0.217	0.259	1.796	0.401
-0.435	-1.014	-0.316	0.718	-0.299	0.619	2.447	-0.457
-1.445	-1.476	-0.235	-1.331	-1.077	0.392	1.527	0.882
-0.597	-1.030	0.007	0.542	-0.378	0.493	0.517	0.235
0.843	1.069	1.065	1.491	0.959	0.170	-1.095	0.859
-1.917	NA	-4.235	-1.253	-2.153	-1.062	NA	0.668
-0.137	-0.054	-0.048	-0.159	-0.111	-0.149	-1.728	0.787
0.383	0.880	0.071	-0.230	0.302	-0.004	-2.009	0.074
-0.830	0.112	-0.267	-0.185	-0.524	0.814	-1.304	0.478
-0.141	-0.800	-0.182	-0.304	-0.214	-0.201	-1.000	0.176

LDL.RegDrink							
					PJoint		
HIS	META	EUR	AFR	ASN	HIS	META	EUR
-0.341	-0.759	5.36E-04	5.16E-05	6.01E-01	1.39E-01	1.23E-08	4.46E-01
-0.992	-0.163	5.10E-01	7.04E-01	3.74E-01	5.20E-01	7.81E-01	5.00E-01
-0.133	-0.098	9.68E-01	5.33E-01	9.04E-01	6.70E-01	9.48E-01	7.59E-01
-0.517	0.049	5.92E-01	4.12E-01	7.86E-01	9.54E-01	7.80E-01	6.83E-01
1.769	-1.583	1.30E-01	2.84E-04	6.48E-01	6.71E-01	3.11E-02	1.41E-01
-0.539	-0.608	5.02E-07	1.54E-01	4.95E-01	8.98E-01	2.79E-07	4.96E-02
0.139	0.124	5.25E-01	1.80E-01	8.92E-01	7.30E-01	5.21E-01	6.03E-01
0.505	0.109	5.43E-01	5.55E-01	5.40E-01	4.79E-01	3.66E-01	9.65E-01
5.257	0.445	NA	3.14E-07	2.09E-01	4.20E-03	2.26E-09	NA
-0.116	0.069	1.45E-08	6.16E-01	5.00E-02	2.18E-01	3.90E-09	3.55E-01
-1.256	-0.263	5.53E-09	1.95E-01	7.83E-01	6.08E-01	3.05E-08	3.70E-01
2.237	-0.424	6.50E-07	8.26E-01	3.21E-02	1.52E-01	4.34E-08	2.71E-01
NA	2.696	3.21E-01	NA	NA	NA	3.21E-01	1.44E-01
0.854	-0.011	8.43E-10	4.28E-02	6.48E-02	3.42E-03	4.21E-13	5.25E-01
-3.016	0.858	1.10E-01	1.39E-01	9.37E-01	5.70E-01	2.13E-01	3.87E-01
4.799	-0.315	3.39E-01	NA	5.68E-01	3.46E-01	3.08E-01	6.78E-01
-2.378	-0.069	2.43E-03	5.83E-03	5.26E-02	8.55E-03	4.20E-06	5.99E-01
1.461	-0.183	1.11E-02	4.26E-01	9.69E-01	4.32E-01	1.61E-01	1.15E-01
-0.950	-0.031	8.13E-16	4.95E-02	6.65E-04	4.65E-03	9.29E-21	2.92E-01
NA	1.477	4.25E-15	NA	7.50E-01	NA	1.75E-14	2.03E-01
-0.581	0.310	4.18E-01	9.22E-01	3.98E-01	3.00E-01	5.14E-01	2.63E-01
NA	1.017	3.06E-176	NA	NA	NA	3.57E-171	2.04E-01
0.276	0.379	1.15E-54	3.50E-04	1.10E-02	1.29E-03	2.16E-57	5.06E-01
0.412	-0.047	4.76E-02	9.53E-01	1.54E-02	3.15E-01	2.76E-03	2.56E-01
-0.668	0.345	0.00E+00	8.97E-35	1.31E-45	6.44E-49	0.00E+00	2.33E-01
-0.163	-0.120	2.53E-01	8.05E-01	5.12E-01	9.18E-01	6.15E-01	7.79E-02
2.260	0.237	8.28E-07	5.37E-01	9.84E-01	6.44E-02	2.15E-05	5.84E-02
-0.601	-0.173	2.65E-15	2.53E-01	1.24E-05	2.90E-04	5.79E-22	7.12E-01
0.599	-0.053	1.85E-01	4.94E-01	8.49E-02	4.60E-01	8.54E-01	6.14E-01
1.639	0.338	1.36E-26	2.15E-02	4.46E-05	3.87E-02	1.05E-31	8.35E-01
0.332	0.191	1.56E-193	2.09E-11	4.37E-13	1.56E-22	5.33E-226	5.50E-01
-0.369	0.255	1.81E-12	2.35E-01	2.78E-02	5.97E-03	1.66E-15	3.39E-01
1.958	-0.054	3.56E-03	2.42E-01	8.96E-02	1.45E-01	1.08E-01	8.15E-02
1.224	0.059	4.20E-74	1.85E-05	1.74E-03	1.15E-09	6.23E-86	7.02E-01
-0.158	0.012	2.07E-12	2.11E-02	6.11E-04	2.04E-04	5.59E-19	6.46E-01
0.143	0.571	3.82E-12	9.33E-02	5.80E-01	1.05E-01	1.67E-12	9.13E-02
-0.268	-0.262	7.04E-10	1.80E-01	1.47E-03	5.17E-02	5.56E-13	6.91E-01
-1.374	-0.483	5.50E-17	2.23E-01	6.94E-01	1.31E-02	1.07E-16	4.22E-01

0.095	-0.221	1.95E-11	4.81E-01	5.95E-02	2.52E-01	9.24E-13	6.86E-01
-0.694	0.127	8.42E-01	3.23E-01	9.35E-01	5.65E-01	6.76E-01	8.18E-01
-0.837	-0.601	1.10E-02	7.79E-01	5.70E-01	7.23E-01	1.26E-02	4.19E-02
-0.936	0.121	3.52E-09	2.41E-01	1.97E-04	2.87E-03	1.08E-13	7.02E-01
1.369	-0.348	2.58E-02	9.08E-02	6.45E-01	2.55E-01	1.35E-01	3.24E-02
0.290	0.421	7.32E-06	5.87E-01	4.49E-01	6.68E-01	1.50E-04	8.30E-01
-1.263	-0.102	7.73E-01	6.37E-01	3.48E-01	3.87E-01	5.78E-01	5.88E-01
0.947	0.256	4.18E-08	7.63E-01	4.94E-02	1.46E-01	6.25E-09	6.12E-01
-1.962	0.136	9.33E-02	2.76E-01	9.23E-02	3.01E-01	3.76E-01	4.51E-01
-0.311	-0.235	2.76E-03	8.97E-01	1.35E-01	1.01E-01	5.90E-03	5.70E-01
4.697	-0.019	4.43E-03	3.29E-01	5.80E-02	3.33E-03	6.65E-04	9.63E-01
0.584	-0.227	2.01E-01	9.39E-01	3.82E-01	8.21E-01	2.10E-01	1.88E-01
-3.652	0.211	1.90E-18	3.87E-03	4.81E-01	2.53E-01	1.40E-18	4.20E-01
0.431	-1.823	0.00E+00	5.64E-02	3.07E-01	1.12E-01	0.00E+00	1.45E-01
-0.650	0.201	2.33E-29	2.73E-02	8.09E-01	1.26E-01	7.83E-25	4.15E-01
-3.897	0.073	3.74E-03	7.51E-01	NA	3.52E-01	2.37E-03	7.98E-01
1.607	-0.224	2.90E-11	1.44E-01	7.17E-01	1.14E-02	5.10E-11	1.88E-01
-2.496	0.255	3.51E-07	7.61E-01	2.01E-01	1.58E-02	1.24E-08	5.78E-01
-1.068	-0.154	3.12E-02	2.74E-01	3.19E-01	2.77E-01	1.17E-02	3.94E-01
-0.266	-0.180	7.10E-04	1.96E-01	3.20E-02	2.95E-01	3.03E-04	6.79E-02
0.334	-0.377	8.73E-07	6.81E-01	6.20E-01	4.70E-01	1.17E-05	1.47E-01
-0.291	0.349	8.66E-11	7.45E-02	7.98E-01	1.41E-01	1.13E-09	1.94E-01
0.506	0.017	8.14E-12	1.40E-01	1.26E-01	1.55E-01	1.49E-13	6.62E-01
0.589	0.253	1.07E-02	7.98E-01	3.34E-01	7.40E-01	1.63E-01	2.21E-01
-0.970	-0.311	2.64E-02	7.09E-01	5.15E-01	4.85E-01	8.26E-03	1.94E-01
-1.902	0.003	3.86E-08	2.46E-02	1.29E-02	4.20E-03	3.54E-11	7.95E-01
-1.531	0.109	1.95E-03	7.53E-01	5.15E-01	5.14E-01	9.73E-03	9.46E-01
0.858	0.109	2.68E-01	8.52E-01	3.55E-01	3.73E-01	8.65E-02	8.09E-01
0.288	0.038	4.93E-01	4.85E-01	8.99E-02	8.80E-01	1.10E-01	7.04E-01
1.021	0.639	5.90E-23	4.40E-02	4.08E-02	1.89E-01	3.33E-24	4.70E-02
-1.552	0.190	1.58E-12	1.90E-01	1.51E-02	7.67E-03	8.82E-16	5.33E-01
2.556	0.820	7.15E-27	5.13E-02	1.85E-01	3.23E-03	2.74E-29	1.71E-01
2.228	0.116	9.95E-01	5.57E-01	7.62E-02	3.57E-01	6.59E-01	6.38E-01
-2.160	2.056	4.69E-01	1.80E-01	NA	9.56E-01	1.17E-01	2.52E-01
-0.219	-0.056	8.89E-04	7.44E-01	4.44E-02	9.58E-01	1.88E-03	4.41E-01
-0.896	-0.001	1.55E-32	1.02E-05	1.91E-07	3.79E-02	6.84E-42	6.05E-01
-0.068	0.411	4.75E-01	6.44E-01	1.91E-01	9.64E-02	7.76E-02	2.63E-01
-0.580	0.103	7.68E-07	1.17E-01	5.13E-01	1.85E-01	2.80E-07	7.07E-01
-1.011	0.251	2.76E-02	4.58E-02	9.15E-01	6.47E-01	1.51E-01	8.30E-01
1.405	0.056	1.05E-18	7.29E-03	2.84E-01	4.42E-01	1.07E-17	1.09E-01
-0.248	-0.249	1.83E-23	4.32E-01	7.16E-05	1.62E-01	2.59E-27	6.31E-01
-0.173	0.047	1.32E-03	9.81E-01	4.90E-02	7.19E-01	1.23E-04	7.01E-01
-0.719	-0.378	3.14E-01	2.07E-01	8.90E-01	7.26E-01	2.65E-01	1.86E-01
0.504	0.737	2.99E-78	7.28E-01	6.03E-10	1.12E-06	1.41E-85	7.07E-02
0.256	0.360	6.08E-01	7.75E-01	1.42E-01	9.45E-01	2.07E-01	5.23E-01
2.600	-0.466	1.00E-01	2.67E-03	6.02E-01	2.15E-01	3.40E-01	2.53E-01
0.688	-0.094	5.61E-10	3.44E-01	1.29E-02	3.84E-04	2.85E-13	7.43E-01

-0.263	0.029	4.24E-103	3.32E-03	3.28E-07	2.14E-08	9.84E-115	3.94E-01
1.029	0.231	3.19E-01	4.62E-01	5.82E-01	5.85E-01	1.32E-01	6.29E-01
-0.802	-0.271	1.26E-06	3.19E-02	4.48E-01	3.62E-01	8.60E-08	2.91E-01
1.129	0.029	8.95E-07	5.27E-03	2.71E-01	9.44E-02	9.87E-09	8.17E-01
0.020	-0.145	2.42E-08	3.55E-01	4.80E-04	3.22E-02	7.38E-13	6.62E-01
-0.281	-0.075	3.88E-01	1.52E-01	6.71E-01	9.40E-01	1.40E-01	5.86E-01
1.011	-0.322	4.65E-11	8.06E-01	9.76E-01	4.81E-01	8.68E-08	2.58E-01
1.583	0.233	8.94E-01	5.88E-01	1.41E-01	1.07E-01	5.51E-01	9.12E-01
1.802	0.250	2.38E-01	5.94E-01	8.94E-01	3.99E-01	1.63E-01	8.43E-01
0.477	0.244	2.41E-01	7.63E-01	3.51E-01	8.89E-01	1.62E-01	4.88E-01
0.834	0.311	3.82E-01	7.59E-01	4.49E-01	7.03E-01	3.49E-01	4.50E-01
-0.347	-0.270	2.63E-47	9.93E-01	1.12E-03	5.84E-08	8.38E-49	8.43E-02
-1.622	0.130	1.08E-01	5.28E-01	7.60E-01	3.70E-01	8.95E-02	1.38E-01
-0.665	0.810	2.80E-12	NA	5.27E-01	6.58E-01	1.18E-11	1.73E-01
0.277	-0.335	7.14E-25	2.04E-01	1.16E-02	7.84E-02	2.57E-22	1.77E-01
1.515	0.226	1.44E-01	3.09E-01	4.94E-01	4.12E-01	1.22E-01	5.88E-01
-1.643	-0.291	9.22E-01	8.20E-01	4.82E-01	3.29E-01	6.00E-01	6.61E-01
0.289	0.330	2.69E-04	6.16E-01	3.02E-01	6.75E-01	2.42E-04	6.16E-02
0.227	-0.164	2.75E-02	4.62E-01	6.57E-01	9.67E-01	8.93E-02	4.29E-01
-0.272	-0.342	1.85E-08	3.81E-03	2.85E-01	1.42E-03	1.68E-11	7.92E-02
-0.674	0.382	2.51E-26	2.73E-01	2.74E-03	2.89E-02	1.51E-25	1.52E-01
-2.394	-0.038	5.37E-02	8.77E-02	1.79E-01	7.52E-02	3.15E-03	6.44E-01
1.124	-0.216	3.54E-01	5.89E-01	5.86E-01	5.70E-01	7.58E-01	5.78E-01
-1.442	-0.392	1.37E-09	9.94E-02	5.96E-02	1.06E-02	1.16E-12	2.55E-01
-0.176	-0.100	1.66E-13	2.12E-02	8.76E-06	2.75E-02	1.59E-19	8.68E-01
-2.152	0.350	6.37E-02	4.57E-02	5.93E-01	7.50E-02	2.17E-01	9.79E-03
2.623	1.004	7.12E-01	NA	NA	5.40E-01	5.76E-01	4.62E-01
-1.955	0.183	8.39E-01	NA	8.28E-01	7.53E-01	7.96E-01	9.22E-01
5.238	0.624	5.32E-01	NA	6.21E-02	2.32E-01	5.98E-01	6.38E-01
0.187	0.166	2.76E-01	5.55E-01	3.05E-04	9.70E-01	5.92E-01	7.53E-01
1.832	0.133	3.82E-01	1.50E-01	5.27E-01	1.30E-01	3.43E-01	7.35E-01
-0.012	0.221	4.17E-01	2.13E-01	2.55E-01	3.85E-01	3.09E-01	6.41E-01
-0.165	0.328	1.77E-10	6.34E-01	9.21E-01	5.37E-01	2.75E-08	7.31E-01
-4.288	-1.519	NA	6.36E-01	NA	3.18E-01	3.72E-01	NA
3.429	0.237	7.84E-01	6.35E-01	1.19E-01	1.73E-02	2.80E-01	3.42E-01
-0.416	0.180	3.43E-43	7.18E-01	2.50E-10	1.45E-06	8.03E-54	6.75E-01
1.887	0.203	3.60E-01	7.87E-01	2.79E-01	2.01E-01	6.71E-01	9.60E-01
-0.233	-0.605	3.63E-03	4.45E-01	7.96E-02	3.77E-01	7.20E-03	3.82E-01
0.723	0.550	4.06E-04	NA	NA	5.70E-01	2.73E-04	6.35E-01
-0.394	-0.309	3.10E-16	4.66E-04	4.54E-03	7.10E-03	5.56E-22	3.76E-01
-1.609	-0.120	3.19E-13	NA	4.36E-01	4.59E-03	1.10E-14	6.82E-01
-8.929	-1.416	8.86E-33	NA	NA	5.26E-02	6.14E-32	4.81E-01
1.844	-0.022	3.54E-04	2.10E-01	6.53E-01	2.24E-02	2.13E-04	9.62E-01
-2.627	0.238	8.72E-05	8.63E-01	6.50E-03	2.22E-02	2.86E-07	1.49E-01
-0.772	0.053	6.38E-01	7.28E-01	6.10E-01	8.23E-01	7.80E-01	6.88E-01
-0.602	-0.139	4.43E-01	2.01E-01	7.32E-02	3.82E-01	6.03E-01	7.08E-01
-1.395	0.600	8.84E-01	NA	3.26E-01	4.90E-01	7.98E-01	8.33E-01

-0.867	0.744	0.00E+00	3.06E-09	4.09E-11	6.81E-19	0.00E+00	6.85E-01
1.075	-2.390	0.00E+00	3.53E-01	1.16E-01	7.87E-03	0.00E+00	3.70E-01
1.467	0.142	7.65E-01	7.25E-02	8.94E-01	2.59E-01	6.70E-01	9.52E-01
-0.345	-1.652	1.65E-177	8.45E-04	2.53E-03	6.38E-02	1.20E-83	9.66E-01
-0.733	-0.425	1.91E-20	4.27E-03	9.74E-05	2.27E-02	1.88E-26	2.22E-01
0.814	0.359	5.97E-01	3.31E-01	7.84E-01	6.94E-01	2.94E-01	8.84E-01
-2.465	0.290	1.22E-01	3.09E-01	3.36E-01	5.53E-02	2.73E-01	3.18E-02
0.649	0.386	9.37E-13	1.20E-01	3.06E-01	5.31E-02	8.43E-11	2.75E-01
-0.135	0.326	1.01E-02	2.05E-01	8.90E-01	4.91E-01	6.05E-02	3.41E-02
-0.726	0.119	1.45E-09	1.22E-01	1.66E-05	1.26E-02	1.90E-15	4.65E-01
-1.003	-0.814	9.73E-10	NA	4.99E-04	3.29E-01	2.51E-12	1.31E-01
1.132	-0.067	4.16E-01	2.25E-01	4.80E-01	6.78E-01	6.05E-01	5.65E-01
-0.418	-0.044	1.20E-02	6.38E-02	9.18E-01	6.66E-01	2.94E-02	9.95E-01
0.839	0.551	7.43E-04	6.30E-01	5.20E-01	6.61E-01	4.08E-03	3.26E-02
0.034	-0.124	1.54E-01	4.23E-02	8.12E-01	7.71E-01	4.91E-02	5.53E-01

PInt					PMain		
AFR	ASN	HIS	META	EUR	AFR	ASN	HIS
6.91E-01	5.31E-01	7.54E-01	4.23E-01	8.71E-04	2.33E-05	5.20E-01	6.66E-02
4.43E-01	8.91E-01	3.63E-01	8.53E-01	3.12E-01	6.48E-01	4.86E-01	3.57E-01
2.47E-01	7.32E-01	8.86E-01	9.63E-01	9.00E-01	7.74E-01	7.51E-01	4.36E-01
3.15E-01	4.95E-01	7.10E-01	9.35E-01	2.90E-01	1.98E-01	9.73E-01	8.62E-01
5.53E-01	3.52E-01	6.37E-01	3.77E-01	6.19E-02	1.83E-03	6.63E-01	6.69E-01
8.50E-01	5.80E-01	7.29E-01	7.64E-02	5.20E-07	7.06E-02	5.56E-01	6.49E-01
2.66E-01	5.37E-01	8.92E-01	6.04E-01	5.40E-01	8.75E-01	7.48E-01	4.67E-01
9.53E-01	5.74E-01	5.29E-01	6.49E-01	4.65E-01	3.21E-01	4.87E-01	4.68E-01
9.26E-01	8.73E-01	1.39E-01	5.60E-01	NA	6.07E-07	2.01E-01	5.86E-02
8.88E-01	1.65E-01	9.57E-01	8.29E-01	2.08E-07	8.00E-01	1.50E-01	1.46E-01
3.39E-01	9.92E-01	3.87E-01	3.98E-01	7.33E-05	1.12E-01	4.63E-01	8.98E-01
6.70E-01	8.25E-01	1.98E-01	4.66E-01	2.09E-06	7.93E-01	2.23E-02	5.99E-01
NA	NA	NA	1.43E-01	7.52E-01	NA	NA	NA
4.04E-01	9.00E-01	3.12E-01	6.05E-01	1.57E-06	1.30E-02	2.44E-02	1.84E-02
7.58E-02	7.37E-01	4.15E-01	4.60E-01	6.06E-01	1.59E-01	9.29E-01	9.57E-01
NA	2.78E-01	3.41E-01	6.48E-01	4.48E-01	NA	4.47E-01	1.51E-01
2.45E-01	3.56E-01	3.22E-02	9.39E-01	1.46E-02	5.12E-02	2.59E-02	4.35E-01
3.07E-01	8.46E-01	2.38E-01	3.17E-01	3.49E-03	2.17E-01	8.56E-01	2.94E-01
2.96E-01	2.35E-01	2.18E-01	9.22E-01	4.85E-11	1.77E-01	2.03E-02	2.96E-02
NA	5.95E-01	NA	2.76E-01	1.47E-05	NA	4.53E-01	NA
6.43E-01	9.76E-01	6.01E-01	3.45E-01	9.69E-01	9.25E-01	3.07E-01	2.61E-01
NA	NA	NA	2.07E-01	1.37E-101	NA	NA	NA
4.06E-01	8.00E-01	7.04E-01	3.41E-01	3.06E-25	1.71E-03	6.98E-03	2.22E-03
7.65E-01	6.00E-01	5.85E-01	3.67E-01	1.83E-01	9.66E-01	3.17E-02	3.15E-01
6.30E-01	1.83E-02	4.60E-01	1.29E-01	1.23E-167	3.13E-30	2.19E-28	1.53E-39
4.74E-01	4.63E-01	8.79E-01	2.89E-01	1.17E-01	5.73E-01	9.60E-01	8.41E-01
5.40E-01	8.50E-01	1.48E-02	3.01E-02	6.66E-06	4.26E-01	8.60E-01	2.65E-01
2.24E-01	4.85E-02	5.53E-01	6.91E-01	9.84E-09	1.24E-01	5.76E-03	1.01E-03
7.69E-01	3.05E-01	4.99E-01	5.49E-01	1.19E-01	2.98E-01	1.69E-01	2.01E-01
1.45E-01	7.55E-01	6.90E-02	3.13E-01	1.12E-13	2.48E-01	1.24E-04	3.92E-01
7.82E-01	9.51E-01	8.14E-01	6.18E-01	1.90E-101	1.18E-10	9.22E-10	2.13E-18
7.18E-01	1.12E-01	6.60E-01	1.67E-01	1.75E-06	1.91E-01	3.53E-01	2.89E-03
3.89E-01	2.28E-01	8.99E-02	8.15E-01	2.32E-01	1.01E-01	2.28E-01	8.46E-02
4.68E-01	2.30E-01	2.92E-01	4.62E-01	3.86E-39	6.33E-05	9.07E-04	1.46E-09
9.24E-01	1.59E-01	8.28E-01	8.75E-01	3.37E-06	1.23E-02	5.28E-05	4.46E-04
6.21E-02	6.43E-01	9.92E-01	6.90E-02	1.08E-09	7.08E-01	3.51E-01	6.09E-02
6.93E-01	4.76E-02	8.04E-01	3.50E-01	1.46E-06	6.16E-02	2.96E-04	2.78E-02
2.14E-01	4.16E-01	1.47E-01	1.12E-01	2.26E-03	1.01E-01	5.12E-01	1.20E-01

9.93E-01	5.41E-01	9.78E-01	5.64E-01	3.90E-06	3.01E-01	4.54E-02	1.37E-01
2.70E-01	3.25E-01	4.87E-01	9.31E-01	6.00E-01	1.29E-01	6.69E-01	7.12E-01
6.51E-01	7.83E-01	5.05E-01	4.79E-02	7.63E-01	9.52E-01	6.67E-01	6.71E-01
7.43E-01	6.21E-02	3.35E-01	7.78E-01	1.98E-05	1.05E-01	4.04E-04	1.79E-02
8.30E-01	4.96E-01	1.66E-01	2.12E-01	6.40E-01	9.28E-02	3.33E-01	1.62E-01
2.73E-01	1.97E-01	6.41E-01	2.86E-01	2.44E-03	9.46E-01	2.03E-01	5.41E-01
6.80E-01	8.64E-01	1.95E-01	5.33E-01	7.73E-01	4.27E-01	2.17E-01	4.87E-01
8.22E-01	4.24E-01	2.74E-01	2.62E-01	4.66E-05	4.65E-01	9.78E-02	3.49E-01
1.99E-01	1.10E-01	1.75E-01	9.90E-01	2.86E-01	6.43E-01	1.76E-01	2.69E-01
7.99E-01	4.26E-01	8.08E-01	3.56E-01	4.97E-03	7.80E-01	6.85E-01	4.55E-02
8.18E-01	1.71E-02	2.23E-02	5.03E-01	6.50E-03	2.16E-01	1.04E-01	2.62E-01
9.93E-01	6.95E-01	5.55E-01	4.72E-01	7.89E-01	7.52E-01	1.28E-01	9.84E-01
1.20E-01	3.73E-01	1.83E-01	9.24E-01	6.01E-09	9.13E-04	2.94E-01	1.11E-01
7.58E-01	3.45E-01	6.25E-01	1.88E-01	1.81E-03	6.41E-02	1.29E-01	8.81E-02
3.51E-02	8.54E-01	4.17E-01	9.40E-01	4.03E-15	1.37E-02	8.25E-01	3.79E-02
8.18E-01	NA	2.72E-01	7.03E-01	3.34E-02	6.74E-01	NA	1.69E-01
9.52E-02	6.06E-01	2.51E-01	1.61E-01	5.66E-09	8.24E-02	5.15E-01	6.99E-02
8.92E-01	6.29E-01	1.83E-01	7.29E-01	2.34E-03	5.06E-01	2.59E-01	3.80E-03
7.31E-01	9.92E-02	3.30E-01	6.38E-01	1.72E-02	1.35E-01	8.68E-01	9.71E-02
2.07E-01	8.62E-02	7.61E-01	2.78E-01	3.77E-01	3.63E-01	6.13E-02	2.23E-01
5.00E-01	3.56E-01	6.90E-01	3.33E-01	2.06E-02	8.16E-01	9.39E-01	2.24E-01
1.13E-02	6.79E-01	8.19E-01	1.16E-01	5.85E-09	7.87E-01	9.57E-01	1.16E-01
3.56E-01	8.92E-01	6.76E-01	9.61E-01	6.90E-07	4.69E-02	8.89E-02	6.16E-02
3.00E-01	1.29E-01	6.03E-01	8.48E-01	3.26E-01	8.37E-01	9.71E-01	9.58E-01
7.77E-01	9.84E-01	3.76E-01	1.98E-01	1.19E-02	5.42E-01	3.24E-01	3.06E-01
5.18E-01	2.22E-02	1.40E-01	9.99E-01	7.52E-06	3.18E-02	9.58E-01	1.10E-03
3.81E-01	1.20E-01	2.52E-01	4.84E-01	4.74E-02	7.30E-01	9.98E-01	5.19E-01
7.92E-01	3.81E-01	4.38E-01	4.21E-01	2.58E-01	5.38E-01	4.75E-01	4.91E-01
7.91E-01	9.18E-01	8.11E-01	7.97E-01	4.91E-01	2.91E-01	1.09E-01	8.61E-01
3.71E-01	5.88E-01	5.20E-01	2.90E-02	6.70E-09	1.09E-01	6.78E-02	2.28E-01
3.44E-01	7.89E-01	1.72E-01	6.91E-01	1.12E-08	7.12E-02	4.69E-03	5.72E-02
1.47E-01	5.19E-01	7.28E-03	1.57E-02	3.00E-09	2.23E-01	2.59E-01	5.94E-01
3.57E-01	4.58E-01	1.85E-01	9.86E-01	9.83E-01	5.50E-01	5.37E-02	9.74E-01
8.94E-02	NA	7.82E-01	4.92E-02	5.37E-01	7.00E-01	NA	8.05E-01
5.74E-01	1.29E-01	7.33E-01	8.10E-01	5.00E-02	4.67E-01	9.85E-02	9.57E-01
5.55E-01	1.00E+00	3.38E-01	8.03E-01	2.03E-19	9.67E-06	5.12E-06	7.73E-02
2.79E-01	3.13E-01	9.72E-01	1.37E-01	2.90E-01	5.69E-01	3.52E-02	6.18E-02
4.07E-01	8.24E-01	5.34E-01	6.58E-01	4.27E-05	3.82E-02	5.35E-01	2.24E-01
3.12E-01	9.19E-01	3.72E-01	8.15E-01	1.90E-01	1.43E-02	9.67E-01	6.53E-01
6.61E-01	6.93E-01	3.10E-01	1.93E-01	1.98E-13	1.87E-02	1.51E-01	2.38E-01
2.88E-01	2.82E-02	8.64E-01	5.20E-01	3.70E-13	6.02E-01	2.00E-02	1.24E-01
7.29E-01	6.47E-01	7.86E-01	9.98E-01	1.25E-02	8.45E-01	1.80E-02	4.39E-01
9.54E-02	8.99E-01	4.33E-01	9.23E-02	2.30E-01	4.18E-01	7.32E-01	5.37E-01
3.30E-01	8.58E-01	6.30E-01	5.45E-02	1.43E-31	9.65E-01	7.81E-07	2.03E-05
7.10E-01	1.80E-02	7.62E-01	9.46E-02	3.18E-01	5.33E-01	1.09E-01	9.07E-01
1.79E-01	9.31E-01	1.38E-01	6.28E-01	6.55E-01	6.62E-02	5.11E-01	7.79E-01
1.97E-01	2.85E-01	5.34E-01	7.59E-01	2.01E-06	6.05E-01	2.72E-02	2.13E-04

9.47E-01	3.80E-01	7.86E-01	2.46E-01	2.21E-36	3.57E-03	5.87E-07	1.09E-07
9.85E-01	6.80E-01	3.32E-01	4.17E-01	6.53E-01	3.12E-01	6.65E-01	7.58E-01
3.01E-01	8.29E-01	4.77E-01	2.42E-01	2.40E-03	4.48E-02	2.58E-01	5.33E-01
7.03E-02	7.99E-01	1.96E-01	7.13E-01	8.71E-04	1.43E-03	3.48E-01	2.97E-02
9.35E-01	1.91E-01	9.75E-01	3.63E-01	2.23E-05	1.80E-01	2.07E-04	2.28E-02
2.55E-01	6.66E-01	7.82E-01	9.95E-01	3.73E-01	2.76E-01	6.59E-01	9.98E-01
8.89E-01	7.68E-01	2.49E-01	4.81E-01	3.78E-05	5.12E-01	9.00E-01	2.92E-01
4.44E-01	3.84E-01	9.33E-02	5.40E-01	7.62E-01	3.76E-01	3.44E-01	4.63E-02
2.60E-01	9.80E-01	2.15E-01	5.94E-01	2.72E-01	9.06E-01	7.28E-01	7.87E-01
7.17E-01	7.80E-01	7.39E-01	5.75E-01	8.87E-01	7.74E-01	2.13E-01	8.67E-01
9.45E-01	6.84E-01	5.41E-01	4.58E-01	6.98E-01	8.55E-01	2.18E-01	7.69E-01
7.23E-01	5.33E-01	7.26E-01	8.10E-02	1.84E-31	9.18E-01	1.05E-03	9.51E-08
9.16E-01	8.49E-01	1.85E-01	5.37E-01	6.51E-01	2.95E-01	5.18E-01	2.63E-01
NA	4.07E-01	7.93E-01	2.87E-01	4.17E-05	NA	3.44E-01	2.76E-01
8.37E-01	3.56E-01	9.27E-01	1.12E-01	2.03E-16	1.47E-01	2.91E-03	6.09E-02
8.54E-01	1.67E-01	2.29E-01	7.68E-01	7.44E-02	1.49E-01	4.03E-01	2.64E-01
7.20E-01	3.02E-01	1.55E-01	6.78E-01	8.98E-01	8.55E-01	4.00E-01	4.78E-01
5.31E-01	8.10E-01	9.14E-01	1.61E-01	1.57E-04	9.98E-01	1.67E-01	3.75E-01
6.55E-01	5.05E-01	7.54E-01	6.70E-01	1.83E-01	4.43E-01	9.88E-01	9.38E-01
1.33E-01	8.01E-01	7.10E-01	4.68E-02	2.60E-03	3.38E-02	2.76E-01	2.45E-03
1.44E-01	2.23E-01	4.09E-01	7.49E-02	1.22E-19	8.08E-01	1.18E-02	5.89E-02
5.45E-01	9.69E-01	8.09E-02	5.03E-01	2.38E-01	3.43E-02	1.05E-01	6.87E-01
4.26E-01	5.55E-01	4.27E-01	9.21E-01	2.62E-01	6.46E-01	3.12E-01	6.79E-01
3.08E-01	2.85E-01	1.44E-01	1.34E-01	7.43E-05	2.49E-01	2.28E-02	1.21E-01
5.53E-02	3.90E-01	9.21E-01	7.72E-01	5.88E-08	7.62E-03	5.53E-04	1.46E-02
1.24E-01	2.47E-01	1.35E-02	9.94E-02	4.87E-02	4.94E-01	7.02E-01	3.13E-01
NA	NA	3.83E-01	3.25E-01	9.69E-01	NA	NA	3.01E-01
NA	8.00E-01	5.04E-01	9.55E-01	5.87E-01	NA	5.51E-01	9.58E-01
NA	3.92E-02	1.77E-01	6.76E-01	7.21E-01	NA	2.81E-02	1.16E-01
8.04E-01	1.59E-01	7.46E-01	4.45E-01	4.18E-01	2.74E-01	5.21E-02	8.40E-01
3.74E-02	3.13E-01	1.45E-01	1.53E-01	6.40E-01	5.71E-01	8.16E-01	5.26E-02
2.91E-01	6.11E-02	9.43E-01	6.72E-01	5.77E-01	5.23E-01	4.01E-02	2.15E-01
7.39E-01	8.90E-01	7.91E-01	7.86E-01	9.97E-06	3.60E-01	9.63E-01	2.89E-01
6.52E-01	NA	3.25E-01	4.23E-01	NA	3.87E-01	NA	1.35E-01
8.33E-01	4.82E-01	4.30E-03	2.37E-01	4.64E-01	5.49E-01	2.33E-01	2.78E-01
4.93E-01	9.81E-01	7.58E-01	7.47E-01	2.25E-23	4.46E-01	3.84E-09	2.62E-06
9.60E-01	9.20E-01	1.05E-01	6.76E-01	3.23E-01	6.29E-01	3.08E-01	1.63E-01
2.85E-01	6.07E-01	7.82E-01	4.41E-01	1.93E-01	8.90E-01	7.80E-01	1.84E-01
NA	NA	8.89E-01	6.19E-01	3.10E-03	NA	NA	3.32E-01
6.45E-01	1.08E-01	6.41E-01	1.00E-01	2.38E-08	2.45E-03	5.09E-02	1.11E-02
NA	2.00E-01	6.16E-01	9.16E-01	6.05E-08	NA	5.49E-01	2.11E-03
NA	NA	4.41E-02	2.61E-01	1.23E-15	NA	NA	9.99E-01
5.93E-01	7.67E-01	3.17E-02	6.37E-01	6.03E-03	9.10E-02	6.46E-01	7.98E-03
4.79E-01	8.49E-01	1.18E-01	4.28E-01	1.45E-04	9.24E-01	3.66E-03	2.56E-01
6.28E-01	2.14E-01	5.39E-01	5.20E-01	3.88E-01	4.86E-01	4.40E-01	7.68E-01
1.40E-01	2.53E-01	5.09E-01	5.00E-01	7.10E-01	1.45E-01	7.62E-01	1.62E-01
NA	1.38E-01	7.80E-01	7.22E-01	8.71E-01	NA	3.66E-01	2.51E-01

1.59E-01	6.98E-01	5.61E-01	7.35E-01	1.77E-172	8.10E-07	7.19E-10	5.31E-16
1.51E-01	1.65E-01	4.99E-01	6.43E-02	1.87E-21	3.34E-01	8.94E-02	2.82E-03
7.61E-01	2.89E-01	9.93E-02	3.86E-01	5.95E-01	3.76E-02	7.01E-01	2.50E-01
8.54E-01	4.28E-01	8.15E-01	7.02E-01	8.11E-89	1.60E-03	2.11E-02	4.86E-02
1.43E-01	4.01E-01	3.97E-01	7.59E-02	4.92E-14	9.55E-04	6.65E-04	6.96E-03
1.36E-01	3.79E-01	3.92E-01	3.24E-01	3.38E-01	2.30E-01	8.34E-01	5.57E-01
1.97E-01	1.69E-01	1.84E-02	4.00E-01	5.60E-02	2.51E-01	4.75E-01	1.87E-01
3.91E-01	4.48E-02	5.71E-01	3.05E-02	9.82E-10	3.95E-02	1.43E-01	2.05E-02
7.49E-01	6.68E-01	7.76E-01	5.55E-02	3.46E-03	9.21E-02	9.53E-01	2.59E-01
4.85E-01	2.29E-01	5.25E-01	4.34E-01	3.83E-05	3.90E-02	1.17E-03	4.57E-03
NA	6.14E-01	8.71E-01	2.11E-01	2.87E-04	NA	1.34E-03	2.82E-01
1.93E-01	1.49E-01	3.49E-01	9.89E-01	5.78E-01	9.45E-01	9.84E-01	8.16E-01
8.67E-02	8.13E-01	7.25E-01	7.41E-01	3.12E-02	6.22E-02	8.14E-01	6.56E-01
3.25E-01	6.94E-01	3.23E-01	4.68E-02	1.75E-04	8.93E-01	9.98E-01	7.24E-01
5.18E-01	6.36E-01	9.67E-01	6.53E-01	4.54E-01	1.12E-01	4.24E-01	5.06E-01

				SNPEffect			
META	EUR	AFR	ASN	HIS	BRA	META	EUR
3.59E-08	-0.001	0.002	0.044	0.006	NA	0.002	0.000
9.31E-01	-0.004	0.004	0.001	0.009	0.013	0.001	0.009
9.21E-01	0.001	0.006	0.006	0.000	0.137	0.004	0.001
4.88E-01	-0.020	-0.006	-0.004	-0.022	0.024	-0.010	0.004
8.36E-02	0.087	-0.011	0.008	-0.016	NA	-0.009	-0.101
3.89E-07	0.000	0.005	0.010	-0.011	0.010	0.003	0.000
6.34E-01	0.014	0.011	0.009	0.037	0.020	0.013	-0.004
4.55E-01	0.012	0.007	0.010	0.007	0.043	0.010	0.002
7.97E-08	NA	0.002	-0.008	-0.001	NA	-0.001	NA
3.51E-07	0.005	0.025	-0.005	0.012	0.019	0.001	-0.004
9.28E-05	-0.009	-0.019	-0.012	0.007	0.039	-0.008	0.003
6.68E-07	0.012	0.017	-0.009	-0.008	NA	0.000	-0.007
6.98E-01	0.069	NA	NA	NA	NA	0.069	0.008
1.02E-09	-0.001	0.001	0.002	-0.015	-0.024	0.000	-0.001
7.86E-01	0.047	0.027	-0.009	0.014	NA	0.038	-0.016
4.49E-01	-0.015	-0.065	-0.041	-0.041	NA	-0.019	-0.004
3.07E-04	-0.014	-0.005	-0.007	-0.027	-0.039	-0.010	-0.001
6.87E-02	0.011	0.013	0.013	0.003	0.026	0.011	0.001
8.37E-13	-0.003	-0.008	-0.005	-0.010	-0.023	-0.005	0.001
1.53E-05	0.041	NA	0.035	0.036	NA	0.040	-0.011
4.17E-01	0.008	-0.011	0.011	0.018	-0.033	0.009	0.001
1.81E-97	-0.018	NA	NA	NA	NA	-0.016	-0.007
2.49E-28	0.035	0.034	0.031	0.057	0.035	0.035	-0.001
1.83E-02	-0.004	-0.012	-0.011	-0.005	-0.039	-0.009	-0.001
3.31E-247	0.005	0.010	0.001	0.015	-0.038	0.005	0.005
2.84E-01	0.012	-0.011	0.005	0.013	-0.011	0.006	-0.010
4.49E-05	-0.008	0.005	-0.009	-0.020	-0.018	-0.008	0.005
1.93E-12	0.006	0.015	0.013	0.011	0.014	0.010	0.002
6.46E-01	0.016	0.012	0.016	0.019	-0.010	0.016	0.005
6.01E-16	0.002	-0.003	0.002	0.011	0.006	0.002	0.004
1.75E-127	0.008	0.013	0.016	0.004	-0.017	0.010	0.002
8.04E-08	0.066	0.048	0.054	0.068	0.057	0.059	-0.004
2.33E-01	-0.019	0.002	-0.003	-0.013	0.002	-0.007	0.001
3.49E-50	-0.002	-0.011	0.011	-0.016	-0.033	-0.003	-0.004
6.07E-13	0.000	-0.007	-0.003	-0.014	0.018	-0.003	-0.003
5.04E-10	0.001	-0.007	-0.010	-0.004	0.058	0.001	-0.008
7.27E-10	-0.003	-0.005	0.009	-0.014	-0.013	-0.003	0.003
2.55E-02	-0.016	-0.023	-0.006	-0.004	-0.013	-0.013	0.001

2.22E-07	-0.004	-0.005	0.001	0.001	0.004	-0.001	0.002
4.53E-01	-0.006	-0.006	-0.010	-0.010	-0.023	-0.008	0.012
5.93E-01	-0.011	-0.008	-0.020	-0.011	0.026	-0.014	-0.005
1.75E-09	-0.002	-0.009	-0.004	-0.004	0.026	-0.004	-0.006
9.24E-01	-0.007	0.003	0.007	-0.003	-0.006	0.000	0.004
5.85E-02	0.016	0.001	0.006	0.000	-0.050	0.008	0.000
7.37E-01	0.004	0.003	0.012	0.018	-0.086	0.009	0.001
8.44E-05	0.021	0.003	0.016	0.001	-0.025	0.015	-0.004
3.75E-01	0.015	0.009	0.034	-0.001	NA	0.012	-0.001
9.89E-03	0.018	0.011	0.016	0.017	-0.013	0.016	-0.002
4.10E-03	-0.012	0.031	-0.079	-0.020	-0.043	-0.013	-0.002
4.47E-01	0.013	0.013	0.007	0.013	-0.005	0.009	-0.002
5.26E-11	-0.003	-0.014	-0.020	0.039	NA	-0.006	-0.002
5.91E-05	0.008	0.003	0.013	0.018	0.033	0.009	0.004
1.41E-13	-0.001	0.006	-0.001	0.015	0.055	0.001	0.000
1.73E-02	-0.009	-0.037	NA	-0.008	-0.117	-0.012	0.012
2.92E-09	0.021	-0.003	0.004	0.006	NA	0.012	-0.003
1.17E-04	-0.003	-0.016	0.000	-0.014	0.124	-0.003	0.007
9.17E-03	0.007	0.007	0.003	0.012	-0.031	0.006	-0.005
2.32E-02	-0.015	-0.021	-0.010	-0.027	-0.017	-0.013	-0.005
2.78E-02	-0.009	-0.033	-0.015	-0.003	-0.058	-0.012	-0.004
5.46E-08	-0.007	-0.015	0.004	-0.009	-0.051	-0.007	0.001
7.69E-09	-0.005	0.010	-0.013	0.001	-0.012	-0.004	-0.002
5.26E-01	0.013	0.010	0.005	0.015	0.039	0.009	0.000
3.62E-03	0.016	0.014	0.008	0.010	-0.002	0.011	0.000
6.06E-08	-0.003	0.002	-0.018	-0.003	-0.036	-0.004	-0.013
4.73E-02	0.001	0.001	0.021	0.011	NA	0.003	0.005
1.84E-01	0.004	-0.027	-0.002	0.007	0.048	0.000	-0.001
1.36E-01	0.008	0.001	0.008	0.005	-0.025	0.007	-0.002
1.58E-09	0.000	-0.003	-0.002	0.009	-0.034	-0.002	0.010
3.22E-11	0.010	0.025	0.012	0.022	0.034	0.012	0.007
8.23E-09	0.001	0.015	0.007	-0.004	0.028	0.004	0.003
4.50E-01	0.077	0.052	0.060	0.074	0.076	0.066	-0.012
5.78E-01	-0.062	-0.016	NA	0.104	NA	-0.017	0.030
2.86E-02	-0.020	-0.018	-0.015	-0.029	-0.054	-0.018	0.008
7.09E-26	0.027	0.032	0.034	0.017	0.042	0.028	-0.015
2.04E-02	0.009	-0.005	0.001	0.010	-0.001	0.005	0.006
1.75E-05	-0.021	-0.010	-0.018	-0.002	-0.064	-0.017	0.005
6.78E-01	0.065	0.044	0.068	0.056	0.038	0.063	0.000
3.77E-13	-0.008	-0.013	-0.003	-0.004	-0.040	-0.005	0.003
1.01E-13	-0.016	-0.014	-0.008	-0.024	0.054	-0.012	0.010
1.07E-03	0.000	0.001	-0.006	0.002	0.027	-0.002	0.007
2.90E-01	0.003	-0.002	0.001	0.019	0.000	0.003	-0.001
1.29E-35	0.044	0.007	0.029	0.042	0.078	0.033	-0.001
1.00E-01	-0.008	-0.014	-0.005	-0.005	-0.005	-0.006	-0.001
6.17E-01	0.004	0.000	-0.004	0.018	-0.038	0.002	0.008
2.03E-08	-0.015	0.001	-0.008	-0.008	-0.007	-0.010	0.002

7.83E-47	0.001	0.035	-0.013	0.007	0.012	-0.005	-0.009
4.63E-01	0.005	0.010	0.002	0.010	0.019	0.005	-0.003
4.16E-04	0.018	0.016	0.017	0.019	0.005	0.017	-0.003
7.41E-06	-0.015	-0.012	-0.019	-0.023	-0.049	-0.018	0.002
1.70E-09	-0.013	0.003	-0.009	-0.010	0.005	-0.009	0.002
2.28E-01	0.014	0.007	0.013	0.024	-0.002	0.014	-0.002
5.04E-04	-0.013	-0.002	0.000	0.002	-0.062	-0.003	0.008
8.44E-01	-0.011	0.004	-0.009	-0.010	-0.021	-0.009	-0.001
3.67E-01	-0.004	-0.013	-0.001	-0.006	-0.049	-0.004	-0.003
4.29E-01	-0.002	-0.013	0.005	0.000	-0.013	0.003	-0.003
8.23E-01	-0.002	0.001	-0.003	0.001	NA	-0.002	-0.006
3.11E-33	-0.029	-0.025	-0.019	-0.037	-0.033	-0.024	0.004
1.66E-01	0.008	0.003	-0.001	0.007	0.038	0.001	-0.005
1.81E-05	0.135	NA	0.136	0.123	NA	0.134	-0.009
4.59E-16	0.002	0.009	0.002	0.038	NA	0.003	0.005
6.14E-02	-0.019	-0.006	0.005	-0.026	NA	-0.011	0.008
6.63E-01	-0.015	-0.029	-0.012	-0.007	0.023	-0.013	0.011
2.10E-04	-0.006	-0.011	-0.004	-0.005	-0.008	-0.006	-0.012
2.02E-01	-0.001	-0.009	-0.003	0.002	-0.007	-0.002	-0.003
2.69E-05	0.004	0.024	0.007	-0.009	-0.023	0.004	0.000
2.12E-18	-0.005	0.009	-0.004	-0.002	0.007	-0.003	0.006
1.65E-02	0.008	-0.007	0.006	-0.002	-0.038	0.005	-0.009
8.36E-01	-0.001	0.000	-0.005	0.010	-0.003	-0.003	-0.008
2.63E-06	-0.014	-0.003	0.011	-0.009	NA	-0.005	0.011
1.28E-12	-0.004	0.009	-0.005	0.009	-0.011	-0.002	0.002
1.33E-01	-0.002	-0.001	-0.009	-0.007	-0.060	-0.006	-0.002
6.25E-01	0.081	NA	-0.106	0.051	-0.027	0.065	-0.044
5.58E-01	-0.101	NA	0.021	-0.085	0.027	-0.090	0.037
8.51E-01	0.077	NA	0.029	0.080	NA	0.072	-0.032
5.02E-01	0.021	0.014	0.020	0.009	0.047	0.019	-0.007
2.05E-01	-0.009	-0.006	-0.002	0.006	-0.013	-0.006	-0.001
5.25E-01	0.004	0.008	-0.014	0.009	NA	0.003	0.003
3.54E-04	0.013	0.001	-0.005	0.029	0.017	0.010	-0.002
1.87E-01	-0.023	-0.016	NA	-0.004	NA	-0.016	0.035
9.42E-02	-0.005	-0.010	-0.015	-0.009	-0.052	-0.011	0.000
6.47E-32	0.008	0.016	0.007	0.008	0.027	0.007	0.010
8.00E-01	0.019	0.013	0.013	0.008	-0.002	0.014	-0.007
4.75E-01	0.008	-0.009	0.006	-0.005	-0.008	0.005	-0.003
1.96E-03	0.070	NA	-0.015	0.110	NA	0.069	0.010
2.04E-11	0.014	0.009	0.009	-0.003	0.058	0.010	-0.007
1.23E-09	-0.029	NA	-0.071	-0.061	NA	-0.039	0.003
5.66E-14	0.021	NA	NA	0.041	NA	0.023	-0.008
3.82E-04	0.007	0.000	0.010	0.013	-0.014	0.008	0.001
2.06E-06	0.004	-0.003	-0.001	-0.011	-0.008	0.000	-0.004
4.66E-01	0.014	0.004	0.006	0.033	-0.029	0.009	-0.007
6.91E-01	0.015	-0.002	0.001	-0.001	0.022	0.005	-0.003
9.52E-01	-0.097	NA	0.013	-0.124	NA	-0.083	-0.005

4.33E-193	0.011	0.005	0.003	-0.002	NA	0.008	-0.001
7.95E-20	-0.060	-0.003	-0.019	-0.008	NA	-0.028	0.017
7.08E-01	0.006	-0.003	0.010	0.004	0.034	0.007	0.003
7.50E-35	0.012	0.001	0.006	0.021	-0.113	0.006	0.004
2.55E-19	0.009	0.018	0.011	0.004	-0.043	0.009	0.003
2.05E-01	0.004	0.002	0.004	-0.009	0.011	0.003	0.002
1.07E-01	0.002	0.020	0.000	0.016	0.031	0.004	0.007
1.53E-10	-0.001	-0.001	0.005	0.005	0.006	0.003	0.003
2.47E-02	0.004	-0.030	-0.007	-0.002	-0.044	-0.005	-0.005
1.39E-09	0.007	-0.009	0.004	-0.003	0.031	0.003	-0.004
4.38E-06	-0.006	NA	-0.021	0.007	0.061	-0.009	0.004
6.24E-01	-0.022	-0.031	-0.023	-0.037	0.041	-0.024	-0.004
3.34E-02	0.004	0.001	0.001	-0.001	-0.016	0.002	-0.003
6.99E-03	-0.004	-0.005	-0.008	-0.011	0.001	-0.007	-0.002
1.26E-01	-0.012	-0.019	-0.009	-0.017	-0.007	-0.011	0.002

		IntEffect				TG.Cu PJo	
AFR	ASN	HIS	BRA	META	EUR	AFR	ASN
-0.003	-0.041	0.036	NA	-0.001	9.94E-01	9.53E-01	6.61E-01
-0.004	0.005	-0.013	-0.010	0.004	6.90E-02	8.11E-01	1.54E-01
-0.023	-0.001	0.027	-0.028	-0.002	8.28E-01	1.59E-01	6.32E-01
-0.006	0.002	-0.007	0.027	-0.003	1.45E-11	8.77E-01	4.06E-01
0.000	0.015	0.037	NA	0.005	5.29E-01	4.88E-01	9.59E-01
0.012	-0.011	0.017	-0.031	-0.002	1.00E+00	5.90E-01	3.14E-01
0.008	0.001	-0.020	-0.008	-0.002	3.89E-07	3.15E-02	3.41E-02
-0.008	-0.002	0.005	-0.013	0.001	1.69E-08	5.02E-01	4.93E-04
0.006	-0.031	0.026	NA	0.001	NA	7.64E-01	1.25E-01
-0.033	0.004	-0.015	-0.075	0.000	2.80E-01	7.47E-02	1.70E-01
0.024	0.063	-0.027	-0.062	0.003	5.31E-02	1.25E-01	5.03E-02
-0.002	0.011	0.005	NA	0.004	4.69E-02	8.13E-01	2.30E-01
NA	NA	NA	NA	0.007	1.96E-04	NA	NA
-0.009	-0.008	0.015	-0.073	-0.003	4.51E-01	5.14E-01	1.70E-01
0.018	0.042	-0.029	NA	-0.010	6.49E-09	5.99E-01	8.32E-01
-0.171	0.045	0.027	NA	0.000	9.95E-04	1.14E-01	5.01E-01
-0.011	-0.005	0.006	0.090	-0.004	4.40E-09	4.90E-01	8.26E-03
-0.001	0.001	0.001	-0.001	0.000	4.03E-07	8.01E-02	2.40E-01
0.011	0.010	0.003	0.094	0.005	3.62E-01	5.05E-01	7.91E-02
NA	-0.041	-0.007	NA	-0.012	9.71E-07	NA	2.60E-01
-0.002	0.004	-0.023	0.031	-0.001	5.96E-04	5.16E-01	4.83E-04
NA	NA	NA	NA	-0.008	4.87E-02	NA	NA
-0.015	0.018	-0.028	0.002	0.001	1.22E-78	3.19E-09	1.09E-37
0.016	-0.002	0.008	0.069	0.003	4.71E-02	2.41E-01	8.64E-07
-0.001	-0.012	0.008	0.052	0.004	1.07E-04	1.89E-01	2.18E-01
0.012	-0.004	-0.017	0.087	-0.005	1.06E-03	3.32E-01	1.57E-01
-0.014	0.009	0.024	0.000	0.006	5.44E-02	4.27E-01	7.27E-03
-0.005	0.005	0.003	-0.058	0.000	2.76E-04	3.25E-01	6.06E-07
0.007	-0.009	0.003	0.025	0.003	9.40E-26	6.14E-02	2.34E-06
0.008	-0.003	0.011	0.012	0.003	1.81E-02	7.83E-01	7.74E-01
-0.015	-0.005	0.007	0.014	-0.001	2.69E-04	1.08E-01	2.79E-01
-0.002	-0.009	0.002	0.024	0.000	1.80E-247	9.73E-08	3.74E-75
-0.008	0.008	0.022	-0.022	-0.002	5.56E-13	8.21E-01	2.76E-01
-0.002	-0.024	0.009	0.033	-0.003	5.01E-02	1.67E-01	2.29E-01
-0.005	-0.001	0.023	-0.042	0.000	2.50E-01	2.74E-01	4.12E-01
0.052	-0.021	-0.011	-0.027	-0.008	1.70E-01	2.96E-01	4.42E-01
0.003	-0.049	0.023	0.054	0.003	7.44E-01	8.52E-01	7.10E-03
0.014	0.002	-0.021	-0.073	-0.002	2.89E-17	2.47E-03	3.66E-01

-0.012	0.002	0.010	-0.002	0.000	4.51E-01	2.63E-02	6.74E-01
0.001	0.006	0.021	-0.064	0.012	3.62E-03	5.57E-01	1.83E-02
0.002	0.006	-0.004	0.049	-0.001	1.40E-16	3.93E-01	5.98E-07
0.009	0.005	-0.004	0.041	-0.002	1.56E-03	4.11E-01	3.40E-01
0.007	-0.015	0.005	0.072	-0.003	4.57E-02	2.58E-01	3.21E-02
-0.001	0.007	0.016	-0.015	0.007	7.22E-14	9.93E-01	5.42E-03
0.007	-0.014	-0.014	0.063	-0.006	2.54E-02	2.84E-01	1.60E-06
0.009	0.000	0.004	-0.027	0.000	7.71E-19	2.73E-01	1.64E-12
0.004	-0.080	0.010	NA	0.001	5.14E-06	1.81E-01	1.48E-01
-0.007	0.006	0.007	0.064	0.001	6.01E-20	2.56E-01	1.11E-15
-0.010	-0.005	0.001	0.040	-0.001	1.08E-03	5.65E-01	4.71E-01
-0.005	0.009	0.002	0.036	0.003	6.35E-08	5.90E-02	2.96E-06
0.013	0.029	-0.031	NA	0.002	5.12E-01	4.63E-01	5.15E-01
0.006	-0.003	-0.003	0.053	0.003	2.71E-05	5.98E-01	1.97E-01
-0.011	0.002	-0.026	-0.076	-0.003	8.70E-01	4.89E-01	9.37E-01
0.028	NA	-0.004	0.087	0.014	2.66E-01	3.91E-01	NA
0.008	-0.004	0.004	NA	0.002	2.98E-19	8.47E-01	6.83E-01
0.063	0.010	0.033	-0.058	0.009	3.65E-01	2.71E-02	9.14E-01
0.025	-0.003	-0.006	0.034	-0.003	1.15E-01	1.10E-01	8.24E-01
0.005	-0.009	0.007	-0.002	-0.006	4.31E-22	5.97E-03	1.01E-08
0.026	0.007	-0.013	0.138	0.000	5.60E-10	5.22E-02	2.52E-04
0.031	0.009	-0.009	0.002	0.003	2.11E-02	3.87E-02	6.82E-01
0.000	0.008	-0.014	0.037	-0.002	1.39E-03	1.38E-01	3.66E-02
-0.013	-0.003	-0.006	-0.011	0.000	9.15E-10	2.46E-01	1.14E-01
0.001	0.008	0.025	-0.003	0.005	3.45E-17	1.09E-02	5.25E-05
0.008	0.029	0.002	0.012	-0.008	4.88E-08	5.30E-01	2.11E-01
0.005	0.004	-0.006	NA	0.002	3.10E-01	7.32E-01	6.97E-01
0.011	-0.006	0.001	-0.061	0.000	2.95E-01	4.10E-02	1.83E-01
0.032	-0.008	-0.002	-0.016	-0.002	1.26E-03	5.71E-05	1.32E-02
-0.007	0.012	-0.017	-0.061	0.010	5.32E-04	6.98E-01	3.30E-02
0.015	0.002	-0.001	-0.090	0.005	2.25E-09	3.09E-02	1.98E-01
-0.021	0.003	0.013	-0.051	-0.001	1.83E-01	4.32E-02	3.55E-01
0.010	-0.009	0.014	0.006	-0.004	7.59E-134	4.94E-10	4.44E-56
-0.007	NA	-0.060	NA	-0.007	1.09E-01	5.60E-03	NA
0.021	0.014	-0.001	0.095	0.008	1.01E-15	8.84E-02	1.15E-05
0.004	-0.026	0.011	-0.002	-0.012	2.88E-07	5.83E-06	1.31E-03
-0.003	0.009	0.000	0.034	0.008	2.20E-13	5.27E-01	4.85E-01
-0.005	0.004	-0.022	0.087	0.001	1.38E-16	2.27E-02	8.18E-12
-0.013	0.000	-0.001	0.015	-0.001	1.40E-215	4.76E-13	5.32E-137
0.012	0.005	0.001	0.103	0.003	3.64E-02	2.55E-01	5.99E-01
0.011	0.007	0.021	-0.035	0.007	1.62E-06	2.69E-01	5.10E-02
0.011	0.010	-0.005	-0.141	0.009	7.52E-04	2.46E-01	8.31E-02
0.000	0.002	-0.019	0.036	0.000	4.27E-01	9.28E-01	7.13E-01
0.000	0.005	-0.002	-0.060	0.006	1.54E-135	2.70E-01	4.59E-47
-0.003	0.009	0.005	-0.014	0.001	3.69E-04	1.42E-01	1.52E-01
0.023	0.028	-0.002	0.008	0.011	1.34E-04	1.28E-01	6.84E-02
-0.007	0.006	-0.009	-0.008	-0.001	4.70E-10	7.11E-01	1.13E-02

-0.035	-0.002	-0.013	-0.080	-0.005	2.95E-03	7.84E-04	1.23E-07
0.008	-0.003	-0.014	0.093	-0.003	3.69E-01	4.34E-02	9.21E-01
0.004	-0.011	-0.002	0.020	-0.004	2.16E-17	7.66E-04	2.31E-10
0.002	0.008	0.017	0.010	0.006	1.99E-12	8.33E-02	3.68E-13
-0.009	-0.010	0.010	-0.061	-0.003	6.39E-08	6.89E-01	5.44E-06
-0.004	-0.013	-0.012	-0.061	-0.005	5.26E-10	6.64E-01	2.19E-05
-0.007	0.000	0.010	0.026	0.001	1.16E-03	4.04E-01	9.87E-01
-0.018	0.004	0.022	-0.029	0.000	9.53E-07	9.93E-02	1.13E-03
0.012	0.004	0.019	-0.009	0.002	1.66E-01	2.13E-01	8.76E-01
0.000	-0.004	-0.006	-0.014	-0.006	3.18E-01	5.69E-01	3.94E-01
-0.010	0.017	-0.003	NA	-0.005	2.42E-02	8.45E-01	5.70E-01
-0.001	0.000	0.003	-0.002	-0.001	2.10E-44	1.20E-05	4.16E-16
0.002	0.009	0.005	0.102	0.005	2.78E-01	7.47E-01	8.33E-02
NA	0.023	-0.015	NA	-0.007	1.85E-136	NA	1.44E-11
-0.045	0.002	-0.036	NA	0.002	2.03E-01	5.36E-01	6.36E-01
-0.009	-0.002	0.024	NA	0.002	3.04E-02	1.31E-01	9.05E-01
0.009	0.012	0.013	-0.027	0.010	6.53E-04	7.29E-02	2.15E-02
0.009	-0.008	-0.007	-0.034	-0.009	4.89E-13	2.23E-01	1.47E-01
0.016	0.006	0.000	-0.011	0.001	2.04E-01	2.57E-01	4.59E-01
-0.025	-0.021	-0.006	0.065	-0.001	1.06E-01	1.31E-01	6.58E-01
-0.012	0.001	0.012	-0.018	0.004	3.13E-01	5.69E-01	2.89E-01
0.001	-0.001	0.008	0.085	-0.004	3.77E-01	6.95E-01	6.67E-02
0.010	0.005	0.006	0.019	-0.001	4.06E-02	9.09E-01	2.99E-01
0.031	-0.017	0.007	NA	0.004	7.21E-03	4.54E-03	1.89E-01
0.001	-0.008	-0.008	0.024	-0.001	3.50E-01	2.79E-01	1.03E-01
0.001	0.006	0.002	0.075	0.003	3.70E-01	9.93E-01	3.87E-02
NA	0.179	-0.028	-0.020	-0.030	2.17E-11	NA	3.25E-01
NA	-0.062	0.027	-0.338	0.026	4.60E-30	NA	8.75E-01
NA	-0.009	-0.030	NA	-0.028	1.57E-10	NA	7.39E-01
0.005	-0.004	0.019	-0.043	-0.004	3.84E-17	6.24E-03	1.96E-16
-0.003	-0.018	-0.008	0.030	-0.003	6.90E-05	2.78E-01	4.21E-01
-0.017	0.057	0.022	NA	0.004	1.93E-02	2.16E-01	1.37E-02
0.008	0.012	-0.017	-0.020	0.001	1.32E-09	3.38E-01	5.24E-01
0.001	NA	-0.001	NA	0.007	7.85E-01	1.65E-01	NA
-0.004	0.014	-0.005	0.096	0.006	2.15E-01	1.12E-01	2.56E-04
0.004	-0.001	0.010	-0.005	0.007	4.15E-12	8.44E-02	1.75E-02
0.004	0.001	0.015	0.000	-0.001	6.83E-12	1.04E-02	6.93E-08
0.007	-0.013	0.028	-0.022	-0.002	7.81E-03	5.05E-01	1.05E-02
NA	-0.048	0.066	NA	0.012	6.66E-21	NA	6.81E-01
-0.009	-0.006	0.008	-0.050	-0.004	4.50E-07	3.17E-01	4.63E-03
NA	0.171	0.012	NA	0.011	1.11E-03	NA	3.49E-01
NA	NA	-0.013	NA	-0.010	4.37E-02	NA	NA
0.004	0.000	0.001	-0.013	0.000	7.97E-05	8.68E-01	2.52E-05
-0.006	0.007	-0.006	0.012	0.000	7.18E-01	8.88E-01	4.81E-01
0.008	0.005	-0.034	0.022	-0.001	3.48E-05	1.64E-01	6.41E-03
0.018	-0.001	0.011	0.059	0.004	7.97E-12	6.26E-02	8.93E-01
NA	-0.110	0.052	NA	-0.018	4.08E-22	NA	2.83E-01

-0.043	-0.011	0.003	NA	-0.001	2.29E-03	8.07E-02	9.12E-01
-0.011	-0.004	-0.017	NA	-0.007	6.66E-47	3.34E-01	5.15E-05
0.018	-0.006	0.003	-0.034	0.000	4.87E-05	9.93E-02	5.71E-04
0.001	-0.008	-0.011	0.222	0.001	2.84E-04	9.67E-01	2.12E-01
-0.008	0.014	-0.005	-0.028	0.003	9.57E-09	9.53E-02	6.84E-02
-0.002	0.000	0.022	0.071	0.003	2.45E-02	9.73E-01	2.13E-01
-0.008	0.004	-0.023	-0.124	0.003	4.68E-03	1.03E-01	7.88E-01
-0.011	0.009	0.013	-0.013	0.002	8.29E-01	4.87E-01	2.30E-03
0.028	-0.001	-0.004	0.067	0.002	5.85E-01	1.33E-03	8.20E-03
0.025	-0.004	-0.003	-0.095	-0.001	1.46E-01	3.89E-02	4.78E-01
NA	0.017	0.055	-0.087	0.012	8.27E-01	NA	2.09E-01
-0.001	0.003	0.033	-0.015	0.000	2.09E-26	4.11E-09	1.16E-10
-0.005	0.000	-0.017	0.027	-0.002	5.44E-01	8.24E-01	8.64E-01
0.000	0.006	0.013	0.030	0.003	4.77E-02	7.60E-01	1.29E-02
0.008	0.001	0.008	-0.036	0.001	3.83E-09	5.35E-03	8.76E-04

rDrink							
int						PInt	
HIS	BRA	META	EUR	AFR	ASN	HIS	BRA
3.36E-01	NA	9.32E-01	9.36E-01	5.92E-01	5.63E-01	4.09E-01	NA
4.95E-01	8.78E-01	6.25E-02	8.30E-02	5.41E-01	1.07E-01	2.25E-01	8.09E-01
1.04E-01	1.51E-02	5.19E-01	7.33E-01	1.32E-01	8.28E-01	1.42E-01	7.24E-01
5.07E-02	6.31E-01	9.63E-10	4.22E-01	6.89E-01	9.30E-01	6.54E-01	7.10E-01
6.42E-01	NA	6.74E-01	3.11E-01	9.33E-01	8.89E-01	3.57E-01	NA
7.12E-01	9.27E-01	7.41E-01	7.08E-01	7.91E-01	4.38E-01	2.94E-01	7.43E-01
7.87E-04	8.53E-01	3.16E-11	3.45E-01	4.25E-01	9.54E-01	2.30E-01	9.03E-01
2.50E-01	2.64E-01	1.80E-11	3.31E-01	3.94E-01	5.30E-01	8.69E-01	7.97E-01
6.49E-01	NA	9.82E-01	NA	5.11E-01	2.20E-01	5.28E-01	NA
4.32E-01	1.54E-01	9.48E-01	4.73E-01	7.07E-02	5.95E-01	3.00E-01	6.50E-02
1.78E-01	2.96E-01	5.00E-02	8.23E-01	2.60E-01	7.17E-02	7.08E-02	3.95E-01
8.58E-01	NA	4.40E-01	4.39E-01	7.99E-01	2.29E-01	8.31E-01	NA
NA	NA	2.68E-04	6.82E-01	NA	NA	NA	NA
1.69E-01	3.34E-02	9.90E-02	5.46E-01	4.27E-01	4.72E-02	2.29E-01	8.94E-02
7.38E-01	NA	1.40E-07	3.63E-01	8.06E-01	6.08E-01	3.29E-01	NA
6.09E-01	NA	5.14E-04	3.24E-01	2.84E-01	4.18E-01	6.53E-01	NA
1.84E-03	1.96E-01	3.38E-12	4.76E-01	5.61E-01	1.32E-01	6.55E-01	7.45E-02
9.08E-01	6.40E-01	2.93E-08	2.61E-01	9.51E-01	9.42E-01	7.48E-01	9.92E-01
2.93E-01	2.11E-01	4.23E-02	6.57E-01	4.58E-01	3.98E-02	7.53E-01	7.81E-02
8.00E-01	NA	6.51E-07	6.46E-01	NA	1.94E-01	8.34E-01	NA
2.54E-01	6.99E-01	2.93E-06	9.93E-01	7.82E-01	7.54E-01	1.45E-01	6.52E-01
NA	NA	6.26E-02	4.46E-01	NA	NA	NA	NA
1.09E-13	1.58E-01	3.02E-130	9.18E-01	2.02E-01	3.31E-03	2.19E-02	9.54E-01
7.44E-01	1.82E-01	6.10E-07	9.66E-01	3.95E-01	7.31E-01	6.10E-01	8.87E-02
1.48E-02	5.01E-01	1.32E-04	3.25E-01	9.20E-01	1.72E-01	5.24E-01	3.23E-01
2.58E-01	1.12E-01	2.45E-03	2.23E-02	2.75E-01	6.84E-01	2.57E-01	4.51E-02
5.72E-02	7.36E-01	2.39E-04	9.43E-02	8.72E-02	1.41E-01	6.11E-02	9.93E-01
1.84E-01	5.42E-01	3.13E-10	3.94E-01	8.58E-01	2.75E-01	6.82E-01	3.28E-01
1.55E-03	8.84E-01	1.22E-32	2.12E-01	5.53E-01	1.86E-01	8.02E-01	6.20E-01
2.02E-02	8.95E-01	1.52E-02	1.85E-01	4.47E-01	2.30E-01	3.12E-01	8.11E-01
4.86E-01	9.16E-01	3.99E-05	4.77E-01	1.19E-01	7.05E-01	5.42E-01	8.21E-01
8.50E-29	1.83E-02	0.00E+00	6.14E-01	5.94E-01	1.01E-01	7.29E-01	5.63E-01
2.61E-01	9.09E-01	1.99E-06	9.68E-01	3.58E-01	1.19E-01	1.84E-01	6.92E-01
2.16E-01	4.86E-01	1.23E-02	4.33E-01	9.47E-01	7.09E-02	4.13E-01	4.58E-01
1.39E-01	7.42E-01	7.33E-02	5.61E-01	9.77E-01	7.56E-01	4.37E-02	4.40E-01
6.76E-01	3.09E-01	1.65E-01	2.42E-01	2.47E-01	7.27E-01	6.31E-01	7.97E-01
2.18E-01	6.78E-01	6.77E-01	6.70E-01	6.70E-01	4.32E-03	9.45E-02	3.80E-01
1.04E-02	7.64E-02	3.57E-19	7.99E-01	2.14E-01	9.08E-01	6.10E-02	9.53E-02

3.35E-01	9.92E-01	7.39E-01	6.04E-01	1.67E-01	4.36E-01	2.93E-01	9.63E-01
2.26E-01	7.04E-02	3.39E-04	3.75E-03	9.17E-01	2.83E-01	8.12E-02	1.98E-01
1.32E-01	9.93E-02	1.53E-21	4.35E-01	8.70E-01	4.93E-01	5.73E-01	2.95E-01
5.86E-01	3.45E-01	2.42E-03	1.28E-01	4.04E-01	2.81E-01	6.91E-01	4.70E-01
9.01E-01	3.81E-01	3.58E-01	7.06E-01	4.24E-01	2.21E-02	7.24E-01	1.87E-01
2.49E-01	6.75E-02	2.20E-13	9.06E-01	9.81E-01	1.94E-01	2.34E-01	8.00E-01
7.49E-02	1.58E-02	6.55E-07	6.29E-01	4.16E-01	8.37E-01	2.64E-01	2.31E-01
8.53E-01	4.42E-01	5.40E-28	2.82E-01	2.43E-01	6.41E-01	7.72E-01	6.48E-01
7.22E-01	NA	3.39E-06	5.51E-01	7.86E-01	1.21E-01	5.80E-01	NA
1.56E-03	4.52E-01	4.68E-36	8.60E-01	7.24E-01	1.42E-01	6.02E-01	2.13E-01
2.95E-01	6.46E-01	6.63E-04	9.53E-01	9.50E-01	9.74E-01	9.54E-01	5.74E-01
7.43E-02	7.67E-01	2.23E-14	7.81E-01	3.57E-01	6.44E-02	8.38E-01	5.26E-01
4.09E-01	NA	4.08E-01	6.10E-01	5.12E-01	4.41E-01	2.24E-01	NA
2.40E-01	1.39E-01	1.71E-06	3.68E-01	7.06E-01	8.51E-01	8.95E-01	3.28E-01
5.45E-02	1.92E-01	5.79E-01	8.11E-01	1.52E-01	8.70E-01	1.84E-02	1.09E-01
8.72E-01	3.23E-02	1.28E-01	1.20E-01	5.57E-01	NA	9.37E-01	4.73E-01
6.16E-01	NA	1.49E-14	6.24E-01	6.25E-01	5.61E-01	8.21E-01	NA
3.50E-01	2.15E-02	1.17E-01	4.66E-01	2.67E-02	4.95E-01	2.99E-01	4.20E-01
5.12E-01	6.73E-01	7.02E-02	3.48E-01	1.52E-01	8.63E-01	7.37E-01	5.30E-01
1.65E-04	7.12E-01	5.99E-34	3.02E-01	9.86E-01	6.88E-02	4.37E-01	9.68E-01
2.26E-01	5.65E-03	8.98E-14	1.16E-01	3.21E-01	1.42E-01	2.53E-01	1.35E-03
1.22E-01	1.98E-01	1.20E-02	9.37E-01	1.52E-02	9.91E-01	5.74E-01	9.65E-01
2.36E-01	7.83E-01	1.71E-03	7.46E-01	9.64E-01	4.08E-01	1.76E-01	4.86E-01
9.43E-02	2.41E-01	8.84E-10	8.39E-01	7.20E-02	8.48E-01	4.98E-01	8.31E-01
2.87E-05	9.92E-01	5.73E-25	5.46E-01	6.71E-01	9.83E-02	3.96E-02	9.59E-01
9.73E-01	5.89E-01	5.17E-06	5.45E-02	3.80E-01	2.76E-01	9.97E-01	8.40E-01
6.03E-01	NA	1.95E-01	5.13E-01	4.17E-01	9.98E-01	6.98E-01	NA
6.05E-01	3.38E-01	9.96E-01	8.51E-01	5.73E-01	2.50E-01	9.01E-01	2.07E-01
7.58E-01	4.08E-01	9.79E-06	5.09E-01	3.67E-04	2.59E-02	8.72E-01	7.31E-01
6.34E-01	2.13E-01	1.46E-04	8.39E-02	9.51E-01	1.90E-02	3.12E-01	3.52E-01
2.78E-02	6.28E-01	4.36E-12	1.27E-01	8.89E-01	8.24E-01	9.82E-01	3.80E-01
4.71E-01	4.19E-01	5.55E-02	5.68E-01	7.41E-02	6.91E-01	2.92E-01	2.46E-01
3.83E-13	4.90E-02	9.03E-203	8.25E-02	5.43E-01	1.95E-01	7.45E-01	9.28E-01
5.81E-01	NA	2.21E-03	6.23E-01	7.77E-01	NA	6.58E-01	NA
1.68E-06	2.46E-02	3.79E-23	7.32E-02	2.91E-02	2.50E-02	8.19E-01	2.83E-02
5.70E-03	6.29E-01	1.89E-15	5.01E-02	8.20E-01	3.17E-02	3.74E-01	9.83E-01
2.23E-01	5.65E-01	4.95E-12	1.47E-01	7.94E-01	2.06E-01	8.51E-01	3.65E-01
1.06E-02	8.31E-02	3.08E-29	2.84E-01	5.86E-01	5.60E-01	5.38E-02	1.26E-01
4.31E-16	1.82E-01	0.00E+00	8.04E-01	2.39E-01	9.01E-01	8.62E-01	7.93E-01
9.39E-01	2.36E-01	4.38E-02	8.73E-01	2.34E-01	3.39E-01	9.04E-01	9.07E-02
4.88E-02	3.90E-02	1.45E-07	3.58E-02	4.57E-01	2.26E-01	1.26E-01	4.76E-01
9.08E-01	1.39E-03	5.05E-04	4.25E-02	2.65E-01	9.43E-02	7.03E-01	3.15E-04
7.95E-02	6.93E-01	2.40E-01	5.49E-01	9.38E-01	6.52E-01	1.52E-01	4.90E-01
1.09E-12	2.77E-02	9.35E-179	3.06E-01	6.77E-01	3.56E-01	9.66E-01	2.51E-01
8.47E-01	8.87E-01	9.45E-04	9.66E-01	8.26E-01	4.37E-02	6.17E-01	8.19E-01
2.28E-01	4.65E-01	3.37E-06	1.43E-01	4.39E-01	5.06E-02	9.64E-01	9.20E-01
1.23E-01	9.36E-01	7.22E-11	6.88E-01	3.86E-01	2.47E-01	5.56E-01	8.83E-01

6.67E-01	2.58E-01	1.42E-06	3.59E-02	1.33E-02	4.77E-01	3.15E-01	1.03E-01
4.46E-01	2.98E-02	8.09E-02	3.55E-01	6.73E-01	7.63E-01	2.02E-01	1.19E-01
2.09E-02	8.32E-01	1.93E-29	4.14E-01	9.45E-01	7.77E-01	9.14E-01	7.39E-01
1.48E-02	1.39E-01	7.15E-27	8.57E-01	8.44E-01	1.05E-01	1.02E-01	8.01E-01
5.39E-01	2.79E-01	1.30E-11	2.56E-01	3.31E-01	9.42E-02	3.43E-01	1.63E-01
6.18E-03	2.51E-01	1.84E-14	1.00E+00	7.97E-01	1.27E-02	2.95E-01	1.71E-01
3.61E-01	1.17E-01	1.08E-01	1.18E-01	6.70E-01	6.59E-01	3.84E-01	6.37E-01
1.63E-01	5.04E-01	1.50E-08	8.95E-01	1.59E-01	2.99E-01	6.46E-02	5.97E-01
4.87E-01	1.71E-01	2.50E-01	5.53E-01	4.82E-01	5.10E-01	2.54E-01	9.04E-01
8.84E-01	9.02E-01	3.26E-01	4.75E-01	9.91E-01	7.05E-01	8.89E-01	8.40E-01
9.87E-01	NA	4.94E-02	2.22E-01	6.69E-01	2.17E-01	9.60E-01	NA
2.05E-08	3.02E-01	5.99E-68	4.60E-01	4.64E-01	5.89E-01	8.90E-01	9.54E-01
4.16E-01	4.88E-03	3.08E-02	2.36E-01	7.76E-01	8.74E-02	7.15E-01	1.84E-02
1.46E-07	NA	3.43E-148	7.58E-01	NA	6.10E-01	9.26E-01	NA
1.19E-01	NA	1.48E-01	5.58E-01	5.00E-01	7.17E-01	1.68E-01	NA
5.59E-02	NA	5.61E-03	5.29E-01	6.04E-01	6.64E-01	1.11E-01	NA
6.15E-01	6.33E-01	1.42E-05	1.85E-01	6.53E-01	8.57E-02	3.60E-01	5.54E-01
2.96E-01	3.61E-01	1.89E-13	5.81E-03	6.91E-01	4.12E-01	6.31E-01	3.83E-01
9.35E-01	8.55E-01	3.62E-01	6.70E-01	9.60E-02	2.17E-01	9.67E-01	8.10E-01
1.62E-01	5.06E-01	2.17E-01	7.84E-01	1.31E-01	3.92E-01	6.77E-01	2.48E-01
4.48E-01	9.22E-01	2.35E-01	1.42E-01	2.57E-01	9.91E-01	2.83E-01	7.12E-01
8.66E-01	2.55E-01	1.22E-01	1.69E-01	9.76E-01	5.90E-01	6.85E-01	1.30E-01
4.05E-01	9.69E-01	1.20E-01	2.92E-01	6.34E-01	2.57E-01	8.23E-01	8.11E-01
5.64E-01	NA	2.52E-01	6.80E-02	1.43E-02	7.80E-01	5.45E-01	NA
5.51E-01	9.09E-01	4.40E-01	5.80E-01	6.46E-01	9.34E-01	4.17E-01	6.78E-01
6.24E-01	1.30E-01	2.08E-02	7.26E-01	7.57E-01	3.00E-01	7.90E-01	1.05E-01
5.61E-02	8.67E-01	9.39E-11	8.50E-03	NA	1.46E-01	4.13E-01	8.65E-01
1.90E-04	8.32E-04	2.27E-31	1.66E-02	NA	6.15E-01	3.52E-01	4.27E-04
7.77E-03	NA	6.72E-12	2.44E-01	NA	9.19E-01	4.13E-01	NA
1.50E-03	2.12E-01	1.94E-36	1.47E-01	5.47E-01	1.84E-01	8.50E-02	4.27E-01
8.38E-01	8.13E-01	5.02E-05	9.85E-01	6.22E-01	5.39E-01	4.97E-01	5.60E-01
1.39E-03	NA	4.73E-03	5.45E-01	1.20E-01	2.30E-02	9.53E-02	NA
7.38E-04	8.64E-01	2.40E-10	7.83E-01	2.95E-01	6.19E-01	1.47E-01	7.36E-01
9.86E-01	NA	2.39E-01	5.05E-01	7.49E-01	NA	9.80E-01	NA
2.69E-01	1.86E-01	1.68E-05	7.04E-01	7.59E-01	4.65E-02	6.44E-01	1.49E-01
1.65E-01	4.93E-01	2.05E-13	4.82E-02	5.45E-01	9.42E-01	5.08E-01	9.27E-01
3.47E-02	9.96E-01	7.39E-21	1.22E-01	8.70E-01	9.74E-01	2.32E-01	9.95E-01
9.08E-03	6.45E-01	1.51E-02	5.46E-01	8.98E-01	6.63E-03	4.50E-03	6.10E-01
2.32E-05	NA	9.95E-23	4.74E-01	NA	5.84E-01	2.92E-01	NA
7.35E-01	1.94E-02	6.40E-09	2.05E-01	4.65E-01	1.62E-01	3.62E-01	2.13E-01
4.73E-03	NA	2.16E-05	7.15E-01	NA	1.48E-01	7.87E-01	NA
4.87E-01	NA	2.98E-02	6.47E-01	NA	NA	8.15E-01	NA
6.44E-02	7.87E-01	1.24E-09	9.25E-01	6.39E-01	9.02E-01	8.96E-01	8.20E-01
3.37E-01	9.64E-01	9.86E-01	2.77E-01	7.73E-01	2.42E-01	7.24E-01	8.51E-01
6.96E-03	7.83E-01	8.45E-08	4.67E-01	4.25E-01	3.55E-01	1.19E-02	7.15E-01
4.28E-01	1.30E-01	1.66E-08	4.54E-01	8.57E-02	3.79E-01	3.44E-01	1.87E-01
2.78E-03	NA	2.00E-23	9.21E-01	NA	2.00E-01	3.85E-01	NA

9.89E-01	NA	1.41E-02	7.05E-01	2.60E-02	7.49E-01	7.88E-01	NA
1.39E-01	NA	4.67E-40	1.42E-01	4.39E-01	4.87E-01	4.03E-01	NA
6.71E-01	5.55E-01	6.21E-08	8.52E-01	9.95E-02	5.30E-01	7.40E-01	5.10E-01
3.18E-01	5.23E-02	4.71E-03	4.42E-01	8.55E-01	2.40E-01	7.32E-01	4.58E-02
9.04E-01	1.41E-01	3.86E-09	4.64E-01	9.60E-01	8.32E-01	7.95E-01	5.89E-01
1.69E-01	2.65E-01	5.15E-03	7.70E-01	9.24E-01	7.32E-01	1.18E-01	1.98E-01
1.52E-01	1.98E-01	6.66E-03	1.35E-01	6.27E-01	5.36E-01	8.37E-02	7.58E-02
1.25E-01	9.65E-01	3.58E-02	8.91E-01	3.34E-01	1.24E-01	3.15E-01	8.06E-01
7.32E-01	3.64E-01	2.58E-02	2.87E-01	1.31E-02	8.04E-01	8.55E-01	1.91E-01
6.96E-01	1.43E-01	2.00E-01	4.55E-01	5.33E-02	3.36E-01	9.01E-01	5.86E-02
4.88E-03	5.02E-01	4.13E-01	9.63E-01	NA	6.58E-01	4.16E-02	3.44E-01
4.41E-03	5.48E-01	8.02E-44	2.38E-01	8.69E-01	5.59E-01	4.67E-02	7.98E-01
6.05E-02	6.99E-01	6.27E-01	5.79E-01	6.89E-01	9.21E-01	7.35E-02	5.77E-01
3.83E-01	6.75E-01	8.26E-04	8.71E-01	5.33E-01	6.47E-01	2.99E-01	5.48E-01
4.33E-02	5.52E-01	7.75E-15	7.32E-01	5.89E-01	5.44E-01	6.12E-01	4.32E-01

				PMain			
META	EUR	AFR	ASN	HIS	BRA	META	EUR
8.00E-01	9.98E-01	8.23E-01	3.66E-01	8.63E-01	NA	7.23E-01	0.000
1.07E-01	3.00E-01	5.45E-01	7.36E-01	3.01E-01	6.16E-01	8.17E-01	0.001
9.96E-01	8.90E-01	5.28E-01	4.22E-01	9.90E-01	5.95E-03	3.33E-01	0.002
6.10E-01	3.13E-05	8.22E-01	2.26E-01	1.28E-01	5.69E-01	3.46E-04	-0.022
8.68E-01	2.71E-01	3.52E-01	8.96E-01	5.59E-01	NA	3.98E-01	0.018
7.14E-01	9.74E-01	7.95E-01	1.66E-01	5.07E-01	7.53E-01	5.10E-01	0.001
4.24E-01	7.94E-04	1.54E-01	3.23E-02	5.47E-04	5.79E-01	1.23E-06	0.013
9.85E-01	5.29E-03	2.23E-01	3.06E-04	4.15E-01	1.57E-01	1.54E-06	0.014
9.21E-01	NA	8.61E-01	5.79E-01	9.47E-01	NA	8.53E-01	NA
3.69E-01	1.37E-01	3.40E-02	1.64E-01	2.17E-01	4.26E-01	5.49E-01	0.000
9.41E-01	9.16E-02	4.95E-02	7.24E-01	5.51E-01	1.29E-01	9.02E-02	-0.007
8.14E-01	4.77E-02	5.85E-01	8.64E-02	6.07E-01	NA	9.71E-01	0.010
6.85E-01	4.60E-02	NA	NA	NA	NA	4.81E-02	0.108
8.40E-02	7.70E-01	8.30E-01	4.18E-01	5.74E-02	2.54E-01	9.40E-01	-0.003
3.23E-01	2.54E-05	5.93E-01	8.31E-01	6.03E-01	NA	1.43E-04	0.041
4.32E-01	1.14E-01	4.90E-01	2.42E-01	3.41E-01	NA	4.46E-02	-0.018
1.88E-01	2.54E-03	6.21E-01	2.33E-01	3.99E-03	2.01E-01	4.31E-04	-0.015
3.00E-01	7.61E-03	9.03E-02	1.15E-01	7.77E-01	4.33E-01	6.47E-04	0.012
4.72E-02	3.35E-01	2.84E-01	1.27E-01	2.02E-01	3.98E-01	1.97E-02	-0.005
3.67E-01	9.36E-04	NA	1.04E-01	6.20E-01	NA	2.28E-04	0.029
8.79E-01	5.77E-02	6.60E-01	4.61E-03	1.17E-01	4.17E-01	7.40E-04	0.006
4.44E-01	3.27E-01	NA	NA	NA	NA	3.71E-01	-0.018
5.65E-01	2.44E-22	7.28E-08	2.71E-17	2.65E-12	1.86E-01	1.65E-53	0.035
8.16E-01	2.83E-01	1.12E-01	1.09E-04	4.46E-01	1.45E-01	3.71E-05	-0.007
7.69E-01	2.54E-01	1.58E-01	9.49E-01	1.15E-01	2.52E-01	9.41E-02	0.006
9.41E-02	4.50E-04	1.39E-01	8.46E-02	1.17E-01	7.03E-01	1.51E-03	0.006
3.43E-02	3.09E-02	5.50E-01	3.43E-03	1.94E-02	5.02E-01	1.07E-04	-0.006
2.04E-01	1.02E-01	2.39E-01	2.37E-04	2.58E-01	6.99E-01	3.94E-05	0.008
7.10E-01	5.20E-06	2.05E-01	3.91E-06	1.81E-02	7.45E-01	3.96E-12	0.018
5.32E-01	5.35E-01	7.58E-01	3.26E-01	2.17E-01	8.62E-01	1.80E-01	0.002
9.99E-01	8.25E-02	4.08E-02	7.02E-02	6.74E-01	6.76E-01	3.44E-03	0.012
1.90E-01	1.50E-72	2.83E-05	1.08E-54	1.20E-15	4.46E-02	2.32E-138	0.069
2.30E-01	5.45E-05	7.77E-01	3.27E-01	1.98E-01	9.38E-01	2.83E-03	-0.020
4.12E-01	6.82E-01	2.09E-01	4.62E-01	1.06E-01	2.46E-01	2.39E-01	-0.003
9.27E-01	9.48E-01	3.62E-01	3.34E-01	1.03E-01	5.89E-01	1.75E-01	-0.002
2.63E-01	8.91E-01	8.04E-01	6.11E-01	8.11E-01	1.73E-01	9.71E-01	-0.003
7.40E-01	4.68E-01	6.19E-01	3.42E-01	1.38E-01	6.67E-01	3.53E-01	-0.001
9.77E-01	6.48E-06	9.17E-04	2.04E-01	6.64E-01	5.72E-01	3.40E-07	-0.015

4.98E-01	2.58E-01	4.16E-01	8.70E-01	8.60E-01	8.97E-01	4.35E-01	-0.003
1.80E-03	1.44E-01	3.50E-01	6.98E-03	2.52E-01	4.29E-01	1.05E-03	0.000
7.57E-01	6.96E-04	2.71E-01	5.55E-06	2.26E-01	3.68E-01	4.68E-08	-0.013
8.16E-01	6.30E-01	1.86E-01	1.52E-01	5.96E-01	3.20E-01	8.30E-02	-0.005
6.18E-01	4.80E-02	5.85E-01	6.00E-02	6.58E-01	7.93E-01	9.96E-01	-0.004
2.55E-01	1.11E-04	9.22E-01	1.54E-01	9.59E-01	4.49E-02	2.81E-03	0.016
8.22E-01	2.51E-01	6.60E-01	6.61E-02	2.69E-02	4.12E-03	1.55E-02	0.002
5.30E-01	5.26E-08	6.10E-01	3.02E-10	9.57E-01	4.18E-01	1.51E-14	0.020
5.43E-01	7.34E-03	2.53E-01	2.86E-01	9.20E-01	NA	7.75E-03	0.017
3.76E-01	2.58E-07	1.13E-01	3.23E-08	3.98E-02	6.51E-01	6.76E-15	0.017
9.90E-01	7.42E-02	3.67E-01	3.35E-01	2.58E-01	3.63E-01	4.12E-02	-0.012
2.37E-01	3.10E-04	3.35E-02	6.13E-03	1.18E-01	8.74E-01	6.56E-07	0.012
8.55E-01	6.83E-01	2.14E-01	2.74E-01	2.10E-01	NA	2.92E-01	-0.004
3.50E-01	1.06E-01	7.54E-01	1.03E-01	1.88E-01	3.34E-01	1.47E-02	0.010
2.55E-01	7.87E-01	3.80E-01	8.35E-01	5.02E-02	1.02E-01	3.70E-01	0.000
1.04E-01	2.10E-01	1.84E-01	NA	7.77E-01	3.40E-02	8.60E-02	-0.005
6.09E-01	2.30E-08	7.33E-01	2.75E-01	6.07E-01	NA	4.06E-06	0.021
1.40E-01	7.13E-01	4.05E-01	9.95E-01	4.08E-01	7.58E-03	6.39E-01	0.001
5.24E-01	6.01E-02	5.55E-01	4.92E-01	3.03E-01	3.99E-01	3.71E-02	0.007
1.05E-01	8.28E-05	7.18E-03	5.57E-04	6.97E-04	5.83E-01	1.83E-10	-0.017
7.46E-01	1.95E-02	1.58E-02	3.99E-05	7.58E-01	4.16E-02	8.64E-07	-0.011
5.99E-01	9.82E-02	6.52E-02	5.62E-01	3.66E-01	1.23E-01	2.93E-02	-0.007
7.58E-01	1.69E-01	1.26E-01	1.51E-02	8.66E-01	6.65E-01	1.22E-01	-0.006
3.30E-01	9.94E-04	1.16E-01	1.38E-01	5.56E-02	1.48E-01	9.87E-05	0.015
2.20E-01	9.05E-06	3.22E-02	1.99E-02	2.29E-01	9.42E-01	2.75E-07	0.014
2.99E-01	5.05E-01	8.14E-01	2.30E-01	8.11E-01	3.53E-01	3.41E-01	-0.009
4.49E-01	9.19E-01	8.61E-01	2.67E-01	3.41E-01	NA	4.83E-01	0.008
3.95E-01	3.54E-01	2.68E-02	7.68E-01	5.07E-01	1.57E-01	9.18E-01	0.008
3.43E-01	1.97E-02	8.72E-01	3.04E-03	5.29E-01	4.01E-01	3.26E-04	0.007
1.08E-02	8.88E-01	8.28E-01	5.16E-01	4.93E-01	3.07E-01	5.25E-01	0.003
2.16E-01	3.39E-02	1.60E-01	1.19E-01	5.36E-02	3.96E-01	7.50E-04	0.015
8.74E-01	7.71E-01	1.66E-02	3.09E-01	6.88E-01	2.72E-01	1.10E-01	-0.001
7.37E-02	7.18E-46	7.53E-06	1.39E-41	1.25E-06	2.07E-02	7.89E-95	0.077
8.52E-01	1.09E-01	5.31E-02	NA	3.35E-01	NA	3.56E-02	-0.039
8.59E-04	1.04E-08	3.56E-02	9.18E-06	4.85E-04	2.89E-02	4.09E-16	-0.020
7.46E-02	6.62E-06	6.18E-04	8.58E-04	9.55E-02	4.17E-01	3.75E-11	0.022
7.97E-02	9.92E-03	5.58E-01	7.62E-01	1.89E-01	9.60E-01	4.80E-02	0.013
6.52E-01	1.65E-07	1.05E-01	4.79E-09	8.11E-01	3.90E-02	7.39E-15	-0.018
6.75E-01	5.55E-59	2.19E-10	3.18E-91	2.70E-09	1.87E-01	6.02E-158	0.061
2.20E-01	8.05E-02	9.67E-02	3.33E-01	7.55E-01	3.56E-01	2.14E-02	-0.004
5.58E-03	1.07E-05	1.11E-01	8.47E-03	1.35E-02	1.16E-02	1.47E-07	-0.012
1.86E-02	8.36E-01	9.54E-01	1.02E-01	8.20E-01	3.26E-01	3.96E-01	0.004
6.52E-01	3.52E-01	8.18E-01	6.84E-01	2.23E-02	9.92E-01	2.03E-01	0.006
7.93E-01	2.55E-38	2.69E-01	7.85E-29	7.87E-08	1.03E-02	3.05E-63	0.043
1.53E-01	5.84E-02	1.39E-01	3.53E-02	5.86E-01	8.83E-01	2.21E-03	-0.008
2.81E-02	3.49E-01	9.36E-01	6.22E-01	1.91E-01	2.64E-01	5.00E-01	0.011
5.30E-01	3.72E-04	9.02E-01	2.55E-03	4.19E-01	8.12E-01	1.76E-05	-0.015

5.14E-03	7.78E-01	1.40E-04	6.32E-05	4.91E-01	6.33E-01	7.98E-02	0.000
3.02E-01	2.72E-01	2.14E-01	7.31E-01	2.48E-01	4.50E-01	7.07E-02	0.000
4.61E-01	2.36E-07	1.58E-02	1.78E-05	3.04E-02	8.88E-01	1.12E-12	0.014
1.70E-01	1.88E-05	7.83E-02	6.70E-12	4.56E-03	8.41E-02	1.70E-18	-0.012
7.45E-01	1.43E-03	6.78E-01	4.08E-03	2.66E-01	8.48E-01	8.28E-05	-0.011
4.72E-02	1.40E-04	3.99E-01	2.23E-05	3.83E-03	9.60E-01	4.00E-10	0.015
1.60E-01	1.45E-03	7.66E-01	8.24E-01	8.00E-01	4.87E-02	5.70E-02	-0.007
5.17E-01	1.10E-02	5.81E-01	4.93E-04	2.40E-01	5.08E-01	4.99E-05	-0.011
5.09E-01	6.31E-01	7.39E-02	8.05E-01	6.04E-01	2.13E-01	1.67E-01	-0.004
4.50E-01	7.97E-01	3.72E-01	2.75E-01	9.96E-01	7.48E-01	5.36E-01	-0.003
4.22E-01	7.11E-01	9.64E-01	7.50E-01	9.23E-01	NA	6.78E-01	-0.004
7.03E-01	9.70E-16	7.82E-04	9.59E-11	3.98E-06	1.69E-01	7.49E-29	-0.029
3.97E-01	1.81E-01	7.19E-01	9.49E-01	5.11E-01	1.93E-01	3.72E-01	0.008
8.60E-01	1.44E-42	NA	2.01E-08	3.49E-05	NA	1.53E-51	0.133
7.52E-01	8.12E-01	7.98E-01	6.26E-01	3.85E-02	NA	3.76E-01	0.006
3.76E-01	5.19E-02	4.41E-01	8.22E-01	1.68E-02	NA	1.67E-02	-0.017
2.73E-02	5.60E-04	4.86E-02	5.31E-03	4.21E-01	3.60E-01	6.07E-06	-0.008
1.40E-02	1.34E-01	9.72E-02	2.56E-01	5.55E-01	7.87E-01	1.45E-02	-0.010
3.81E-01	8.72E-01	2.00E-01	2.42E-01	8.23E-01	7.96E-01	2.21E-01	-0.004
7.71E-01	3.04E-01	4.24E-02	5.21E-01	3.60E-01	4.29E-01	2.49E-01	0.006
3.33E-01	1.66E-01	3.02E-01	1.84E-01	8.89E-01	7.95E-01	1.16E-01	-0.002
3.41E-01	1.69E-01	4.70E-01	3.51E-02	8.63E-01	2.74E-01	3.87E-02	0.013
7.20E-01	8.86E-01	9.93E-01	1.31E-01	4.88E-01	9.29E-01	2.08E-01	-0.003
1.01E-02	3.99E-03	7.42E-01	8.13E-01	2.88E-01	NA	6.68E-03	-0.009
9.54E-01	3.16E-01	2.68E-01	1.11E-01	2.92E-01	6.94E-01	3.73E-01	0.000
5.21E-01	7.08E-01	9.08E-01	4.79E-03	4.31E-01	5.07E-02	1.03E-02	-0.006
1.32E-02	2.83E-08	NA	2.06E-01	2.77E-02	6.54E-01	1.14E-07	0.070
5.14E-02	3.77E-16	NA	7.99E-01	6.19E-04	6.90E-01	8.36E-17	-0.093
1.69E-01	2.84E-06	NA	4.88E-01	7.63E-03	NA	1.55E-07	0.071
1.89E-01	6.36E-09	4.52E-02	6.68E-16	2.76E-01	8.11E-02	3.63E-24	0.016
6.11E-01	3.50E-02	3.51E-01	8.61E-01	5.94E-01	6.42E-01	5.40E-02	-0.008
4.14E-01	3.29E-01	2.62E-01	3.12E-01	3.29E-01	NA	1.66E-01	0.009
8.78E-01	1.51E-04	8.58E-01	9.56E-01	4.83E-04	5.90E-01	6.06E-05	0.012
9.27E-01	6.24E-01	1.30E-01	NA	9.20E-01	NA	1.31E-01	NA
1.89E-01	3.88E-01	1.80E-01	9.12E-05	3.75E-01	1.13E-01	4.94E-05	-0.004
1.13E-01	7.29E-02	1.56E-01	2.84E-02	4.41E-01	3.01E-01	1.68E-03	0.015
4.84E-01	7.25E-07	5.97E-02	2.41E-06	3.70E-01	9.33E-01	3.76E-12	0.018
1.41E-01	3.09E-02	2.09E-01	1.51E-02	5.27E-01	7.73E-01	1.34E-02	0.011
3.85E-01	8.43E-05	NA	7.92E-01	1.52E-02	NA	1.73E-05	0.061
8.00E-02	2.52E-05	1.34E-01	8.05E-04	6.95E-01	5.05E-03	8.71E-08	0.011
5.39E-01	5.54E-02	NA	3.35E-01	7.95E-03	NA	1.97E-03	-0.021
6.18E-01	7.32E-02	NA	NA	3.26E-01	NA	4.90E-02	0.025
8.85E-01	3.89E-02	9.82E-01	6.14E-05	1.17E-01	6.40E-01	1.09E-05	0.007
8.85E-01	4.39E-01	7.89E-01	6.62E-01	4.21E-01	8.09E-01	9.30E-01	0.002
8.46E-01	6.37E-04	5.01E-01	5.60E-02	1.74E-03	4.95E-01	4.14E-05	0.012
3.93E-01	1.93E-05	7.83E-01	5.59E-01	8.92E-01	3.46E-01	6.60E-02	0.012
9.73E-01	7.64E-06	NA	7.63E-01	2.22E-03	NA	2.35E-06	-0.095

3.51E-01	4.61E-02	7.29E-01	9.89E-01	9.01E-01	NA	8.47E-02	0.009
9.64E-01	1.34E-20	7.74E-01	1.02E-03	5.55E-01	NA	3.56E-14	-0.047
8.04E-01	8.93E-02	5.96E-01	4.40E-03	6.42E-01	2.80E-01	1.83E-03	0.008
6.55E-01	1.20E-01	9.20E-01	1.69E-01	1.63E-01	2.13E-02	5.52E-02	0.012
5.76E-01	1.67E-02	4.83E-02	2.41E-01	6.57E-01	1.78E-01	4.41E-03	0.010
3.47E-01	3.03E-01	7.91E-01	1.74E-01	3.00E-01	7.19E-01	1.64E-01	0.003
4.85E-01	6.82E-01	6.32E-02	8.51E-01	8.11E-02	4.28E-01	2.56E-01	0.004
2.57E-01	8.41E-01	8.41E-01	1.32E-01	5.60E-01	8.34E-01	2.54E-01	0.000
8.40E-01	3.47E-01	2.90E-04	1.70E-02	8.25E-01	1.97E-01	2.59E-02	0.001
5.26E-01	8.74E-02	2.23E-01	2.04E-01	7.21E-01	2.51E-01	1.45E-01	0.003
3.60E-01	5.99E-01	NA	1.09E-01	7.28E-01	2.99E-01	2.84E-01	-0.002
9.31E-01	2.10E-06	6.96E-06	6.01E-09	1.04E-03	2.99E-01	1.72E-19	-0.019
3.87E-01	2.89E-01	8.53E-01	7.73E-01	8.27E-01	4.16E-01	4.56E-01	0.004
3.75E-01	3.33E-01	6.40E-01	4.04E-02	1.69E-01	9.70E-01	1.22E-02	-0.007
3.96E-01	3.33E-04	4.46E-03	2.73E-04	2.64E-02	7.53E-01	9.71E-10	-0.012

SNPEffect					IntEffect		
AFR	ASN	HIS	META	EUR	AFR	ASN	HIS
0.001	0.059	0.032	0.003	-0.002	-0.006	-0.083	-0.012
0.007	0.002	0.010	0.003	0.003	-0.023	0.003	-0.030
0.000	0.004	0.015	0.003	-0.003	-0.024	0.004	-0.002
-0.021	-0.003	-0.023	-0.013	0.010	0.043	-0.002	-0.022
-0.014	0.007	-0.021	-0.012	-0.086	0.008	0.013	0.069
-0.009	0.009	-0.008	0.002	0.000	0.025	-0.010	0.025
0.016	0.005	0.036	0.013	-0.004	-0.003	0.010	-0.033
0.006	0.010	0.006	0.011	-0.002	-0.006	-0.002	0.016
0.006	-0.002	-0.001	0.003	NA	-0.006	-0.047	0.024
0.029	-0.004	0.000	-0.001	0.006	-0.077	0.002	0.017
-0.010	-0.006	0.004	-0.006	0.001	0.013	0.060	-0.042
0.001	-0.006	-0.007	0.002	-0.006	-0.001	0.003	0.007
NA	NA	NA	0.106	-0.031	NA	NA	NA
-0.004	0.002	-0.010	-0.001	0.001	0.002	-0.009	0.011
0.025	-0.031	0.017	0.035	-0.012	0.065	0.090	-0.068
NA	-0.037	-0.043	-0.018	0.003	NA	0.045	0.058
-0.001	-0.004	-0.028	-0.010	0.000	-0.021	-0.009	0.013
0.012	0.017	0.000	0.011	-0.002	0.002	-0.015	0.013
-0.001	-0.005	-0.014	-0.005	0.006	-0.003	0.011	0.019
NA	0.031	NA	0.029	0.007	NA	-0.037	NA
-0.004	0.009	0.010	0.007	0.002	-0.014	0.009	-0.028
NA	NA	NA	-0.017	-0.015	NA	NA	NA
0.031	0.032	0.044	0.034	0.000	-0.025	0.019	-0.005
-0.009	-0.009	-0.001	-0.008	0.005	0.030	-0.006	-0.002
0.010	-0.005	0.022	0.005	0.005	-0.005	0.001	-0.011
-0.007	0.005	0.007	0.005	-0.004	0.003	-0.004	-0.014
0.000	-0.009	-0.012	-0.007	0.004	-0.005	0.008	0.015
0.014	0.014	0.010	0.010	-0.002	-0.007	0.006	0.011
0.009	0.014	0.019	0.016	0.002	0.024	-0.005	0.009
-0.002	0.003	0.014	0.003	0.007	0.022	-0.006	0.010
0.010	0.018	0.010	0.012	-0.006	-0.020	-0.010	-0.008
0.058	0.052	0.066	0.062	-0.011	-0.015	-0.006	0.013
-0.003	-0.002	-0.002	-0.009	0.004	0.011	0.006	-0.001
-0.011	0.004	-0.017	-0.005	-0.002	-0.012	-0.012	0.021
-0.010	-0.003	-0.009	-0.003	-0.001	-0.003	0.000	0.025
0.014	-0.007	-0.011	-0.003	-0.005	0.061	-0.032	0.005
-0.004	0.008	-0.005	-0.001	0.000	0.006	-0.053	0.012
-0.018	-0.005	-0.009	-0.013	0.000	-0.006	0.001	-0.022

-0.008	0.001	0.007	-0.001	0.002	-0.025	0.002	-0.004
-0.006	-0.010	0.000	-0.004	0.007	0.004	0.007	0.001
-0.005	-0.021	-0.014	-0.014	-0.003	-0.014	0.005	0.002
-0.006	-0.003	0.002	-0.004	-0.001	0.002	0.001	-0.029
0.007	0.006	-0.001	0.000	0.001	0.007	-0.014	-0.002
-0.001	0.004	0.004	0.009	0.000	0.010	0.012	0.012
0.002	0.003	0.018	0.004	0.006	0.014	0.002	-0.028
0.002	0.020	-0.003	0.017	-0.005	0.031	-0.007	0.020
0.009	0.022	0.002	0.014	-0.005	0.000	-0.108	0.003
0.012	0.016	0.019	0.016	-0.001	-0.015	0.008	0.006
0.016	-0.081	-0.016	-0.012	-0.002	-0.027	0.000	-0.019
0.011	0.007	0.017	0.010	0.004	-0.002	0.009	-0.009
-0.006	-0.026	0.026	-0.005	-0.002	-0.008	0.024	-0.012
0.007	0.014	0.019	0.011	0.003	0.010	-0.005	-0.014
0.006	-0.001	0.012	0.001	-0.003	-0.026	0.004	-0.038
-0.024	NA	-0.011	-0.006	0.012	0.024	NA	-0.007
-0.005	0.007	0.005	0.015	-0.004	0.013	-0.012	0.008
0.012	-0.001	-0.004	0.001	0.006	0.026	0.017	0.028
0.009	0.001	0.015	0.007	-0.007	0.006	0.001	-0.019
-0.019	-0.011	-0.025	-0.015	-0.004	0.005	-0.007	0.008
-0.014	-0.013	-0.010	-0.012	-0.001	-0.039	0.003	0.001
-0.006	0.000	-0.013	-0.006	0.001	0.037	0.023	-0.001
0.009	-0.008	0.001	-0.004	0.001	0.005	-0.005	-0.029
0.010	0.004	0.014	0.009	-0.003	-0.022	0.000	-0.008
0.015	0.006	0.020	0.012	0.004	0.008	0.013	0.013
0.004	-0.017	0.004	-0.006	-0.008	0.006	0.031	-0.017
0.005	0.025	0.003	0.007	-0.005	-0.002	0.007	0.020
-0.027	-0.002	0.009	0.002	-0.008	-0.010	-0.005	-0.005
0.012	0.008	0.005	0.008	-0.003	0.024	-0.010	-0.002
-0.003	-0.001	0.004	0.001	0.006	-0.036	0.010	-0.017
0.043	0.008	0.021	0.016	-0.001	-0.036	0.009	0.008
0.004	0.006	-0.003	0.000	0.007	-0.003	0.011	0.028
0.053	0.062	0.075	0.069	-0.014	-0.019	-0.014	0.023
-0.016	NA	0.097	-0.017	0.013	-0.021	NA	-0.111
-0.014	-0.014	-0.032	-0.018	0.010	0.027	0.015	0.010
0.041	0.032	0.020	0.026	-0.011	-0.028	-0.030	0.007
-0.002	0.003	0.012	0.010	0.001	-0.020	0.003	-0.004
-0.014	-0.018	-0.010	-0.017	0.000	0.006	0.005	-0.018
0.032	0.066	0.060	0.060	0.005	0.017	0.006	-0.019
-0.010	-0.004	-0.004	-0.004	-0.002	0.022	0.008	0.005
-0.006	-0.009	-0.018	-0.011	0.006	-0.019	0.011	0.018
0.004	-0.004	-0.002	0.001	0.004	0.010	0.006	0.002
-0.003	0.002	0.011	0.004	-0.005	0.005	0.001	-0.008
0.007	0.030	0.038	0.034	0.001	0.000	0.004	0.011
-0.010	-0.006	-0.006	-0.007	-0.001	-0.001	0.011	0.015
0.010	0.002	0.007	0.009	-0.002	0.001	0.020	0.038
0.003	-0.008	-0.012	-0.010	0.002	-0.010	0.005	0.001

0.025	-0.012	0.006	-0.003	-0.003	-0.024	-0.005	-0.023
0.009	0.003	0.008	0.002	0.006	0.030	-0.009	-0.016
0.019	0.012	0.014	0.014	0.002	-0.009	-0.005	0.012
-0.014	-0.018	-0.018	-0.015	-0.002	0.005	0.006	0.016
0.004	-0.011	-0.008	-0.009	-0.001	-0.031	-0.005	0.013
0.004	0.012	0.021	0.014	-0.005	0.003	-0.012	-0.015
-0.006	0.002	0.004	-0.002	0.001	-0.004	-0.003	0.009
-0.008	-0.009	-0.005	-0.010	-0.003	0.011	0.004	0.027
-0.007	-0.001	-0.003	-0.003	-0.007	-0.001	0.004	0.022
-0.014	0.005	-0.008	0.001	-0.002	-0.024	-0.005	0.018
0.004	0.004	-0.007	-0.003	-0.004	-0.013	0.000	0.023
-0.031	-0.020	-0.032	-0.025	0.003	0.009	0.004	-0.013
0.005	-0.001	0.010	0.003	-0.005	0.001	0.012	0.001
NA	0.138	0.110	0.131	-0.011	NA	0.021	-0.016
-0.020	0.001	0.030	0.003	-0.001	-0.034	0.004	-0.041
-0.010	0.015	-0.016	-0.010	0.007	0.008	-0.024	0.010
-0.019	-0.012	-0.008	-0.009	0.004	0.001	0.011	0.028
-0.007	-0.006	-0.010	-0.009	-0.010	0.010	-0.004	0.005
0.000	-0.003	0.003	-0.003	0.002	0.003	0.005	-0.002
0.017	0.016	-0.014	0.005	-0.005	-0.028	-0.053	0.002
0.002	-0.004	0.007	-0.002	0.003	-0.001	0.002	-0.007
-0.010	0.006	0.009	0.007	-0.017	0.022	-0.001	-0.036
0.000	-0.005	0.013	-0.003	-0.007	-0.022	0.006	0.001
0.011	0.010	-0.007	-0.003	0.007	0.000	-0.021	0.008
0.011	-0.006	0.003	0.000	-0.005	-0.013	-0.008	0.007
-0.004	-0.010	-0.013	-0.008	0.007	0.000	0.009	0.029
NA	NA	0.047	0.065	-0.052	NA	NA	-0.036
NA	0.017	-0.087	-0.090	0.046	NA	-0.068	0.061
NA	-0.001	0.075	0.068	-0.039	NA	-0.013	-0.059
0.016	0.020	0.016	0.018	-0.001	-0.003	-0.006	0.011
-0.003	-0.002	0.003	-0.005	-0.004	0.000	-0.013	-0.001
0.000	-0.008	0.016	0.007	-0.006	-0.002	0.056	0.018
0.006	-0.001	0.026	0.011	-0.001	-0.005	0.002	-0.028
-0.017	NA	-0.017	-0.017	NA	0.004	NA	0.040
-0.013	-0.016	-0.011	-0.011	-0.003	0.008	0.020	-0.006
0.018	0.007	0.006	0.010	0.000	-0.009	-0.001	0.025
0.017	0.014	0.015	0.016	-0.010	-0.006	-0.002	0.005
0.000	0.006	-0.002	0.007	-0.010	-0.002	-0.013	0.043
NA	-0.158	0.135	0.063	0.022	NA	0.015	0.028
0.005	0.009	-0.001	0.009	-0.006	-0.010	-0.008	0.005
NA	-0.009	-0.055	-0.027	-0.003	NA	0.043	-0.004
NA	NA	0.022	0.024	-0.020	NA	NA	0.035
0.004	0.011	0.008	0.009	0.003	-0.017	-0.003	0.020
-0.001	-0.001	-0.002	0.001	-0.003	0.010	0.006	-0.048
0.008	0.007	0.025	0.010	-0.009	0.010	0.005	-0.033
0.007	-0.001	0.006	0.006	0.000	0.001	0.002	-0.004
NA	-0.006	-0.131	-0.096	-0.001	NA	-0.046	0.116

-0.017	0.009	0.004	0.007	0.001	-0.016	-0.036	-0.019
-0.012	-0.020	-0.020	-0.030	0.001	0.016	-0.001	0.014
0.002	0.010	0.007	0.008	0.000	0.012	-0.008	-0.009
0.002	0.004	0.014	0.006	0.003	0.000	-0.003	0.008
0.016	0.010	0.007	0.010	0.004	-0.001	0.017	-0.022
-0.006	0.003	-0.003	0.002	0.004	0.040	0.004	0.022
0.014	-0.001	0.008	0.003	0.005	0.023	0.004	-0.015
-0.003	0.005	0.010	0.003	0.001	-0.004	0.010	0.010
-0.020	-0.006	-0.006	-0.004	-0.003	0.013	-0.006	0.007
-0.001	0.000	-0.005	0.001	0.002	0.024	0.004	0.001
NA	-0.019	0.026	-0.002	0.000	NA	0.017	0.031
-0.028	-0.023	-0.023	-0.022	-0.012	-0.011	0.000	0.011
0.003	0.000	-0.005	0.002	-0.004	-0.021	0.003	-0.021
-0.006	-0.006	-0.005	-0.007	0.002	-0.004	0.004	-0.001
-0.010	-0.009	-0.013	-0.011	0.002	-0.011	0.003	-0.004

			TG.RegDrink				
			PJoint				
META	EUR	AFR	ASN	HIS	META	EUR	AFR
-0.005	9.67E-01	9.11E-01	4.12E-01	3.75E-01	7.93E-01	7.13E-01	7.51E-01
0.000	2.88E-01	1.41E-01	2.38E-01	6.08E-02	1.08E-01	5.36E-01	1.02E-01
-0.003	8.30E-01	3.23E-01	7.05E-01	3.02E-01	5.73E-01	5.86E-01	2.24E-01
0.003	2.03E-11	5.22E-01	4.34E-01	1.76E-02	3.45E-09	2.61E-02	5.58E-01
0.015	5.79E-01	4.83E-01	9.71E-01	3.75E-01	4.84E-01	4.69E-01	6.37E-01
-0.001	9.32E-01	7.39E-01	4.11E-01	5.85E-01	7.75E-01	9.52E-01	3.94E-01
-0.002	4.00E-07	3.43E-02	2.42E-02	2.67E-04	9.34E-11	6.51E-01	9.04E-01
0.000	3.45E-08	5.39E-01	3.88E-04	1.37E-01	2.64E-11	9.57E-01	5.45E-01
-0.019	NA	7.93E-01	9.22E-02	8.54E-01	4.74E-01	NA	9.10E-01
0.004	9.94E-02	4.75E-04	2.55E-01	4.40E-01	3.33E-01	7.65E-02	4.79E-04
0.000	5.12E-02	5.07E-01	1.04E-01	6.13E-02	4.85E-02	7.28E-01	4.98E-01
0.000	7.81E-02	1.00E+00	4.43E-01	8.47E-01	7.47E-01	2.55E-01	9.52E-01
-0.029	9.60E-10	NA	NA	NA	3.55E-09	6.24E-01	NA
-0.002	4.14E-01	7.36E-01	1.68E-01	3.11E-01	2.47E-01	8.51E-01	7.13E-01
-0.009	2.00E-09	5.67E-01	5.63E-01	3.00E-01	5.96E-08	5.97E-01	5.80E-01
0.005	5.82E-03	NA	5.36E-01	4.70E-01	4.51E-03	9.21E-01	NA
-0.004	1.74E-08	5.86E-01	1.03E-02	1.49E-03	1.20E-10	4.88E-01	4.55E-01
-0.001	5.17E-07	8.49E-02	1.51E-01	6.59E-01	5.43E-08	7.32E-01	8.69E-01
0.008	9.32E-02	9.59E-01	6.49E-02	8.10E-02	3.69E-03	6.38E-02	6.92E-01
0.003	1.45E-06	NA	3.12E-01	NA	1.65E-06	7.54E-01	NA
0.002	2.68E-03	7.62E-01	2.67E-04	2.83E-01	9.04E-06	8.39E-01	4.66E-01
-0.016	8.15E-03	NA	NA	NA	1.11E-02	1.08E-01	NA
0.003	2.83E-72	8.82E-09	7.36E-39	2.05E-12	3.41E-123	6.21E-01	5.96E-02
0.002	1.86E-02	8.91E-02	1.00E-06	9.65E-01	1.08E-06	1.59E-01	4.44E-02
0.003	2.89E-04	2.20E-01	4.15E-01	1.31E-02	7.67E-04	3.24E-01	8.46E-01
-0.003	2.66E-02	5.26E-01	1.64E-01	4.36E-01	1.30E-02	1.18E-01	7.26E-01
0.006	5.88E-02	9.40E-01	1.19E-02	2.25E-01	6.08E-04	1.30E-01	3.58E-01
-0.001	3.98E-03	3.34E-01	3.42E-07	1.71E-01	7.40E-09	6.08E-01	7.10E-01
0.002	1.25E-24	5.75E-02	1.71E-05	9.78E-04	8.94E-31	9.42E-01	7.71E-02
0.004	1.60E-03	3.72E-01	4.88E-01	1.98E-02	3.55E-03	5.70E-02	7.60E-02
-0.008	1.72E-04	1.05E-01	2.12E-01	4.60E-01	6.49E-06	3.78E-01	8.43E-02
-0.006	1.10E-237	5.36E-09	6.58E-75	8.88E-29	0.00E+00	2.06E-03	7.01E-01
0.001	3.02E-13	7.99E-01	4.79E-01	9.65E-01	2.91E-06	4.86E-01	5.77E-01
-0.001	5.93E-02	1.27E-01	7.56E-01	9.03E-02	1.40E-02	8.08E-01	3.69E-01
0.001	4.61E-01	2.50E-01	4.63E-01	1.64E-01	1.09E-01	9.99E-01	7.38E-01
-0.005	1.98E-01	3.84E-01	4.13E-01	7.57E-01	1.55E-01	5.77E-01	5.35E-01
-0.001	9.43E-01	8.98E-01	5.37E-03	7.08E-01	7.63E-01	4.37E-01	4.30E-01
-0.001	3.84E-16	1.26E-03	4.03E-01	1.37E-02	4.02E-18	5.88E-01	7.03E-01

0.000	4.78E-01	4.57E-03	6.57E-01	4.99E-01	7.50E-01	5.81E-01	6.52E-02
0.008	7.26E-02	5.97E-01	1.75E-02	9.97E-01	3.63E-02	1.24E-01	8.66E-01
-0.002	1.69E-15	1.97E-01	2.66E-07	1.17E-01	8.03E-22	6.96E-01	2.84E-01
-0.002	4.61E-03	5.29E-01	5.96E-01	4.36E-02	1.98E-03	8.37E-01	8.38E-01
-0.004	1.30E-01	1.58E-01	6.46E-02	9.64E-01	3.48E-01	8.03E-01	6.79E-01
0.007	9.52E-13	7.43E-01	3.11E-03	3.95E-01	6.47E-13	7.64E-01	2.48E-01
0.003	1.30E-02	3.20E-01	1.75E-01	1.34E-02	9.82E-04	1.22E-01	2.70E-01
-0.002	2.14E-17	3.45E-02	6.34E-15	2.82E-01	7.76E-29	3.70E-01	7.59E-03
-0.003	1.11E-06	3.02E-01	2.40E-01	9.22E-01	2.71E-06	5.64E-01	9.00E-01
0.002	2.16E-17	1.48E-01	1.43E-15	1.52E-03	1.27E-33	9.92E-01	4.40E-01
-0.003	3.32E-03	8.84E-01	4.68E-01	2.35E-01	1.33E-03	6.09E-01	7.88E-01
0.005	4.48E-10	6.62E-02	5.09E-06	5.53E-02	1.47E-16	4.34E-01	7.07E-01
-0.001	4.10E-01	6.24E-01	4.17E-01	4.48E-01	3.26E-01	6.33E-01	8.32E-01
0.002	5.93E-05	3.15E-01	1.71E-01	2.36E-01	2.91E-06	3.28E-01	9.04E-01
-0.005	4.55E-01	1.11E-01	8.24E-01	7.94E-03	2.13E-01	7.06E-01	1.34E-02
0.013	1.80E-01	5.92E-01	NA	8.28E-01	1.64E-01	4.20E-02	5.86E-01
-0.002	1.05E-18	7.41E-01	2.15E-01	6.37E-01	7.89E-14	1.59E-01	4.48E-01
0.007	1.52E-01	4.14E-01	8.06E-01	5.44E-01	8.14E-02	5.54E-01	4.70E-01
-0.006	3.31E-02	6.64E-01	8.94E-01	2.52E-01	2.32E-02	1.45E-01	6.18E-01
-0.005	5.54E-21	1.37E-02	1.26E-08	1.53E-04	3.27E-32	3.03E-01	9.90E-01
0.000	2.56E-08	3.11E-02	2.43E-04	3.79E-01	1.46E-12	4.35E-01	8.79E-02
0.002	1.52E-02	8.49E-02	4.33E-01	1.89E-01	1.78E-02	9.40E-01	1.46E-02
-0.002	4.71E-03	1.47E-01	6.35E-02	3.63E-02	3.38E-03	6.75E-01	6.66E-01
-0.001	3.46E-10	1.06E-01	1.77E-01	9.00E-02	1.39E-09	1.33E-01	8.17E-02
0.008	2.64E-18	3.20E-03	1.89E-05	1.57E-04	2.23E-26	3.14E-01	5.16E-01
-0.008	4.74E-07	7.12E-01	2.37E-01	6.27E-01	1.12E-05	1.62E-01	7.25E-01
-0.002	1.49E-01	7.69E-01	5.47E-01	3.52E-01	8.90E-02	5.65E-01	8.89E-01
-0.005	3.02E-02	1.56E-02	2.79E-01	5.70E-01	3.80E-01	1.67E-01	7.62E-01
-0.004	3.07E-03	2.39E-03	7.73E-03	6.99E-01	6.74E-06	6.17E-01	7.93E-02
0.008	4.79E-03	1.32E-01	7.66E-02	7.04E-01	2.68E-03	1.48E-01	6.78E-02
-0.001	2.03E-08	1.50E-02	2.76E-01	1.45E-02	4.35E-11	9.16E-01	5.51E-01
0.007	5.56E-02	7.15E-01	1.95E-01	7.34E-02	9.06E-03	1.04E-01	9.82E-01
-0.010	4.84E-136	5.22E-06	2.04E-57	2.27E-13	3.50E-200	3.27E-02	4.80E-01
-0.017	2.04E-01	4.36E-03	NA	5.18E-01	2.29E-03	7.63E-01	2.25E-01
0.011	2.04E-17	7.93E-02	1.34E-05	1.05E-06	6.25E-25	1.10E-02	1.63E-01
-0.014	9.91E-07	1.62E-06	2.41E-03	8.08E-03	5.18E-15	7.03E-02	1.75E-01
0.003	1.21E-12	2.32E-01	6.71E-01	1.83E-01	9.91E-11	7.20E-01	1.95E-01
0.000	2.77E-16	2.08E-02	2.22E-11	2.19E-02	1.88E-28	9.07E-01	7.07E-01
0.007	2.15E-198	9.35E-11	9.14E-136	4.62E-16	0.00E+00	3.91E-01	3.22E-01
0.002	7.64E-02	2.34E-01	3.10E-01	9.24E-01	7.22E-02	6.35E-01	9.15E-02
0.007	5.25E-06	1.97E-01	1.54E-02	7.28E-02	2.97E-08	1.11E-01	2.61E-01
0.006	4.73E-03	3.97E-01	3.66E-01	9.72E-01	1.52E-02	1.47E-01	6.14E-01
-0.002	1.12E-01	8.86E-01	6.97E-01	2.83E-01	1.19E-01	1.57E-01	7.74E-01
0.006	3.30E-127	3.29E-01	2.10E-46	1.66E-12	4.01E-169	9.75E-01	7.90E-01
0.003	9.75E-04	5.15E-01	7.56E-02	5.11E-01	1.83E-03	8.09E-01	9.59E-01
0.002	5.44E-04	5.82E-01	1.53E-01	4.27E-02	4.32E-05	6.91E-01	9.53E-01
0.001	4.92E-10	7.85E-01	1.82E-02	1.57E-01	4.16E-10	5.29E-01	3.58E-01

-0.001	4.85E-01	8.63E-03	2.38E-07	3.53E-01	1.36E-02	1.51E-02	2.44E-01
0.002	2.23E-01	7.21E-03	6.24E-01	4.10E-01	1.55E-01	1.76E-01	4.90E-02
0.000	1.87E-16	2.62E-03	1.02E-06	1.43E-02	1.96E-24	6.92E-01	5.14E-01
0.003	3.57E-12	5.10E-02	1.35E-12	2.51E-02	2.93E-25	2.66E-01	8.29E-01
-0.004	1.78E-07	7.47E-02	7.39E-06	4.67E-01	8.87E-12	6.45E-01	1.96E-02
-0.007	1.85E-10	6.89E-01	4.06E-05	5.91E-03	4.22E-15	5.13E-01	7.97E-01
-0.002	8.48E-03	3.41E-01	7.54E-01	4.18E-01	1.78E-01	7.60E-01	8.72E-01
0.001	6.15E-07	2.85E-01	1.26E-03	1.18E-01	1.10E-08	6.16E-01	5.38E-01
-0.001	8.56E-02	4.46E-01	8.58E-01	4.72E-01	2.58E-01	1.97E-01	8.69E-01
-0.004	4.31E-01	2.47E-01	4.49E-01	6.56E-01	6.29E-01	3.30E-01	5.25E-01
-0.004	5.65E-02	9.08E-01	8.91E-01	5.54E-01	1.33E-01	3.42E-01	7.78E-01
0.002	5.69E-44	4.88E-07	2.35E-16	1.48E-08	4.65E-68	4.98E-01	3.23E-01
0.004	9.40E-02	6.16E-01	4.23E-02	4.29E-01	2.45E-02	6.05E-01	8.91E-01
-0.009	2.51E-132	NA	1.25E-11	4.26E-06	5.52E-142	3.11E-01	NA
0.001	3.27E-01	5.49E-01	5.02E-01	1.15E-01	1.90E-01	8.12E-01	6.34E-01
0.002	1.70E-02	3.17E-01	3.01E-01	1.88E-01	1.55E-02	5.20E-01	7.27E-01
0.007	1.63E-02	2.86E-01	2.64E-02	1.89E-01	3.53E-04	8.11E-01	7.50E-01
-0.008	4.91E-12	3.55E-01	1.36E-01	3.18E-01	4.64E-12	1.54E-02	4.14E-01
0.002	2.62E-01	9.68E-01	4.61E-01	9.01E-01	2.79E-01	3.13E-01	6.51E-01
-0.005	5.95E-02	2.05E-01	1.10E-01	1.40E-01	1.13E-01	2.57E-01	2.20E-01
0.002	6.99E-01	9.78E-01	3.09E-01	6.29E-01	4.73E-01	4.99E-01	9.82E-01
-0.007	9.02E-03	5.07E-01	6.29E-02	1.57E-01	7.77E-03	9.30E-03	2.84E-01
-0.001	3.86E-02	8.47E-01	2.52E-01	3.98E-01	1.05E-01	2.40E-01	5.96E-01
0.001	2.08E-02	1.92E-01	2.41E-01	5.72E-01	3.39E-01	2.06E-01	8.79E-01
-0.006	1.55E-01	2.93E-01	1.11E-01	6.36E-01	9.22E-02	2.14E-01	3.17E-01
0.009	9.50E-02	8.32E-01	1.25E-02	5.07E-02	3.41E-04	5.48E-02	6.61E-01
-0.048	5.31E-12	NA	NA	5.51E-02	2.10E-12	5.60E-04	NA
0.045	1.14E-31	NA	8.63E-01	1.12E-04	3.09E-33	1.36E-03	NA
-0.039	2.23E-11	NA	9.84E-01	1.93E-02	5.48E-12	3.29E-02	NA
-0.003	6.44E-15	1.65E-02	8.11E-17	5.24E-03	8.39E-34	9.83E-01	6.23E-01
-0.005	5.72E-05	7.86E-01	6.38E-01	9.41E-01	1.80E-04	4.12E-01	7.86E-01
-0.002	8.57E-03	9.88E-01	8.33E-02	2.13E-03	4.96E-03	2.00E-01	7.02E-01
-0.001	1.62E-09	5.43E-01	9.74E-01	3.37E-04	4.91E-10	9.79E-01	8.30E-01
0.011	NA	1.93E-01	NA	7.61E-01	2.06E-01	NA	9.36E-01
0.006	1.26E-01	1.10E-01	3.29E-05	2.29E-01	1.16E-05	9.82E-01	5.24E-01
0.002	9.51E-11	1.71E-01	1.69E-02	7.48E-02	1.76E-11	7.23E-01	7.70E-01
-0.006	1.27E-11	7.88E-03	4.34E-08	5.34E-02	4.77E-21	1.70E-02	7.08E-01
-0.007	2.12E-04	9.81E-01	1.29E-02	7.88E-04	4.08E-04	1.06E-02	6.27E-01
0.021	8.42E-20	NA	6.11E-02	3.90E-05	5.07E-21	1.87E-01	NA
-0.005	2.39E-06	5.79E-01	2.50E-03	9.06E-01	1.13E-07	2.70E-01	3.33E-01
0.001	5.86E-03	NA	9.36E-01	1.58E-02	5.13E-04	8.71E-01	NA
-0.018	1.36E-02	NA	NA	4.14E-01	1.26E-02	1.18E-01	NA
0.001	6.66E-05	3.73E-01	5.83E-06	2.02E-02	3.89E-10	4.22E-01	2.67E-01
-0.001	7.71E-01	9.52E-01	6.08E-01	3.05E-02	9.65E-01	4.41E-01	8.36E-01
-0.004	5.45E-05	1.25E-01	4.53E-03	1.27E-02	6.76E-08	2.67E-01	3.61E-01
0.003	1.30E-10	3.30E-01	9.09E-01	6.64E-01	1.08E-06	8.57E-01	8.23E-01
0.006	1.74E-19	NA	8.98E-01	9.49E-04	4.23E-21	9.80E-01	NA

-0.001	7.20E-03	2.62E-01	4.33E-01	6.61E-01	3.90E-02	8.12E-01	6.87E-01
-0.006	8.04E-44	2.52E-01	2.44E-05	1.68E-01	2.15E-39	9.11E-01	5.45E-01
-0.002	1.53E-04	4.52E-01	2.54E-04	5.28E-01	1.20E-07	4.91E-01	4.15E-01
0.001	1.91E-03	9.59E-01	5.10E-01	3.08E-01	9.96E-03	9.77E-01	9.10E-01
0.003	1.62E-09	9.20E-02	7.24E-02	2.41E-01	4.19E-10	1.36E-01	9.25E-01
0.006	4.02E-02	7.15E-02	1.89E-01	2.33E-01	3.07E-03	3.86E-01	1.73E-02
0.004	1.49E-02	6.20E-02	8.50E-01	4.72E-01	1.53E-02	1.98E-01	3.82E-01
0.004	9.60E-01	8.40E-01	1.01E-03	1.56E-01	1.70E-02	6.51E-01	7.54E-01
-0.001	8.12E-01	1.78E-02	5.41E-03	6.78E-01	3.82E-02	4.85E-01	3.11E-01
0.004	2.13E-01	1.78E-01	6.88E-01	7.30E-01	1.51E-01	2.71E-01	4.40E-02
0.004	9.39E-01	NA	2.73E-01	3.47E-02	8.98E-01	9.07E-01	NA
-0.007	4.70E-27	9.03E-08	5.19E-11	3.48E-02	1.21E-43	4.16E-02	7.09E-01
-0.003	3.28E-01	2.26E-01	7.60E-01	5.17E-02	4.94E-01	2.66E-01	1.53E-01
0.002	1.67E-02	5.58E-01	3.88E-02	7.09E-01	4.18E-04	4.67E-01	7.13E-01
0.001	4.73E-08	4.79E-02	5.61E-04	4.24E-02	4.16E-13	8.23E-01	7.48E-01

PInt					PMain		
ASN	HIS	META	EUR	AFR	ASN	HIS	META
3.01E-01	9.02E-01	5.51E-01	9.13E-01	8.72E-01	2.01E-01	1.71E-01	5.39E-01
2.88E-01	1.93E-02	8.60E-01	6.26E-01	1.89E-01	4.18E-01	1.47E-01	8.90E-02
9.35E-01	9.50E-01	4.41E-01	5.83E-01	9.78E-01	6.19E-01	1.69E-01	3.24E-01
6.52E-01	3.81E-01	1.97E-01	4.56E-10	3.01E-01	3.68E-01	6.60E-02	1.46E-07
9.11E-01	1.62E-01	3.81E-01	6.57E-01	2.36E-01	9.00E-01	4.26E-01	2.34E-01
4.81E-01	3.59E-01	9.70E-01	7.48E-01	5.50E-01	1.74E-01	5.07E-01	5.44E-01
2.39E-01	4.26E-02	8.04E-01	9.39E-06	1.26E-02	1.55E-01	4.91E-05	7.20E-09
6.70E-01	2.04E-01	9.43E-01	5.95E-06	2.66E-01	3.51E-04	4.12E-01	1.88E-08
7.87E-02	6.04E-01	3.41E-01	NA	4.88E-01	8.63E-01	9.56E-01	6.65E-01
9.52E-01	2.38E-01	2.32E-01	8.97E-01	3.37E-03	2.63E-01	9.92E-01	9.07E-01
1.21E-01	2.34E-02	5.98E-01	6.44E-02	2.49E-01	9.67E-01	7.04E-01	9.14E-02
7.21E-01	8.19E-01	5.22E-01	3.96E-02	9.42E-01	2.32E-01	5.63E-01	5.65E-01
NA	NA	6.28E-01	2.24E-07	NA	NA	NA	6.73E-07
7.50E-02	3.18E-01	3.52E-01	3.07E-01	4.60E-01	5.77E-01	1.26E-01	3.63E-01
3.04E-01	1.16E-01	4.88E-01	2.38E-07	5.12E-01	4.58E-01	4.76E-01	2.78E-06
4.55E-01	3.96E-01	8.96E-01	1.38E-02	NA	2.70E-01	2.31E-01	8.33E-03
8.04E-02	4.23E-01	1.37E-01	1.39E-05	9.31E-01	2.56E-01	5.77E-04	8.98E-06
3.54E-01	4.57E-01	7.47E-01	3.22E-05	5.53E-02	2.11E-02	9.83E-01	3.33E-06
3.08E-02	1.01E-01	2.82E-03	3.16E-02	9.28E-01	1.42E-01	2.87E-02	3.59E-03
2.19E-01	NA	9.02E-01	1.14E-03	NA	1.31E-01	NA	4.01E-04
3.01E-01	1.17E-01	7.37E-01	3.94E-02	7.76E-01	9.31E-03	2.55E-01	9.02E-04
NA	NA	1.09E-01	1.57E-01	NA	NA	NA	1.88E-01
1.46E-03	6.53E-01	5.50E-01	4.13E-38	1.28E-09	1.46E-19	3.45E-11	3.33E-69
3.64E-01	9.71E-01	3.85E-01	6.58E-03	1.16E-01	2.98E-04	8.62E-01	2.77E-06
9.84E-01	4.61E-01	5.15E-01	4.50E-02	7.65E-02	3.49E-01	4.75E-03	1.29E-02
5.80E-01	2.40E-01	9.47E-02	1.22E-02	2.68E-01	5.94E-02	2.64E-01	4.22E-03
1.91E-01	1.92E-01	4.71E-02	2.02E-02	9.43E-01	4.19E-03	9.27E-02	1.53E-04
1.79E-01	5.59E-01	7.20E-01	9.03E-03	1.63E-01	9.77E-05	2.47E-01	2.14E-06
3.61E-01	4.67E-01	9.68E-01	8.70E-13	2.54E-01	2.09E-05	4.86E-03	1.05E-17
1.64E-01	4.62E-01	2.72E-01	4.49E-01	8.39E-01	2.72E-01	5.09E-02	9.85E-02
5.83E-01	5.42E-01	1.05E-01	1.90E-04	5.45E-02	5.09E-02	2.01E-01	2.18E-06
3.45E-01	3.76E-01	6.51E-03	2.68E-146	5.99E-09	8.74E-58	1.06E-21	1.07E-221
1.91E-01	9.56E-01	1.47E-01	2.63E-09	6.86E-01	4.35E-01	8.71E-01	2.93E-05
3.28E-01	1.74E-01	7.84E-01	2.16E-01	1.43E-01	9.91E-01	3.08E-02	3.57E-02
9.08E-01	6.51E-02	7.51E-01	4.92E-01	1.79E-01	2.53E-01	2.16E-01	6.26E-02
5.17E-01	7.95E-01	5.77E-01	5.11E-01	5.65E-01	7.13E-01	4.64E-01	4.43E-01
3.70E-03	4.18E-01	3.22E-01	7.83E-01	6.84E-01	4.11E-01	5.26E-01	7.30E-01
9.86E-01	7.71E-02	9.46E-01	6.90E-10	1.51E-03	2.34E-01	1.88E-01	1.73E-11

4.18E-01	7.58E-01	7.11E-01	2.31E-01	1.26E-01	8.16E-01	2.54E-01	3.93E-01
2.44E-01	8.80E-01	5.89E-02	8.26E-01	2.93E-01	4.71E-03	9.77E-01	3.99E-02
5.48E-01	8.58E-01	7.69E-01	6.96E-08	3.70E-01	1.40E-06	5.62E-02	1.29E-12
6.92E-01	2.43E-02	9.24E-01	3.89E-02	2.49E-01	2.99E-01	7.49E-01	2.24E-02
4.96E-02	9.13E-01	5.03E-01	1.09E-01	1.57E-01	1.05E-01	9.19E-01	8.01E-01
7.17E-02	4.86E-01	2.12E-01	1.38E-07	9.01E-01	1.90E-01	5.67E-01	2.04E-05
6.73E-01	2.50E-02	2.52E-01	5.05E-01	6.85E-01	1.36E-01	5.42E-03	2.66E-02
2.71E-01	1.22E-01	6.53E-01	1.27E-12	6.78E-01	7.54E-12	6.80E-01	1.11E-18
1.51E-01	7.92E-01	6.04E-01	1.38E-05	1.64E-01	4.25E-01	8.31E-01	2.69E-05
7.11E-02	6.33E-01	3.18E-01	1.17E-10	5.16E-02	4.63E-09	3.34E-03	2.47E-20
1.00E+00	5.14E-01	5.04E-01	2.33E-02	6.36E-01	2.88E-01	2.89E-01	1.41E-02
9.96E-02	4.84E-01	1.83E-01	7.84E-05	3.32E-02	1.34E-03	2.01E-02	7.63E-09
6.71E-01	8.50E-01	6.51E-01	4.38E-01	5.32E-01	1.84E-01	2.32E-01	3.14E-01
8.45E-01	6.04E-01	4.62E-01	7.90E-03	3.21E-01	8.49E-02	8.45E-02	4.34E-04
6.96E-01	1.56E-03	1.52E-01	9.23E-01	2.92E-01	8.85E-01	7.05E-02	4.89E-01
NA	8.51E-01	4.33E-02	3.41E-01	2.83E-01	NA	6.57E-01	2.33E-01
1.90E-01	6.85E-01	1.04E-01	5.78E-14	4.38E-01	1.11E-01	6.20E-01	1.38E-10
3.59E-01	2.33E-01	2.80E-01	8.01E-01	4.70E-01	9.71E-01	7.96E-01	7.28E-01
7.49E-01	2.79E-01	1.93E-01	9.96E-03	4.51E-01	7.42E-01	1.06E-01	6.17E-03
8.64E-02	5.11E-01	1.05E-01	8.90E-10	4.97E-03	1.31E-04	8.84E-05	3.10E-16
5.65E-01	9.29E-01	5.74E-01	9.22E-05	2.11E-01	1.89E-04	2.08E-01	2.78E-08
4.63E-01	8.88E-01	5.42E-01	3.15E-02	4.41E-01	8.90E-01	1.22E-01	1.87E-02
4.75E-01	1.90E-02	6.93E-01	1.26E-02	9.06E-02	1.12E-01	8.41E-01	6.14E-02
7.67E-01	4.99E-01	1.59E-01	1.55E-07	7.88E-02	1.86E-01	2.84E-02	2.30E-07
1.41E-02	2.93E-01	1.24E-02	2.07E-08	4.57E-03	3.78E-02	2.56E-03	1.30E-11
3.13E-01	3.53E-01	2.22E-01	1.95E-02	5.81E-01	2.24E-01	6.97E-01	5.98E-02
9.31E-01	2.62E-01	8.42E-01	6.68E-02	4.83E-01	2.49E-01	7.65E-01	4.57E-02
4.37E-01	6.55E-01	1.00E-01	9.48E-03	1.40E-02	6.85E-01	2.90E-01	2.26E-01
2.07E-02	8.85E-01	1.47E-01	4.37E-03	3.41E-02	3.72E-03	4.33E-01	8.97E-06
2.34E-02	4.48E-01	3.05E-02	3.00E-01	7.46E-01	6.30E-01	6.68E-01	7.98E-01
8.82E-01	7.25E-01	9.70E-01	6.43E-06	4.43E-03	2.38E-01	2.26E-02	3.91E-08
2.56E-01	2.80E-02	2.05E-02	7.07E-01	3.69E-01	4.29E-01	6.38E-01	9.06E-01
7.07E-02	3.59E-01	7.42E-03	2.81E-83	1.25E-06	3.51E-47	1.08E-09	2.94E-135
NA	4.58E-01	3.05E-01	1.59E-01	2.27E-02	NA	2.56E-01	1.50E-02
1.21E-02	5.65E-01	1.90E-04	7.65E-15	3.81E-02	3.28E-06	1.03E-06	5.91E-24
1.18E-02	6.46E-01	1.11E-02	2.26E-06	2.26E-07	6.42E-04	1.56E-02	1.46E-14
4.97E-01	7.20E-01	8.92E-01	4.25E-07	6.79E-01	8.26E-01	7.36E-02	6.84E-06
3.19E-01	1.50E-01	7.72E-01	4.47E-09	7.68E-03	1.14E-10	1.62E-01	1.35E-19
3.43E-01	1.86E-01	2.67E-01	8.56E-97	1.40E-08	2.65E-92	4.16E-15	2.87E-195
2.25E-01	7.02E-01	4.15E-01	1.88E-01	1.25E-01	3.14E-01	6.79E-01	4.13E-02
1.43E-01	2.07E-01	3.13E-02	8.49E-06	4.40E-01	5.65E-03	2.16E-02	2.39E-08
3.33E-01	9.32E-01	7.51E-02	1.48E-01	4.86E-01	2.50E-01	8.01E-01	6.93E-01
7.78E-01	4.22E-01	3.29E-01	3.64E-02	5.93E-01	5.54E-01	1.22E-01	5.70E-02
4.48E-01	4.11E-01	5.66E-01	9.57E-65	1.74E-01	7.10E-32	2.88E-09	6.13E-93
3.78E-02	2.83E-01	1.52E-01	1.24E-02	2.89E-01	3.95E-02	4.18E-01	7.00E-04
1.04E-01	7.63E-02	5.45E-01	2.33E-03	3.71E-01	8.21E-01	5.07E-01	2.80E-03
3.41E-01	9.72E-01	3.91E-01	1.13E-06	6.43E-01	5.51E-03	8.95E-02	1.37E-07

3.90E-01	1.85E-01	5.85E-03	6.47E-01	1.62E-03	3.67E-05	4.34E-01	3.22E-02
4.27E-01	2.59E-01	3.18E-01	8.33E-01	1.58E-01	5.66E-01	2.62E-01	3.32E-01
3.49E-01	3.84E-01	7.98E-01	1.16E-08	8.35E-04	1.35E-06	4.36E-02	5.13E-16
1.90E-01	1.98E-01	7.65E-01	8.48E-07	1.77E-02	1.08E-11	7.14E-03	8.48E-19
2.70E-01	3.56E-01	5.78E-01	2.11E-04	5.29E-01	3.70E-04	2.48E-01	3.94E-06
2.92E-02	2.26E-01	4.05E-02	1.52E-08	5.04E-01	6.45E-05	1.66E-03	6.65E-13
8.91E-01	4.84E-01	9.83E-01	1.89E-02	2.24E-01	9.65E-01	5.29E-01	1.30E-01
3.87E-01	4.38E-02	3.89E-01	6.31E-04	1.03E-01	4.51E-04	4.47E-01	2.10E-07
5.03E-01	2.31E-01	8.16E-01	4.88E-01	2.25E-01	7.92E-01	7.57E-01	2.92E-01
5.65E-01	4.50E-01	3.19E-01	4.92E-01	2.67E-01	2.00E-01	4.44E-01	8.39E-01
6.62E-01	3.06E-01	5.81E-01	2.66E-01	7.58E-01	6.56E-01	5.34E-01	3.95E-01
7.01E-01	3.12E-01	4.87E-01	1.14E-27	5.57E-07	1.20E-13	1.56E-06	4.55E-48
3.50E-02	9.48E-01	1.84E-01	3.88E-02	4.13E-01	8.13E-01	2.57E-01	1.85E-01
6.90E-01	8.56E-01	3.67E-01	3.73E-74	NA	4.30E-09	7.57E-06	1.74E-81
4.39E-01	1.55E-01	8.29E-01	2.67E-01	5.05E-01	6.97E-01	4.33E-02	2.45E-01
8.66E-01	5.75E-01	4.25E-01	1.46E-02	1.25E-01	6.53E-01	7.43E-02	3.68E-03
1.23E-01	5.98E-02	1.57E-01	1.09E-02	1.30E-01	7.83E-03	3.32E-01	1.20E-04
6.02E-01	7.58E-01	6.57E-02	1.44E-03	1.62E-01	1.49E-01	1.37E-01	9.11E-05
4.02E-01	8.74E-01	1.90E-01	1.46E-01	9.33E-01	2.97E-01	6.36E-01	1.25E-01
3.60E-02	9.61E-01	1.29E-01	1.85E-02	8.80E-02	2.35E-01	7.37E-02	3.57E-02
7.67E-01	5.46E-01	5.86E-01	4.63E-01	8.54E-01	1.32E-01	3.14E-01	2.28E-01
7.77E-01	6.37E-02	4.66E-02	3.88E-03	3.17E-01	4.10E-02	3.20E-01	1.80E-03
2.13E-01	9.90E-01	9.16E-01	4.86E-01	9.58E-01	9.53E-02	2.50E-01	1.45E-01
5.79E-01	5.24E-01	2.35E-01	6.34E-03	1.05E-01	7.37E-01	2.92E-01	4.92E-02
8.00E-01	5.54E-01	2.26E-01	9.06E-01	1.11E-01	1.33E-01	6.64E-01	8.94E-01
2.50E-01	3.03E-02	5.80E-03	3.45E-02	5.67E-01	4.09E-03	4.90E-02	7.99E-05
NA	3.53E-01	4.04E-04	3.35E-12	NA	NA	1.72E-02	1.53E-12
5.94E-01	1.01E-01	5.02E-04	2.71E-27	NA	8.20E-01	2.86E-05	7.87E-29
7.74E-01	2.61E-01	1.75E-02	2.06E-10	NA	9.89E-01	5.29E-03	3.63E-11
1.06E-01	4.64E-01	3.41E-01	1.09E-09	6.05E-03	2.13E-17	1.80E-02	3.81E-27
8.52E-01	9.61E-01	3.79E-01	1.41E-02	5.46E-01	7.53E-01	7.60E-01	3.07E-02
5.71E-02	1.88E-01	5.67E-01	2.83E-03	9.91E-01	6.09E-01	2.23E-02	2.64E-03
8.23E-01	2.44E-02	4.90E-01	3.98E-06	2.75E-01	7.02E-01	6.26E-05	7.70E-08
NA	4.73E-01	7.21E-01	NA	8.86E-02	NA	5.97E-01	7.99E-02
4.64E-03	7.95E-01	7.89E-02	2.94E-01	3.96E-02	1.80E-05	2.03E-01	8.78E-06
9.55E-01	1.15E-01	6.49E-01	1.49E-06	6.50E-02	1.84E-02	4.64E-01	4.47E-07
7.13E-01	7.74E-01	4.96E-02	1.22E-10	2.27E-03	9.38E-08	5.16E-02	3.84E-19
7.62E-03	8.85E-04	4.71E-03	4.82E-05	8.58E-01	2.46E-02	7.41E-01	1.17E-04
9.14E-01	6.83E-01	1.68E-01	1.72E-07	NA	4.01E-02	3.25E-04	1.96E-08
6.62E-02	7.16E-01	4.68E-02	6.01E-06	3.37E-01	3.27E-04	8.86E-01	1.03E-07
7.29E-01	9.36E-01	8.87E-01	3.36E-02	NA	9.08E-01	1.37E-02	4.12E-03
NA	5.57E-01	1.63E-01	3.71E-03	NA	NA	5.16E-01	3.73E-03
8.71E-01	1.13E-01	5.78E-01	1.08E-02	4.00E-01	3.27E-05	2.18E-01	1.63E-06
3.33E-01	3.38E-02	7.12E-01	6.21E-01	9.73E-01	7.87E-01	8.48E-01	9.14E-01
3.07E-01	5.30E-02	7.17E-01	2.76E-05	1.60E-01	3.94E-02	4.26E-03	5.04E-07
6.92E-01	6.93E-01	7.40E-01	1.65E-06	2.16E-01	7.97E-01	3.62E-01	7.30E-04
7.22E-01	8.63E-02	6.66E-01	5.07E-11	NA	9.23E-01	1.93E-04	3.72E-13

2.08E-01	3.34E-01	4.26E-01	2.66E-02	2.18E-01	6.82E-01	7.09E-01	5.17E-02
5.94E-01	5.63E-01	9.12E-01	1.13E-23	1.13E-01	1.76E-04	5.99E-02	4.37E-22
2.61E-01	4.36E-01	2.34E-01	3.23E-03	7.07E-01	6.92E-04	2.70E-01	8.56E-06
6.18E-01	7.50E-01	7.74E-01	2.65E-02	8.31E-01	3.01E-01	2.62E-01	3.13E-02
7.13E-01	1.05E-01	3.01E-01	9.03E-05	4.04E-02	2.42E-01	2.96E-01	7.08E-06
3.01E-01	9.17E-02	3.80E-02	3.52E-01	4.59E-01	2.60E-01	6.51E-01	3.10E-01
6.71E-01	3.00E-01	2.70E-01	2.19E-01	1.48E-01	8.84E-01	2.79E-01	1.61E-01
6.56E-02	4.91E-01	3.29E-01	7.29E-01	6.57E-01	1.14E-01	2.09E-01	1.13E-01
2.54E-01	5.95E-01	4.00E-01	6.16E-01	4.41E-03	5.30E-02	4.02E-01	5.64E-02
8.15E-01	9.98E-01	2.43E-01	3.53E-01	8.43E-01	4.18E-01	4.64E-01	4.30E-01
6.66E-01	2.65E-01	5.34E-01	9.44E-01	NA	1.13E-01	9.59E-02	8.34E-01
9.72E-01	4.74E-01	1.39E-01	8.41E-09	1.07E-06	9.85E-09	1.20E-02	3.49E-22
5.66E-01	1.14E-01	2.60E-01	1.30E-01	6.10E-01	9.23E-01	4.56E-01	3.21E-01
8.60E-01	9.87E-01	5.94E-01	2.17E-02	3.77E-01	5.24E-02	4.63E-01	2.04E-03
3.19E-01	8.71E-01	5.08E-01	6.51E-06	7.58E-02	7.74E-05	4.32E-02	7.51E-11

Web Table 7: Stage 1 genetic main effect of the index variants at the 18 novel lo

SNP	Chromosome	Position	Closest Gene(s)	Alleles
rs190528931	11	63911273	*MACROD1*	A/C
rs7904973	10	1.25E+08	*C10orf88*	T/G
rs73729083	7	1.38E+08	*CREB3L2*	T/C
rs80080062	3	1.86E+08	*ETV5*	C/G
rs7140110	13	1.15E+08	*GAS6-AS1*	T/C
rs34311866	4	951947	*TMEM175*	T/C
rs2911971	8	6607634	*AGPAT5*	C/G
rs56076449	5	1.32E+08	*HSPA4 / FSTL4*	T/G
rs41274050	10	52573772	*A1CF*	T/C
rs7035578	9	78745177	*PCSK5*	A/G
rs201445483	2	17890087	*SMC6*	D/I
rs72729610	4	1.54E+08	*TRIM2*	A/G
rs143528679	4	1.25E+08	*SPRY1 / LINC01091*	A/G
rs2111622	2	53984823	*ASB3 / GPR75-ASB3*	A/G
rs13284665	9	1.32E+08	*ZER1*	A/G
rs4898521	12	49755162	*DNAJC22 / SPATS2*	A/T
rs6063050	20	45604240	*EYA2*	T/C
rs2963472	5	1.58E+08	*LOC101927697 / EBF1*	A/G

ɔci.

	1 DF Genetic Main Effect	
Most Significant 2 DF Model	**Beta**	**P-value**
META - HDL-C – CURDRINK	-0.0237	2.96E-08
META - LDL-C - CURDRINK	0.8892	4.18E-08
META - LDL-C - CURDRINK	3.6971	1.32E-08
META - HDL-C - REGDRINK	0.008	4.61E-06
META - TG - CURDRINK	-0.0199	6.96E-10
EUR - TG – CURDRINK	-0.0216	3.64E-08
META - LDL-C - CURDRINK	-1.0836	9.41E-10
META - TG - REGDRINK	0.0149	2.83E-07
EUR - TG – REGDRINK	0.1108	1.80E-07
EUR - LDL-C - CURDRINK	-1.4575	1.15E-07
META - LDL-C - CURDRINK	1.8262	3.98E-08
META - HDL-C - REGDRINK	0.0082	6.15E-06
AFR - LDL-C - CURDRINK	-4.3353	3.34E-07
EUR - HDL-C - CURDRINK	-0.0061	7.44E-05
EUR - LDL-C - CURDRINK	1.8836	9.01E-07
EUR - HDL-C - REGDRINK	0.0214	4.29E-08
META - TG - CURDRINK	0.0143	4.34E-07
EUR - TG – REGDRINK	0.0171	9.92E-08

Web Table 8: Effect allele frequencies and *P* -values of 314 known published lipid variants. If a vari
column E, otherwise, the values presented here come from the Stage 1 + 2 combined analyses.

rsID	Locus	CHR	BP	Stage 1 Only	Effect Alle		
					EUR	AFR	ASN
rs1077514	*ASAP3*	1	23,766,233	TRUE	0.8591	0.5120	0.6479
rs10903129	*TMEM57*	1	25,768,937	FALSE	0.4528	0.2895	0.6775
rs12027135	*LDLRAP1*	1	25,775,733	FALSE	0.4678	0.5149	0.6767
rs12748152	*PIGV-NR0B2*	1	27,138,393	FALSE	0.0802	0.0227	0.0162
rs4660293	*PABPC4*	1	40,028,180	FALSE	0.7595	0.9503	0.8608
rs2479409	*PCSK9*	1	55,504,650	FALSE	0.6608	0.7388	0.4270
rs1998013		1	55,958,030	TRUE	0.0132	NA	NA
rs10493326	*DOCK7*	1	62,953,373	TRUE	0.2494	0.0762	0.1535
rs2131925		1	63,025,942	FALSE	0.6672	0.3444	0.7328
rs4587594		1	63,133,930	FALSE	0.3318	0.4424	0.1913
rs6603981	*EVI5*	1	92,993,807	TRUE	0.7955	0.9247	0.9581
rs7515577		1	93,009,438	TRUE	0.7966	0.9250	0.9542
rs12133576	*DR1*	1	93,816,400	FALSE	0.3600	0.7613	0.3772
rs629301	*SORT1*	1	109,818,306	FALSE	0.7781	0.6441	0.8959
rs646776	*CELSR2*	1	109,818,530	FALSE	0.7776	0.6441	0.8983
rs1010167	*GSTM4*	1	110,198,727	FALSE	0.6064	0.6946	0.5033
rs267733	*ANXA9-CERS2*	1	150,958,836	TRUE	0.8459	0.9368	0.9493
rs12145743	*HDGF-PMVK*	1	156,700,651	TRUE	0.6614	0.9299	0.8611
rs4650994	*ANGPTL1*	1	178,515,312	TRUE	0.5160	0.1975	0.5392
rs1689797	*ZNF648*	1	182,150,978	FALSE	0.3258	0.2108	0.2650
rs1689800		1	182,168,885	FALSE	0.6510	0.6784	0.7358
rs2642438	*MOSC1*	1	220,970,028	FALSE	0.2892	0.0908	0.1873
rs2642442	*MARC1*	1	220,973,563	FALSE	0.6924	0.7809	0.8373
rs903319		1	220,985,811	TRUE	0.7402	0.9466	0.7309
rs4846914	*GALNT2*	1	230,295,691	FALSE	0.5971	0.1414	0.2538
rs6680658		1	230,419,344	TRUE	0.2302	0.1666	0.1226
rs2587534		1	234,849,339	FALSE	0.5277	0.8510	0.7049
rs514230	*IRF2BP2*	1	234,858,597	FALSE	0.4732	0.2528	0.3031
rs1367117	*APOB*	2	21,263,900	FALSE	0.3185	0.1164	0.0990
rs515135		2	21,286,057	FALSE	0.1813	0.4943	0.1187
rs1260326	*GCKR*	2	27,730,940	FALSE	0.3932	0.1475	0.4980
rs3817588		2	27,731,212	FALSE	0.8047	0.9505	0.6991
rs780094		2	27,741,237	FALSE	0.3846	0.1783	0.4965
rs4299376	*ABCG8*	2	44,072,576	FALSE	0.6973	0.8403	0.7465
rs6544713		2	44,073,881	FALSE	0.3016	0.1653	0.2467
rs4148218		2	44,099,582	FALSE	0.1889	0.2737	0.1220
rs350721	*ASB3*	2	52,980,427	TRUE	0.1174	0.1051	0.1072
rs2710642	*EHBP1*	2	63,149,557	FALSE	0.6631	0.8623	0.7513
rs17508045	*DDX18*	2	118,576,719	FALSE	0.9183	0.9816	0.9373
rs17526895	*LOC102723413*	2	118,815,958	FALSE	0.9246	0.9815	0.9441

rs10490626	*INSIG2*	2	118,835,841	FALSE	0.0755	0.0190	0.0567
rs2030746	*LOC84931*	2	121,309,488	TRUE	0.4082	0.5030	0.5019
rs16831243	*MAP3K19*	2	135,762,344	TRUE	0.1367	0.3939	0.3752
rs7570971	*RAB3GAP1*	2	135,837,906	FALSE	0.3591	0.8688	0.7105
rs197273	*TANK*	2	161,894,663	TRUE	0.4773	0.3232	0.5325
rs12328675	*COBLL1*	2	165,540,800	FALSE	0.8767	0.8365	0.8943
rs7607980		2	165,551,201	FALSE	0.8766	0.8421	0.8945
rs355838		2	165,619,163	TRUE	0.3849	0.0897	0.5066
rs2287623	*ABCB11*	2	169,830,155	FALSE	0.5968	0.5654	0.7294
rs11694172	*FAM117B*	2	203,532,304	TRUE	0.7529	0.9368	0.7612
rs1047891	*CPS1*	2	211,540,507	FALSE	0.3212	0.3505	0.1764
rs1250229	*FN1*	2	216,304,384	TRUE	0.2654	0.1876	0.2149
rs2972146	*IRS1*	2	227,100,698	FALSE	0.6392	0.8309	0.8875
rs1515110		2	227,122,216	FALSE	0.6289	0.5750	0.8802
rs11563251	*UGT1A1*	2	234,679,384	TRUE	0.1072	0.3583	0.1190
rs2606736	*ATG7*	3	11,400,249	TRUE	0.6285	0.4243	0.6334
rs9875338		3	12,296,469	TRUE	0.4037	0.3822	0.1169
rs2290159	*RAF1*	3	12,628,920	FALSE	0.2136	0.2922	0.0507
rs7640978	*CMTM6*	3	32,533,010	TRUE	0.0875	0.2787	0.0497
rs2290547	*SETD2*	3	47,061,183	TRUE	0.1709	0.0434	0.1760
rs2240327	*RBM6*	3	50,113,034	FALSE	0.5016	0.6423	0.1722
rs2013208	*RBM5*	3	50,129,399	FALSE	0.4995	0.5812	0.8283
rs13326165	*STAB1*	3	52,532,118	TRUE	0.2041	0.3307	0.0644
rs13315871	*PXK*	3	58,381,287	TRUE	0.0896	0.0534	0.0787
rs6805251	*GSK3B*	3	119,560,606	TRUE	0.3877	0.8734	0.5427
rs17404153	*ACAD11*	3	132,163,200	TRUE	0.1220	0.0307	0.1467
rs17345563	*DNAJC13*	3	132,209,203	TRUE	0.8858	0.9740	0.8799
rs645040		3	135,926,622	TRUE	0.7780	0.7080	0.8272
rs687339	*MSL2L1*	3	135,932,359	FALSE	0.7840	0.7267	0.8175
rs1482852	*LINC02029*	3	156,798,294	FALSE	0.5814	0.4768	0.4259
rs10513688	*SLC2A2*	3	170,727,218	TRUE	0.1008	0.2811	0.1257
rs6831256	*LRPAP1*	4	3,473,139	TRUE	0.5733	0.3979	0.6008
rs10019888	*C4orf52*	4	26,062,990	TRUE	0.8330	0.7855	0.8851
rs11940694	*KLB*	4	39,414,993	TRUE	0.4103	0.4116	0.5767
rs442177	*KLHL8*	4	88,030,261	FALSE	0.5815	0.4869	0.5278
rs10029254		4	88,160,140	TRUE	0.2306	0.0706	0.3494
rs3822072	*FAM13A*	4	89,741,269	TRUE	0.4584	0.5149	0.6381
	ADH5	4	100,001,040	TRUE	NA	NA	NA
rs2602836		4	100,014,805	TRUE	0.4255	0.6588	0.1518
	ADH4	4	100,061,878	TRUE	NA	NA	NA
	ADH6	4	100,132,244	TRUE	NA	NA	NA
	ADH1A	4	100,204,854	TRUE	NA	NA	NA
	ADH1B	4	100,234,346	TRUE	NA	NA	NA
	ADH1C	4	100,265,916	TRUE	NA	NA	NA
	ADH7	4	100,345,156	TRUE	NA	NA	NA
rs13107325	*SLC39A8*	4	103,188,709	FALSE	0.0661	0.0204	0.0210
rs6822892	*PDGFC*	4	157,734,675	TRUE	0.6638	0.2626	0.5863

rs6450176	*ARL15*	5	53,298,025	TRUE	0.2555	0.2928	0.4414
rs9686661	*MAP3K1*	5	55,861,786	FALSE	0.1903	0.2297	0.1083
rs4976033		5	67,714,246	TRUE	0.5817	0.3247	0.5553
rs7703051		5	74,625,487	FALSE	0.3845	0.3393	0.5400
rs12916	*HMGCR*	5	74,656,539	FALSE	0.5924	0.7509	0.4689
rs4530754	*CSNK1G3*	5	122,855,416	TRUE	0.5519	0.7742	0.3484
rs6882076	*TIMD4*	5	156,390,297	FALSE	0.3658	0.6260	0.2198
rs2294261		6	16,109,163	FALSE	0.4925	0.1165	0.1158
rs3757354	*MYLIP*	6	16,127,407	FALSE	0.2203	0.3429	0.4081
rs1800562	*HFE*	6	26,093,141	TRUE	0.0654	0.0145	NA
rs2247056	*LOC105375015*	6	31,265,490	FALSE	0.2540	0.1367	0.1310
rs3177928	*HLA*	6	32,412,435	TRUE	0.1412	0.1104	0.1760
rs2814982	*C6orf106*	6	34,546,560	TRUE	0.1056	0.2749	0.0699
rs205262		6	34,563,164	TRUE	0.7232	0.3636	0.8528
rs2758886	*KCNK17*	6	39,250,837	TRUE	0.2948	0.1693	0.0581
rs4714556	*CCND3-TAF8*	6	41,993,229	TRUE	0.6144	0.6229	0.4142
rs998584	*VEGFA*	6	43,757,896	FALSE	0.4806	0.1994	0.5658
rs2239620	*TRAM2*	6	52,452,585	TRUE	0.3600	0.4188	0.3013
rs2239619		6	52,453,220	TRUE	0.6263	0.5066	0.6905
rs17789218	*LOC105377911*	6	100,600,097	FALSE	0.7756	0.9471	0.8405
rs9488822	*FRK*	6	116,312,893	TRUE	0.6481	0.6262	0.8364
rs868943		6	116,337,503	FALSE	0.4001	0.3966	0.0949
rs719726	*LOC105377989*	6	127,414,801	FALSE	0.5621	0.6886	0.5433
rs1936800	*RSPO3*	6	127,436,064	FALSE	0.5161	0.5308	0.5007
rs9491696		6	127,452,639	FALSE	0.5098	0.6178	0.4908
rs9376090	*HBS1L*	6	135,411,228	TRUE	0.7426	0.9457	0.7886
rs605066	*CITED2*	6	139,829,666	FALSE	0.5776	0.4456	0.3373
rs634869		6	139,831,757	FALSE	0.4221	0.5562	0.6615
rs12525163	*ESR1*	6	152,040,291	TRUE	0.7350	0.7466	0.8487
rs2297374	*SLC22A1*	6	160,575,985	FALSE	0.3817	0.5192	0.3233
rs1564348	*LPA*	6	160,578,860	FALSE	0.8415	0.8909	0.8597
rs1997243	*GPR146*	7	1,083,777	TRUE	0.8469	0.9668	0.8863
rs702485	*DAGLB*	7	6,449,272	TRUE	0.5518	0.2188	0.1563
rs17286602	*ISPD*	7	16,152,174	TRUE	0.4174	0.2162	0.6500
rs10282707	*SNX13*	7	17,911,038	FALSE	0.3971	0.6996	0.5066
rs4142995		7	17,919,258	FALSE	0.3916	0.7027	0.4973
rs12670798	*DH11*	7	21,607,352	TRUE	0.7691	0.6812	0.5449
rs4722551	*MIR148A*	7	25,991,826	FALSE	0.8353	0.9507	0.9671
rs2072183	*NPC1L1*	7	44,579,180	FALSE	0.2421	0.2200	0.3624
rs2073547		7	44,582,331	FALSE	0.7937	0.7149	0.6414
rs217386		7	44,600,695	FALSE	0.4208	0.4705	0.0709
rs4917014	*IKZF1*	7	50,305,863	TRUE	0.6787	0.9119	0.7005
rs6943555	*AUTS2*	7	69,806,023	TRUE	0.2455	0.5263	0.3672
rs10950202		7	69,930,098	TRUE	0.8582	0.8390	0.9048
rs13238203	*TYW1B*	7	72,129,667	TRUE	0.0345	NA	NA
rs17145738	*MLXIPL*	7	72,982,874	FALSE	0.1214	0.0910	0.0992
rs799160		7	73,060,006	FALSE	0.5058	0.4295	0.7694

rs139906208		7	80,322,438	FALSE	NA	0.8958	NA
rs38855	*MET*	7	116,358,044	TRUE	0.5297	0.7911	0.4201
rs4731702	*KLF14*	7	130,433,384	FALSE	0.4840	0.2741	0.3177
rs3996352	*LOC105375508*	7	130,444,934	FALSE	0.5178	0.7297	0.6827
rs17173637	*TMEM176A*	7	150,529,449	TRUE	0.9120	0.9367	0.9452
rs9987289	*PPP1R3B*	8	9,183,358	FALSE	0.0912	0.1839	0.0271
rs4240624	*LOC157273*	8	9,184,231	FALSE	0.9096	0.8175	0.9729
rs9693857	*LOC105379231*	8	9,267,117	TRUE	0.4528	0.5613	0.2286
rs11776767	*PINX1*	8	10,683,929	TRUE	0.3722	0.6589	0.2613
rs4332136		8	15,799,853	TRUE	0.0148	0.0393	0.1365
rs4921914		8	18,272,438	FALSE	0.7741	0.6202	0.4159
rs1495741	*T2*	8	18,272,881	FALSE	0.7728	0.6190	0.4158
rs12678919	*LPL*	8	19,844,222	FALSE	0.9003	0.8902	0.8823
rs894210		8	19,865,843	FALSE	0.5498	0.8650	0.3052
rs10102164	*SOX17*	8	55,421,614	FALSE	0.2009	0.1715	0.2081
rs2326077		8	59,385,919	FALSE	0.6548	0.7573	0.7839
rs2081687	*CYP7A1*	8	59,388,565	FALSE	0.3452	0.2413	0.2110
rs6982451	*NCOA2*	8	71,014,079	TRUE	0.2070	0.2360	0.3351
rs10504476		8	71,267,629	TRUE	0.1018	0.0537	0.3694
rs2293889	*TRPS1*	8	116,599,199	FALSE	0.4166	0.1102	0.2631
rs2737252		8	116,663,898	TRUE	0.2728	0.1431	0.2935
rs4871137	*SNTB1*	8	121,868,551	FALSE	0.6584	0.3024	0.6379
rs2980885		8	126,474,306	FALSE	0.7807	0.8548	0.7896
rs2954022		8	126,482,621	FALSE	0.4685	0.3627	0.4800
rs2954029	*TRIB1*	8	126,490,972	FALSE	0.5315	0.6602	0.5249
rs4075205		8	144,284,709	TRUE	0.5503	0.6573	0.6098
rs7832643	*PLEC*	8	145,022,657	TRUE	0.4100	0.6404	0.2228
rs11136341		8	145,043,543	TRUE	0.6363	0.4961	0.8073
rs3780181	*VLDLR*	9	2,640,759	TRUE	0.9294	0.7884	0.9086
rs686030	*TTC39B*	9	15,304,782	FALSE	0.8576	0.9122	0.9655
rs191247983		9	15,305,378	FALSE	0.8160	0.5012	0.9033
rs7033354		9	16,904,846	TRUE	0.6644	0.6559	0.3340
	ALDH1B1	9	38,395,659	TRUE	NA	NA	NA
		9	75,605,468	TRUE	NA	NA	NA
rs1883025	*ABCA1*	9	107,664,301	FALSE	0.2486	0.3355	0.2804
rs2472509		9	107,684,230	FALSE	0.6683	0.8635	0.6601
rs8176720	*ABO*	9	136,132,873	FALSE	0.6647	0.5331	0.5518
rs579459		9	136,154,168	FALSE	0.7826	0.8632	0.7527
rs635634		9	136,155,000	FALSE	0.1970	0.1061	0.2503
rs1781930	*AKR1C8P*	10	5,196,273	TRUE	0.1706	0.0451	0.1434
rs1832007	*AKR1C4*	10	5,254,847	TRUE	0.8493	0.9595	0.8982
rs10904908	*VIM-CUBN*	10	17,260,290	TRUE	0.5639	0.6358	0.3090
rs970548	*MARCH8-ALOX5*	10	46,013,277	TRUE	0.7538	0.8044	0.8691
rs10761731	*JMJD1C*	10	65,027,610	FALSE	0.5800	0.6751	0.5454
rs7897379	*REEP3*	10	65,301,725	FALSE	0.5125	0.6650	0.5244
rs2068888	*CYP26A1*	10	94,839,642	FALSE	0.4561	0.3110	0.6457
rs2255141	*GPAM*	10	113,933,886	FALSE	0.2860	0.0799	0.2249

rs10886863	*WDR11-FGFR2*	10	122,929,493	TRUE	0.0228	0.4694	0.2679
	CYP2E1	10	135,354,317	TRUE	NA	NA	NA
rs2923084	*AMPD3*	11	10,388,782	TRUE	0.8168	0.5308	0.5979
rs2303975	*SPON1*	11	14,276,999	TRUE	0.1120	0.1909	0.1617
rs10128711	*SPTY2D1*	11	18,632,984	TRUE	0.2581	0.7802	0.4668
rs10832962		11	18,656,271	TRUE	0.7413	0.2207	0.5249
rs3136441	*LRP4*	11	46,743,247	FALSE	0.8608	0.9639	0.4590
rs326214	*MADD*	11	47,298,360	FALSE	0.6756	0.3628	0.3463
rs17788930	*FNBP4*	11	47,752,775	FALSE	0.6565	0.9009	0.6879
rs7395662	*MADD-FOLH1*	11	48,518,893	TRUE	0.3791	0.5602	0.6040
rs10742937		11	49,320,438	FALSE	0.8429	0.4430	0.8332
		11	50,873,764	TRUE	NA	NA	NA
rs11246602	*OR4C46*	11	51,512,090	TRUE	0.8678	0.9381	0.8615
rs12226802		11	55,324,308	FALSE	0.8694	0.9470	0.8529
rs174532	*MYRF*	11	61,548,874	FALSE	0.3000	0.0724	0.0792
rs174546	*FADS1-2-3*	11	61,569,830	FALSE	0.3397	0.0820	0.3659
rs1535	*FADS2*	11	61,597,972	FALSE	0.6579	0.8612	0.6330
rs12801636	*KAT5*	11	65,391,317	TRUE	0.2203	0.2575	0.3606
rs499974	*MOGAT2-DGAT2*	11	75,455,021	TRUE	0.1719	0.3431	0.2150
rs10790162		11	116,639,104	FALSE	0.0689	0.0189	0.2550
rs2160669	*APOA5-A4-C3-A1*	11	116,647,607	FALSE	0.9295	0.9417	0.7448
rs964184	*APOA1*	11	116,648,917	FALSE	0.8637	0.7955	0.7362
rs603446	*ZPR1*	11	116,654,435	FALSE	0.4374	0.1952	0.2322
rs186808413	*PAFAH1B2*	11	117,042,408	TRUE	NA	NA	NA
rs142953140	*PCSK7*	11	117,089,205	TRUE	NA	NA	NA
rs11603023	*PHLDB1*	11	118,486,067	TRUE	0.4272	0.4998	0.3282
rs7941030	*UBASH3B*	11	122,522,375	TRUE	0.6133	0.5675	0.6911
rs7117842		11	122,534,504	TRUE	0.6209	0.5856	0.6904
rs11220462	*ST3GAL4*	11	126,243,952	FALSE	0.1402	0.0485	0.3488
rs10743940	*CD163-APOBEC1*	12	7,651,138	TRUE	0.0299	0.3385	0.2682
rs1419980		12	7,774,892	TRUE	0.9342	0.7000	0.6581
rs4883201	*PHC1-A2ML1*	12	9,082,581	TRUE	0.8979	0.9745	0.7067
rs11045163		12	20,463,526	TRUE	0.5678	0.7024	0.7346
rs7134375	*PDE3A*	12	20,473,758	TRUE	0.4389	0.3175	0.2654
rs11613352	*LRP1*	12	57,792,580	FALSE	0.2401	0.0972	0.0884
rs3741414	*INHBC*	12	57,844,049	FALSE	0.2391	0.0972	0.0775
rs10861661	*RIC8B*	12	107,174,646	TRUE	0.7654	0.7706	0.6899
rs2241210	*UBE3B*	12	109,950,144	FALSE	0.4709	0.2784	0.6855
rs7134594	*MVK*	12	110,000,193	FALSE	0.5289	0.7213	0.3172
rs653178	*ATXN2*	12	112,007,756	TRUE	0.5078	0.9081	0.9462
rs11065987	*BRAP*	12	112,072,424	TRUE	0.5664	0.9185	0.9554
	ALDH2	12	112,226,240	TRUE	NA	NA	NA
rs6489818	*MAPKAPK5*	12	112,310,580	FALSE	0.1784	0.6760	0.7250
rs1186380		12	121,376,416	FALSE	0.2487	0.7279	0.3225
rs1169288	*HNF1A*	12	121,416,650	FALSE	0.6742	0.8828	0.5172
rs4759375	*SBNO1*	12	123,796,238	FALSE	0.1014	0.1162	0.2537
rs4765127	*ZNF664*	12	124,460,167	FALSE	0.3347	0.3608	0.1493

rs838876		12	125,259,888	FALSE	0.3341	0.6293	0.1507
rs838880	*SCARB1*	12	125,261,593	FALSE	0.6640	0.3241	0.5022
rs10773105	*SCARB1*	12	125,283,766	FALSE	0.5222	0.8216	0.7346
rs4942486	*BRCA2*	13	32,953,388	FALSE	0.4796	0.5002	0.4021
rs1341267	*GPR180*	13	95,284,980	TRUE	0.5928	0.8757	0.3538
rs8017377	*NYNRIN*	14	24,883,887	FALSE	0.4643	0.1813	0.1064
rs10144765	*NID2-PTDGR*	14	52,559,930	TRUE	0.9247	0.8894	0.7802
rs4983559	*ZBTB42-AKT1*	14	105,277,209	TRUE	0.6120	0.4104	0.2125
rs2412710	*CAPN3*	15	42,683,787	FALSE	0.0227	0.0692	0.0130
rs492571	*FRMD5*	15	44,211,273	FALSE	0.9583	0.8176	0.9452
rs2929282		15	44,245,931	FALSE	0.9509	0.6846	0.9669
rs1532085	*LIPC*	15	58,683,366	FALSE	0.3807	0.5147	0.5612
rs261342		15	58,731,153	FALSE	0.7756	0.4027	0.3891
rs2652834	*LACTB*	15	63,396,867	FALSE	0.2007	0.3044	0.1961
rs1035744	*PARP6*	15	72,566,615	TRUE	0.7323	0.4170	0.4438
rs8030477	*ADPGK*	15	73,085,815	TRUE	0.6806	0.3874	0.3786
rs8027181		15	73,088,869	TRUE	0.3197	0.6009	0.6217
rs3198697	*PDXDC1*	16	15,129,940	TRUE	0.3816	0.0861	0.2103
rs11649653	*CTF1*	16	30,918,487	TRUE	0.5929	0.9156	0.3388
rs749671	*ZNF646*	16	31,088,347	TRUE	0.3800	0.1103	0.7028
rs9930333	*FTO*	16	53,799,977	TRUE	0.5718	0.5730	0.7485
rs1121980		16	53,809,247	TRUE	0.4287	0.4677	0.2680
rs9989419	*NUP93/HERPUD1/CETP*	16	56,985,139	FALSE	0.3937	0.5867	0.3310
rs3764261	*CETP*	16	56,993,324	FALSE	0.3194	0.3102	0.2252
rs5880		16	57,015,091	FALSE	0.0507	0.0161	0.0899
rs868213	*EXOC3L1*	16	67,220,457	FALSE	0.9274	0.5738	0.9515
rs16942887	*LCAT*	16	67,928,042	FALSE	0.1250	0.2145	0.0713
rs2288002	*DHODH*	16	72,057,282	FALSE	0.4281	0.4300	0.5228
rs2000999	*HPR*	16	72,108,093	FALSE	0.1977	0.0801	0.3785
rs2925979	*CMIP*	16	81,534,790	FALSE	0.3032	0.3140	0.3380
rs314253	*DLG4*	17	7,091,650	TRUE	0.6551	0.6230	0.6073
rs4791641	*PFAS*	17	8,161,149	TRUE	0.5053	0.2751	0.2924
	ALDH3A2	17	19,566,180	TRUE	NA	NA	NA
rs11869286	*STARD3*	17	37,813,856	FALSE	0.6640	0.2570	0.5396
rs931992	*TCAP*	17	37,821,435	FALSE	0.6635	0.2356	0.5317
rs8077889	*MPP3*	17	41,878,166	TRUE	0.7875	0.8121	0.8429
rs7225700	*THCAT158*	17	45,391,804	TRUE	0.3489	0.3084	0.3410
rs7206971	*OSBPL7*	17	45,425,115	FALSE	0.4839	0.4721	0.3035
rs1801689	*APOH-PRXCA*	17	64,210,580	TRUE	0.9667	NA	NA
rs12602912	*BPTF*	17	65,870,073	TRUE	0.2005	0.1141	0.5575
rs4148008	*ABCA8*	17	66,875,294	FALSE	0.6814	0.4493	0.5783
rs4148005		17	66,882,466	FALSE	0.6848	0.4518	0.6166
rs4969178	*PGS1*	17	76,388,202	FALSE	0.3876	0.3670	0.5425
rs4129767		17	76,403,984	FALSE	0.5060	0.3467	0.4170
rs7241918	*LIPG*	18	47,160,953	FALSE	0.8324	0.9457	0.8894
rs4939883		18	47,167,214	FALSE	0.1721	0.4552	0.1941
rs11660468	*LOC105372112*	18	47,209,143	FALSE	0.4009	0.1679	0.2066

rs952044		18	57,798,110	TRUE	0.3328	0.4425	0.2367
rs12967135	*MC4R*	18	57,849,023	FALSE	0.2364	0.2773	0.2478
rs941408	*THOP1*	19	2,814,181	TRUE	0.2845	0.2306	0.4130
rs7248104	*INSR*	19	7,224,431	FALSE	0.4102	0.3073	0.3616
rs2278236	*ANGPTL4*	19	8,431,581	FALSE	0.5229	0.4685	0.2014
rs7255436		19	8,433,196	FALSE	0.5268	0.6560	0.2093
rs6511720	*LDLR*	19	11,202,306	FALSE	0.1123	0.1222	0.0770
rs688		19	11,227,602	FALSE	0.4407	0.1102	0.1773
rs737337	*ANGPTL8*	19	11,347,493	FALSE	0.9139	0.5836	0.7526
rs145464906		19	11,350,874	TRUE	NA	NA	NA
rs10401969	*CILP2*	19	19,407,718	FALSE	0.9221	0.8306	0.8994
rs731839	*PEPD*	19	33,899,065	TRUE	0.6634	0.6137	0.4299
rs1688030	*HPN-AS1*	19	35,556,744	TRUE	0.0665	0.1963	0.1949
rs6859	*NECTIN2*	19	45,382,034	FALSE	0.4305	0.4527	0.3416
rs7254892		19	45,389,596	FALSE	0.0373	0.1390	0.0425
rs4420638	*APOE*	19	45,422,946	FALSE	0.8210	0.7998	0.8891
rs492602	*FLJ36070*	19	49,206,417	FALSE	0.5313	0.5030	0.6922
rs17695224	*HAS1*	19	52,324,216	FALSE	0.2603	0.1503	0.2512
rs386000	*LILRA3*	19	54,792,761	FALSE	0.2325	0.1972	0.6863
rs103294		19	54,797,848	FALSE	0.2112	0.0934	0.6154
rs364585	*SPTLC3*	20	12,962,718	TRUE	0.3833	0.1737	0.4177
rs2328223	*SNX5*	20	17,845,921	FALSE	0.8123	0.8104	0.7510
rs2277862	*ERGIC3*	20	34,152,782	TRUE	0.1462	0.1894	0.1845
rs7264396	*FER1L4*	20	34,154,741	TRUE	0.2267	0.3720	0.3489
rs2902940	*MAFB*	20	39,091,487	TRUE	0.6974	0.5201	0.7007
rs6016381		20	39,180,436	FALSE	0.6270	0.5346	0.4745
rs6029526	*TOP1*	20	39,672,618	FALSE	0.4775	0.7799	0.7822
rs6065311		20	39,724,338	FALSE	0.5213	0.2181	0.2104
rs1800961	*HNF4A*	20	43,042,364	FALSE	0.0338	NA	0.0136
rs6065906	*PLTP*	20	44,554,015	FALSE	0.8145	0.8365	0.9537
rs4465830	*ZNF335*	20	44,585,420	FALSE	0.8133	0.9560	0.9553
rs114139997	*COL18A1*	21	46,875,775	TRUE	NA	0.0237	NA
rs181362	*UBE2L3*	22	21,932,068	FALSE	0.2165	0.4181	0.4650
rs5763662	*MTMR3*	22	30,378,703	TRUE	0.0229	0.0136	0.1530
rs138777	*TOM1*	22	35,711,098	TRUE	0.3441	0.7801	0.4605
rs5756931	*PLA2G6*	22	38,546,033	TRUE	0.6288	0.8754	0.7659
rs3761445		22	38,595,411	FALSE	0.5986	0.3756	0.6744
rs4253772	*PPARA*	22	46,627,603	TRUE	0.1105	0.0307	0.0474
rs4253776		22	46,629,479	TRUE	0.8851	0.5655	0.9482

iant was available for analysis only in Stage 1, it will be marked as TRUE in

le Frequency			EUR		AFR		ASI
HIS	BRA	META	P.2df	P.Int	P.2df	P.Int	P.2df
0.7926	NA	0.7808	0.0017	0.0877	0.5630	0.7425	0.3225
0.4938	0.4522	0.4984	0.5286	0.6957	0.7367	0.4631	0.2437
0.5358	0.5025	0.5254	0.5203	0.5180	0.5570	0.2793	0.2214
0.0409	0.0557	0.0599	**8.20E-18**	0.0915	0.1904	0.1969	0.0189
0.8577	0.8169	0.8018	**3.28E-14**	0.7050	0.6829	0.6882	4.63E-07
0.4771	0.5988	0.5988	0.5203	0.2111	0.2749	0.1368	0.9545
NA	NA	0.0132	NA	NA	NA	NA	NA
0.2101	NA	0.2114	0.5851	0.2389	0.0592	0.7667	0.3244
0.5949	0.6217	0.6554	1.59E-06	0.2617	0.4848	0.3576	0.3965
0.3601	0.3207	0.3080	1.98E-06	0.2241	0.0057	0.0528	0.4128
0.8700	NA	0.8259	0.1626	0.0413	0.3927	0.4848	0.3960
0.8701	NA	0.8289	0.1481	0.0396	0.4380	0.4909	NA
0.4817	0.4361	0.3981	**3.80E-16**	0.3664	0.0222	0.3628	**3.83E-12**
0.7687	0.7597	0.7967	**1.37E-26**	0.0194	0.0178	0.5554	0.0211
0.7687	0.7594	0.7960	**3.49E-25**	0.1003	0.0427	0.4749	0.0153
0.4698	0.5459	0.5948	0.6147	0.1765	0.6250	0.7644	0.2106
0.9078	NA	0.8686	0.0011	0.5217	0.7718	0.4944	0.5250
0.7684	NA	0.7251	0.0042	0.3546	0.7446	0.8106	0.8420
0.3807	NA	0.4600	6.98E-06	0.2641	0.2056	0.4693	0.6793
0.3015	0.3310	0.3019	**6.21E-13**	0.1018	0.4040	0.7193	5.86E-06
0.6743	0.6416	0.6749	**2.42E-11**	0.0648	0.0896	0.5323	7.21E-07
0.2009	0.2479	0.2459	**2.74E-17**	0.1346	0.7465	0.6178	8.75E-06
0.7770	0.7189	0.7374	**2.21E-16**	0.0656	0.1247	0.0182	0.0002
0.7343	NA	0.7717	0.6676	0.2408	0.0029	0.0013	0.0267
0.5401	0.5486	0.4772	**5.12E-50**	0.0418	0.0070	0.1924	**4.33E-09**
0.1836	NA	0.2094	0.0292	0.4562	0.8959	0.6571	0.5305
0.6941	0.6237	0.6036	0.0137	0.4687	0.1117	0.3339	0.0178
0.3171	0.3905	0.4052	0.0271	0.4000	0.3525	0.1313	0.0383
0.2710	0.2733	0.2464	**4.46E-09**	0.2452	0.2212	0.2918	0.0064
0.2200	0.2245	0.1901	0.0036	0.4990	0.9556	0.8126	0.1409
0.3389	0.3959	0.3995	0.0123	0.2522	0.0006	0.1041	0.0027
0.8984	0.8640	0.7901	0.3866	0.1817	0.2470	0.8763	0.0042
0.3448	0.4013	0.3963	0.1032	0.4463	0.0006	0.0237	0.0050
0.7844	0.7235	0.7185	0.9764	0.5799	0.2682	0.0747	0.0036
0.2134	0.2707	0.2802	0.6853	0.3530	0.4884	0.1905	0.0029
0.2973	0.2364	0.1843	0.5052	0.5514	0.2589	0.1696	0.1136
0.0759	NA	0.1135	0.4163	0.5502	0.2783	0.3215	NA
0.6781	0.6805	0.6993	0.0673	0.4884	0.1995	0.1285	0.0869
0.9567	0.9392	0.9254	5.59E-05	0.3997	0.0797	0.0750	0.2339
0.9601	0.9463	0.9311	0.0304	0.3316	0.0560	0.1294	0.0219

0.0403	0.0537	0.0691	0.0220	0.3057	0.0515	0.1261	0.0304
0.4159	NA	0.4332	0.1336	0.1504	0.5698	0.3020	0.8197
0.2742	NA	0.2005	0.0066	0.2397	0.9457	0.7031	0.7250
0.7903	0.6819	0.4615	6.56E-05	0.6572	0.0349	0.2311	0.0846
0.3618	NA	0.4537	0.6970	0.7052	0.4842	0.2721	0.2759
0.8991	0.8619	0.8751	**2.78E-22**	0.0553	0.0140	0.5463	0.4794
0.8990	0.8603	0.8757	**5.33E-23**	0.0571	0.0039	0.5401	0.6489
0.3629	NA	0.3473	1.97E-06	0.1811	0.2509	0.4017	0.6661
0.4832	0.5675	0.6219	0.0008	0.1032	0.5529	0.2730	0.7129
0.7850	NA	0.7827	0.4496	0.6788	0.8912	0.5275	0.8935
0.3077	0.3207	0.2874	**9.96E-14**	0.6201	0.4601	0.4356	0.0025
0.2309	NA	0.2470	0.3329	0.3368	0.9830	0.8909	0.0993
0.7784	0.6545	0.7206	**3.23E-24**	0.2950	0.6612	0.2588	0.0008
0.7387	0.6049	0.6916	**3.25E-26**	0.1762	0.0754	0.0733	0.0014
0.1116	NA	0.1503	0.6022	0.1872	0.1505	0.0921	0.2966
0.4793	NA	0.5882	0.0420	0.0365	0.0269	0.0200	0.2454
0.2843	NA	0.3734	0.4917	0.2552	0.1409	0.0530	0.1232
0.1883	0.2034	0.1803	0.0005	0.2821	0.0261	0.0195	0.4531
0.0896	NA	0.1189	0.7224	0.7984	0.8407	0.5876	0.8421
0.1401	NA	0.1623	1.23E-05	0.4418	0.2050	0.0783	0.2613
0.3936	0.4818	0.4259	**5.25E-13**	0.3526	0.0691	0.3194	0.0018
0.6388	0.5557	0.5935	**3.13E-13**	0.3722	0.0012	0.0659	0.0016
0.1891	NA	0.2213	6.63E-05	0.3853	0.0851	0.0562	NA
0.0568	NA	0.0817	0.2878	0.3844	0.4696	0.2704	NA
0.4120	NA	0.4772	0.0491	0.0894	0.3090	0.4122	0.2281
0.1474	NA	0.1112	0.0821	0.6193	0.6619	0.4537	0.3607
0.8652	NA	0.8966	0.2264	0.6276	0.4759	0.1966	0.7195
0.7756	NA	0.7683	1.17E-05	0.1749	0.7569	0.4832	0.2665
0.7838	0.7640	0.7877	**7.23E-16**	0.7578	0.1499	0.1872	0.4680
0.5357	0.5470	0.5329	**1.14E-14**	0.0366	0.0122	0.1483	0.0122
0.1119	NA	0.1344	0.0916	0.3963	0.1286	0.3528	NA
0.4752	NA	0.5412	0.0605	0.3343	0.5816	0.2708	0.6126
0.8532	NA	0.8263	**4.49E-08**	0.2421	0.1697	0.1946	NA
0.5410	NA	0.4289	0.5161	0.5118	0.0613	0.3426	0.4713
0.6457	0.6160	0.5650	**7.39E-12**	0.7612	0.0303	0.0323	0.0098
0.1261	NA	0.2104	0.0221	0.1371	0.8330	0.5559	0.2703
0.4484	NA	0.4825	2.31E-06	0.2654	0.0419	0.2832	0.2780
NA	NA	NA	NA	NA	NA	NA	NA
0.5348	NA	0.4540	0.0030	0.1720	0.7665	0.4791	0.6951
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
0.0484	0.0639	0.0619	**4.70E-30**	0.0123	0.1849	0.3506	NA
0.6102	NA	0.5850	0.0086	0.5843	0.1640	0.0684	0.0082

0.2717	NA	0.2815	0.0010	0.4573	0.0259	0.1346	0.3737
0.2229	0.2476	0.1754	**3.00E-15**	0.0768	0.0176	0.3933	0.5411
0.5583	NA	0.5339	0.0078	0.0845	0.0010	0.7417	0.2898
0.3779	0.3672	0.4199	0.0044	0.0347	0.1719	0.1355	0.1587
0.6172	0.6280	0.5743	0.0220	0.0988	0.0150	0.0040	0.1472
0.5345	NA	0.5725	0.1646	0.7691	0.8722	0.2324	0.0796
0.3065	0.4051	0.3451	0.8637	0.7616	0.5568	0.3724	0.5877
0.3256	0.4120	0.3658	0.4847	0.3638	0.5683	0.5883	0.4009
0.3037	0.2301	0.2810	0.7834	0.3167	0.2302	0.0865	0.0073
0.0213	NA	0.0586	0.6432	0.0830	0.6469	0.4605	NA
0.1527	NA	0.2032	0.0020	0.2773	0.1515	0.1464	0.0019
NA	NA	0.1413	0.0229	0.1487	0.1881	0.3641	NA
0.0995	NA	0.1329	4.37E-05	0.8384	0.4749	0.2259	0.1068
0.7313	NA	0.6734	1.80E-05	0.3370	0.8919	0.7414	0.2607
0.2398	NA	0.2623	0.1586	0.3503	0.2805	0.0717	NA
0.5430	NA	0.5968	0.0017	0.9701	0.6949	0.5998	0.3146
0.4931	0.4647	0.4839	**3.28E-15**	0.3756	0.0058	0.0589	4.39E-06
0.2271	NA	0.3609	0.1209	0.0319	0.3226	0.2370	0.1012
0.7489	NA	0.6134	0.1883	0.0407	0.2568	0.2020	0.2271
0.8345	0.7813	0.7942	0.3171	0.0439	0.2061	0.4277	0.1072
0.5856	NA	0.6545	0.0046	0.0683	0.1240	0.2282	0.8114
0.4439	0.4313	0.3342	0.0266	0.0762	0.0624	0.2715	0.0020
0.6121	0.5595	0.5684	**5.69E-12**	0.1764	0.0181	0.0156	0.0820
0.5013	0.4660	0.5122	**3.54E-12**	0.0216	0.0105	0.0039	0.1064
0.5430	0.5784	0.5152	**1.79E-12**	0.0064	0.1579	0.0323	0.1119
0.8438	NA	0.7835	8.35E-06	0.0583	0.2407	0.1330	0.0543
0.5523	0.5809	0.5065	**6.69E-17**	0.2054	0.3715	0.3998	0.0830
0.4477	0.4188	0.4907	**2.10E-16**	0.1457	0.5818	0.5654	0.1398
0.7180	NA	0.7460	0.0002	0.3152	0.1067	0.0192	0.2761
0.3207	0.3871	0.3737	0.0835	0.2801	0.3957	0.1490	0.2379
0.7899	0.8271	0.8434	0.3065	0.1169	0.5739	0.6408	0.2469
0.8982	NA	0.8680	0.0003	0.3064	0.3413	0.8688	NA
0.3912	NA	0.4593	0.0008	0.0502	0.7162	0.1364	0.3745
0.4075	NA	0.4029	0.0013	0.5995	0.1635	0.2543	0.4642
0.4838	0.4631	0.4494	**2.93E-22**	0.2936	0.0006	0.3640	3.18E-06
0.4843	0.4661	0.4442	**9.23E-22**	0.3620	0.0019	0.1927	9.68E-08
0.8062	NA	0.7353	0.8901	0.4469	0.3461	0.5328	0.4424
0.8502	0.8615	0.8742	0.0189	0.1540	0.0881	0.0309	0.5010
0.2379	0.2140	0.2718	0.0685	0.1868	0.4007	0.2399	0.4908
0.7330	0.7883	0.7434	0.0261	0.5005	0.1733	0.2150	0.5935
0.3350	0.4216	0.3371	0.0172	0.0174	0.2097	0.4619	0.1334
0.5389	NA	0.7137	0.0059	0.6154	0.0139	0.4169	0.3602
0.2841	NA	0.3011	0.5106	0.2902	0.1716	0.0409	0.5470
0.8914	NA	0.8590	0.7253	0.6223	0.0703	0.0505	0.6509
NA	NA	0.0345	0.1444	0.2252	NA	NA	NA
0.0746	0.0875	0.1109	**2.58E-20**	0.4232	0.4190	0.2851	3.67E-06
0.5966	0.5088	0.5734	**9.23E-11**	0.4206	0.1596	0.2117	0.0034

0.9882	0.9881	0.9335	NA	NA	**3.11E-25**	0.4542	NA
0.4603	NA	0.5612	0.0947	0.3501	0.8137	0.6638	0.0165
0.3894	0.3932	0.4220	**2.67E-29**	0.0319	0.0375	0.1984	0.0014
0.6110	0.6111	0.5802	**4.62E-32**	0.0488	0.0445	0.1706	0.0005
0.9469	NA	0.9182	0.0018	0.1138	0.2757	0.2280	NA
0.1920	0.0888	0.0894	**1.51E-75**	0.0262	**7.79E-12**	0.0413	**4.79E-09**
0.8076	0.9137	0.9113	**3.08E-79**	0.0205	**1.00E-11**	0.0350	**6.23E-09**
0.3547	NA	0.4605	0.3408	0.4363	0.0139	0.0596	NA
0.3268	NA	0.4125	0.0094	0.0573	0.1369	0.0734	0.6912
0.1224	NA	0.0704	NA	NA	0.0208	0.7581	0.4175
0.6716	0.7347	0.6674	0.2409	0.1643	0.0021	0.5229	0.0887
0.6702	0.7323	0.6649	0.2208	0.1506	0.0029	0.7131	0.0468
0.9215	0.9126	0.8963	**4.85E-229**	0.5448	2.88E-07	0.7136	**8.01E-91**
0.5273	0.5855	0.5125	**4.26E-107**	0.1012	6.47E-07	0.0473	**2.51E-55**
0.1341	0.1404	0.1965	0.7113	0.3795	0.2250	0.1264	0.0148
0.7719	0.6895	0.7006	0.4183	0.0381	0.0473	0.2767	0.0936
0.2277	0.3101	0.2969	0.4300	0.0447	0.0511	0.2647	0.2878
0.1897	NA	0.2220	0.0081	0.1686	0.5397	0.2562	0.2391
0.0948	NA	0.1168	0.0721	0.1517	0.1763	0.1540	0.0856
0.3201	0.3445	0.3516	**1.96E-18**	0.5101	0.0108	0.1784	**6.47E-13**
0.2990	NA	0.2537	0.3535	0.1986	0.0667	0.0522	0.4222
0.6565	0.5907	0.6281	**4.14E-08**	0.6154	0.4152	0.6705	7.23E-07
0.7881	0.7531	0.7884	**2.79E-20**	0.2977	0.6676	0.4270	0.0002
0.3844	0.4243	0.4592	**7.06E-41**	0.0971	0.6300	0.5839	8.88E-05
0.6185	0.5817	0.5440	**1.56E-41**	0.0971	0.8244	0.7305	0.0002
0.5630	NA	0.5748	1.39E-06	0.3987	0.2337	0.5359	0.5501
0.3692	NA	0.4342	0.0477	0.0093	0.8484	0.3625	0.0385
0.7001	NA	0.6268	0.0806	0.0127	0.9180	0.4866	0.0104
0.8978	NA	0.9024	0.5760	0.4314	0.3997	0.8023	0.2140
0.9056	0.8539	0.8886	**2.85E-38**	0.7195	0.2677	0.8177	0.0001
0.8092	0.7220	0.8136	**5.08E-31**	0.2080	0.6661	0.3870	0.0073
0.4933	NA	0.6295	0.0439	0.2049	0.0421	0.0223	0.5692
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
0.2855	0.2632	0.2650	**5.28E-77**	0.4884	0.0024	0.0402	**1.45E-77**
0.6493	0.6782	0.6793	**5.80E-10**	0.5238	0.0162	0.0121	5.12E-05
0.5273	0.6176	0.6198	0.2873	0.4235	0.2090	0.0447	0.0232
0.8326	0.7855	0.7832	0.0023	0.2777	0.0308	0.4347	0.0012
0.1492	0.1940	0.2011	0.0005	0.1862	0.1185	0.2034	0.0009
0.1591	NA	0.1490	0.0407	0.0226	0.3171	0.1899	0.5397
0.8399	NA	0.8705	0.1293	0.1248	0.4982	0.5958	0.7712
0.6195	NA	0.5599	0.1015	0.2657	0.4535	0.2860	0.1203
0.7099	NA	0.7692	2.13E-05	0.5551	0.3057	0.1633	0.1459
0.6943	0.6121	0.5845	9.34E-06	0.5137	0.0244	0.3558	0.3285
0.6680	0.5751	0.5347	1.74E-06	0.1164	0.0792	0.4838	0.0484
0.4378	0.4192	0.4912	**1.78E-08**	0.0780	1.10E-05	0.7822	1.22E-06
0.2833	0.3030	0.2569	**5.18E-17**	0.2352	0.0030	0.1936	7.91E-08

0.1567	NA	0.1684	0.0082	0.0613	0.3916	0.1816	0.0688
NA	NA	NA	NA	NA	NA	NA	NA
0.6248	NA	0.7427	0.0001	0.0509	0.0051	0.1902	0.4370
0.1017	NA	0.1294	0.0043	0.0831	0.0866	0.5234	0.0312
0.3574	NA	0.3658	0.1013	0.0671	0.2713	0.6191	0.4163
0.6421	NA	0.6331	0.1465	0.0736	0.1666	0.4148	0.5283
0.7363	0.8916	0.7558	**1.15E-30**	0.5974	0.1472	0.1640	0.0009
0.5908	0.6972	0.5632	**8.98E-41**	0.4338	0.0695	0.6821	1.71E-06
0.6635	0.6801	0.6804	**1.52E-26**	0.6670	0.2405	0.4546	0.0148
0.3780	NA	0.4267	1.55E-05	0.0587	0.1493	0.4342	0.0807
0.8186	0.8358	0.8100	**6.98E-19**	0.1918	0.3050	0.9095	0.7164
NA	NA	NA	NA	NA	NA	NA	NA
0.9018	NA	0.8861	1.42E-05	0.2405	0.3321	0.1378	0.2357
0.9026	0.9189	0.8726	**7.24E-18**	0.6723	0.6842	0.4281	0.6341
0.1782	0.2470	0.2666	**2.69E-10**	0.4946	0.2757	0.1515	0.9226
0.4994	0.3449	0.3370	**1.09E-48**	0.1205	0.0021	0.1782	0.0069
0.4858	0.6422	0.6576	**1.47E-47**	0.1402	0.0001	0.0346	0.0066
0.3826	NA	0.2446	0.0069	0.9018	0.0681	0.1293	0.0732
0.1577	NA	0.2038	0.0002	0.1318	0.9060	0.7990	0.2036
0.1221	0.0678	0.1204	**9.66E-69**	0.4242	0.0607	0.1288	**1.81E-46**
0.8700	0.9188	0.8797	**1.22E-71**	0.2275	0.0006	0.2366	**7.54E-46**
0.7362	0.8206	0.8208	**3.57E-182**	0.0156	0.1492	0.1838	**4.52E-53**
0.2758	0.3660	0.3636	0.0459	0.1122	0.1334	0.5305	**1.14E-21**
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
0.3118	NA	0.4264	0.0115	0.2854	0.4202	0.6640	0.6555
0.6450	NA	0.6151	0.0001	0.1847	0.3200	0.6724	0.1299
0.6500	NA	0.6233	0.0003	0.3014	0.1638	0.3276	0.1030
0.1180	0.0926	0.1870	0.0063	0.4643	0.4278	0.7261	0.4815
0.1475	NA	0.1105	0.0027	0.3314	0.1883	0.5467	0.6793
0.7022	NA	0.8604	0.0030	0.3229	0.1392	0.3048	0.0008
0.9259	NA	0.8894	0.0002	0.4128	0.0011	0.3933	0.3957
0.5587	NA	0.6034	2.65E-05	0.5573	0.6879	0.5213	0.8610
0.4469	NA	0.4033	7.38E-06	0.7296	0.9825	0.9280	0.7163
0.3076	0.1978	0.1969	**9.57E-19**	0.1497	0.0924	0.5011	0.0316
0.3073	0.2025	0.1909	**1.26E-18**	0.2442	0.0872	0.4026	0.0312
0.7462	NA	0.7583	0.0001	0.0917	0.5245	0.6162	0.1736
0.4810	0.4314	0.5102	**9.19E-17**	0.7185	0.0009	0.2210	1.11E-07
0.5213	0.5681	0.4878	**2.53E-17**	0.7777	0.0011	0.2777	6.58E-08
0.7015	NA	0.5993	0.0003	0.2263	0.0585	0.2277	NA
0.7222	NA	0.6457	0.0104	0.1494	0.0106	0.3026	NA
NA	NA	NA	NA	NA	NA	NA	NA
0.3574	0.2807	0.3538	0.0959	0.2537	0.0441	0.7740	0.0065
0.2848	0.3275	0.3020	0.0185	0.3791	0.5741	0.3652	0.1055
0.6725	0.7102	0.6516	3.28E-06	0.2929	0.3429	0.3734	0.0001
0.1315	0.1323	0.1441	**1.15E-13**	0.2159	0.1117	0.0638	**1.77E-14**
0.3022	0.3378	0.2896	**2.96E-31**	0.3739	0.0569	0.5156	0.0005

0.2821	0.3686	0.3084	**9.25E-30**	0.0855	0.3170	0.5274	0.5055
0.5886	0.6096	0.5948	**4.01E-25**	0.3438	0.6108	0.5027	1.25E-06
0.6581	0.5861	0.6035	**5.47E-25**	0.3547	0.0364	0.5436	0.0807
0.4888	0.4956	0.4624	0.0167	0.5832	0.1486	0.0905	0.0519
0.4574	NA	0.6176	0.5267	0.3211	0.5317	0.5100	0.1878
0.2747	0.3732	0.3445	0.2327	0.1373	0.0907	0.5924	0.0358
0.8765	NA	0.9075	0.2240	0.7649	0.0223	0.1177	0.0077
0.4785	NA	0.5536	8.32E-05	0.9175	0.3622	0.1954	0.0634
0.0397	0.0516	0.0298	**3.84E-09**	0.3349	0.2098	0.1732	0.1795
0.9426	0.9210	0.9427	**4.30E-20**	0.1883	0.3484	0.2034	0.9212
0.8941	0.8992	0.9313	**2.23E-16**	0.4195	0.4794	0.4405	0.4106
0.3905	0.3943	0.4370	**1.89E-194**	0.2548	7.52E-08	0.1771	**1.52E-116**
0.5346	0.6838	0.6380	**2.26E-170**	0.3983	0.0006	0.6178	**2.36E-63**
0.1567	0.2175	0.2075	**3.37E-08**	0.5025	0.0471	0.2164	0.6024
0.6358	NA	0.6524	0.2162	0.1531	0.0180	0.0616	0.8152
0.5651	NA	0.6027	0.8677	0.3418	0.3070	0.2201	0.0425
0.4334	NA	0.3955	0.8710	0.3496	0.4877	0.3456	0.0414
0.2480	NA	0.3213	0.0027	0.4812	0.5699	0.1787	NA
0.5925	NA	0.6271	0.0059	0.0735	0.4969	0.3580	0.3135
0.4130	NA	0.3615	0.0027	0.0316	0.1563	0.0547	0.5379
0.6547	NA	0.5928	1.07E-05	0.2680	0.2743	0.3184	0.2995
0.3566	NA	0.4184	8.66E-06	0.2891	0.0830	0.0537	0.3437
0.3758	0.4111	0.4033	**0**	0.4866	0.3745	0.9458	**1.82E-32**
0.3078	0.2732	0.2941	**0**	0.0427	**7.49E-71**	0.1580	**0**
0.0687	0.0389	0.0525	**0**	0.0228	0.0044	0.6514	**4.67E-29**
0.8798	0.8799	0.9043	**4.73E-13**	0.2541	**8.64E-11**	0.2261	0.0053
0.1586	0.1413	0.1212	**4.78E-52**	0.0578	**3.63E-19**	0.0223	**5.72E-09**
0.5457	0.4496	0.4581	0.5082	0.5365	0.0937	0.4553	0.1929
0.1809	0.1997	0.2334	0.3173	0.5426	0.0044	0.0052	0.1133
0.2097	0.2448	0.3076	**4.71E-28**	0.0354	0.0028	0.3780	**2.22E-14**
0.5609	NA	0.6428	0.6455	0.0890	0.7565	0.7095	0.4948
0.3499	NA	0.4484	0.2258	0.3450	0.3485	0.0470	0.4600
NA	NA	NA	NA	NA	NA	NA	NA
0.5470	0.5666	0.5976	**5.09E-35**	0.3219	0.1698	0.6530	0.0010
0.5427	0.5575	0.5930	**4.53E-34**	0.3627	0.2116	0.6962	0.0010
0.8513	NA	0.7955	0.0439	0.0114	0.0092	0.0039	NA
0.4529	NA	0.3447	0.0642	0.0977	0.7604	0.6268	0.2925
0.3933	0.4332	0.4330	9.32E-07	0.0161	0.5583	0.5762	0.2523
0.9697	NA	0.9669	0.3161	0.4279	NA	NA	NA
0.2485	NA	0.2238	0.0058	0.0609	0.6280	0.1869	0.7765
0.6438	0.6546	0.6376	**5.10E-14**	0.6095	0.0286	0.5836	0.0100
0.6449	0.6547	0.6492	**1.25E-14**	0.7163	0.0203	0.6073	0.0129
0.3470	0.3606	0.4223	**6.57E-19**	0.4331	0.0003	0.3364	1.63E-06
0.5259	0.4949	0.4733	**2.26E-16**	0.0567	0.0011	0.6333	5.08E-05
0.9133	0.8709	0.8588	**1.59E-92**	0.1252	0.0017	0.6618	**1.19E-10**
0.1638	0.2157	0.1975	**8.53E-92**	0.1562	0.0005	0.4733	**2.70E-22**
0.2651	0.3499	0.3293	**3.73E-41**	0.1950	0.0078	0.1658	**1.15E-11**

0.2667	NA	0.3432	8.17E-06	0.1801	0.1769	0.7099	0.0436
0.1591	0.1984	0.2378	**7.68E-11**	0.6076	0.0366	0.4470	0.0014
0.2722	NA	0.2845	0.1757	0.3787	0.2117	0.1793	0.4403
0.3747	0.4042	0.3889	1.59E-06	0.0848	0.1874	0.0788	0.4249
0.4811	0.5131	0.4382	**7.12E-19**	0.3046	0.0714	0.0825	0.0001
0.5118	0.5432	0.4551	**2.38E-18**	0.2493	0.0632	0.2984	4.96E-05
0.0945	0.1308	0.1099	5.75E-06	0.6790	0.6894	0.5842	0.1589
0.3907	0.3690	0.3514	0.0043	0.0724	0.2528	0.1776	0.4496
0.7603	0.8366	0.8385	**1.02E-23**	0.0054	**3.62E-12**	0.2042	**7.21E-18**
NA	NA	NA	NA	NA	NA	NA	NA
0.9279	0.9292	0.9102	4.76E-05	0.0561	0.3854	0.3927	0.0456
0.6047	NA	0.6290	4.80E-05	0.4464	0.1917	0.0955	0.1439
0.0653	NA	0.0980	0.1732	0.1419	0.6168	0.4857	0.5075
0.3051	0.3734	0.4014	**9.74E-14**	0.0270	0.0419	0.2663	3.13E-05
0.0366	0.0462	0.0431	**1.32E-10**	0.2518	3.40E-05	0.5636	**4.21E-08**
0.8881	0.8419	0.8406	**1.35E-71**	0.0991	0.3068	0.3649	**2.44E-31**
0.6384	0.5849	0.5452	0.0004	0.5392	0.0225	0.0756	0.0057
0.2966	0.2796	0.2522	**6.37E-15**	0.4652	0.1194	0.0747	0.0001
0.3815	0.2298	0.3541	**3.19E-50**	0.0658	0.0362	0.1839	0.0002
0.2389	0.1483	0.3060	**1.30E-52**	0.1142	5.95E-05	0.2555	2.94E-06
0.3376	NA	0.3481	0.8342	0.8025	0.4383	0.8261	0.1983
0.7666	0.7913	0.7936	0.0527	0.1287	0.8413	0.6928	0.7523
0.1933	NA	0.1580	0.0400	0.5341	0.0037	0.2919	0.5448
0.2999	NA	0.2614	0.0311	0.3235	0.0513	0.4132	0.1368
0.7096	NA	0.6678	0.2925	0.2551	0.2172	0.1015	0.2572
0.6720	0.6489	0.5847	0.1455	0.3847	0.3262	0.1105	0.7269
0.5360	0.5384	0.5773	0.1458	0.1508	0.1211	0.0839	0.0096
0.4324	0.4584	0.4210	0.0931	0.0834	0.1942	0.1576	0.0170
0.0443	0.0472	0.0292	**2.40E-50**	0.2845	NA	NA	4.32E-07
0.8689	0.8327	0.8507	**2.52E-65**	0.0324	8.75E-05	0.0947	0.0957
0.8863	0.8559	0.8586	**7.13E-65**	0.0300	0.0084	0.0200	0.1401
NA	NA	0.0237	NA	NA	0.0056	0.1776	NA
0.3990	0.2806	0.3044	**1.36E-13**	0.7477	0.2327	0.1411	**1.38E-12**
0.1008	NA	0.0371	0.0102	0.1741	0.2361	0.1058	0.7361
0.4308	NA	0.4336	0.2256	0.0579	0.0018	0.3462	0.0055
0.6114	NA	0.6806	0.0002	0.4949	0.2700	0.6425	0.0430
0.5182	0.5313	0.5977	**1.94E-09**	0.4088	0.4855	0.8878	0.1871
0.0724	NA	0.0956	0.7624	0.3655	0.2217	0.0614	NA
0.8793	NA	0.8278	0.7389	0.3455	0.2167	0.1071	NA

HDL-C							
N	HIS		BRA		META		EU
P.Int	P.2df	P.Int	P.2df	P.Int	P.2df	P.Int	P.2df
0.6380	0.1177	0.0430	NA	NA	0.0259	0.3399	0.0013
0.4433	0.0547	0.0583	0.7876	0.7094	0.1246	0.3861	**5.47E-15**
0.4364	0.1645	0.1441	0.8563	0.8871	0.1675	0.3893	**6.18E-15**
0.2444	0.0822	0.4130	0.1398	0.6219	**1.33E-20**	0.0833	5.73E-07
0.3690	0.0002	0.0075	0.0040	0.3544	**1.93E-23**	0.3925	0.1879
0.8509	0.1348	0.0490	0.4332	0.9036	0.6318	0.1429	**1.43E-39**
NA	NA	NA	NA	NA	NA	NA	NA
0.4532	0.1894	0.5834	NA	NA	0.5162	0.3791	8.62E-05
0.5461	0.0505	0.4977	0.8801	0.3087	5.18E-06	0.4775	**2.14E-55**
0.3228	0.0792	0.2236	0.9572	0.9166	1.07E-06	0.4825	**1.02E-56**
0.4646	0.3507	0.1689	NA	NA	0.3484	0.0654	6.16E-05
NA	0.3530	0.1671	NA	NA	0.3088	0.0753	0.0002
0.4068	0.1170	0.8925	0.0156	0.7119	**5.11E-30**	0.3535	0.0459
0.0860	4.27E-05	0.3288	0.1062	0.0253	**3.37E-31**	0.0702	**0**
0.0366	4.45E-05	0.3270	0.1160	0.0265	**2.15E-29**	0.1836	**0**
0.2854	0.2014	0.2688	0.7062	0.4345	0.6307	0.1955	**1.29E-08**
0.5976	0.4060	0.7455	NA	NA	0.0006	0.5706	7.59E-05
0.5108	0.5227	0.4311	NA	NA	0.0059	0.3633	0.0914
0.6112	0.3922	0.2378	NA	NA	2.80E-05	0.2125	0.5808
0.4024	0.0114	0.3095	0.0176	0.5507	**5.94E-20**	0.3567	9.32E-07
0.6167	0.0440	0.5005	0.0784	0.4067	**8.50E-20**	0.0670	0.0002
0.5051	0.1303	0.4788	0.0656	0.8632	**1.36E-21**	0.5458	**2.65E-15**
0.0851	0.4689	0.7055	0.0675	0.5772	**7.43E-17**	0.6982	**2.90E-15**
0.0704	0.0271	0.2726	NA	NA	0.2939	0.1186	2.56E-05
0.4719	0.0511	0.8238	0.4631	0.2156	**5.49E-56**	0.0930	0.0538
0.6550	0.8802	0.6437	NA	NA	0.0700	0.5671	0.1171
0.4756	0.5223	0.6582	0.5876	0.9031	0.0002	0.2789	**1.73E-28**
0.5031	0.2983	0.2828	0.5244	0.7333	0.0015	0.2857	**3.30E-27**
0.0017	0.0006	0.4202	0.6600	0.9600	**1.79E-09**	0.0703	**2.81E-192**
0.1734	0.7653	0.4364	0.6052	0.3455	0.0086	0.2566	**5.02E-200**
0.1439	0.2323	0.4474	0.0789	0.0862	0.0010	0.1211	**3.59E-16**
0.0284	0.0129	0.0054	0.6927	0.6674	0.0115	0.0366	**4.28E-09**
0.1681	0.2005	0.3456	0.0657	0.1557	0.0026	0.1637	**8.03E-14**
0.1207	0.8312	0.6882	0.0688	0.1752	0.0784	0.1526	**7.84E-76**
0.0522	0.6908	0.4789	0.0688	0.1057	0.0430	0.0662	**3.03E-70**
0.2798	0.3571	0.2001	0.3831	0.0992	0.0827	0.2027	**1.25E-15**
NA	0.8908	0.6606	NA	NA	0.3026	0.4181	0.6075
0.4194	0.4409	0.1996	0.9496	0.2598	0.3651	0.5862	**6.68E-12**
0.1139	0.2335	0.7124	0.6142	0.7199	0.0002	0.4113	**6.95E-16**
0.0115	0.2984	0.7553	0.7542	0.6556	0.0172	0.3001	**3.54E-14**

0.0167	0.2699	0.6067	0.7504	0.6431	0.0107	0.3282	**1.75E-14**
0.7992	0.6548	0.6077	NA	NA	0.0995	0.1020	0.0004
0.1994	0.9086	0.7138	NA	NA	0.0946	0.4170	0.0002
0.1631	0.8789	0.6919	0.4043	0.4875	7.77E-06	0.7120	**7.04E-10**
0.3547	0.3839	0.4287	NA	NA	0.6530	0.4572	0.6106
0.2670	0.1504	0.3626	0.5796	0.6546	**5.21E-22**	0.0824	0.0777
0.3377	0.1432	0.4059	0.7782	0.7652	**4.07E-23**	0.0751	0.0920
0.8808	0.4197	0.2594	NA	NA	8.97E-06	0.2818	0.0173
0.7150	0.0177	0.2516	0.8050	0.3573	0.0003	0.4998	**3.84E-11**
0.3355	0.6064	0.7530	NA	NA	0.4356	0.6074	0.0013
0.1264	0.0087	0.7174	0.6815	0.7318	**3.19E-16**	0.5180	0.6720
0.0295	0.2242	0.4365	NA	NA	0.3812	0.7746	0.0026
0.3204	0.0650	0.4357	0.0281	0.8589	**9.62E-28**	0.0838	0.0218
0.1185	0.2910	0.6544	0.0269	0.9072	**1.78E-29**	0.0215	0.0132
0.3646	0.1876	0.1596	NA	NA	0.4308	0.1498	1.30E-05
0.3740	0.4202	0.4102	NA	NA	0.0224	0.0044	0.6202
0.3406	0.3236	0.3284	NA	NA	0.2899	0.2473	7.64E-06
0.3343	0.2425	0.1477	0.7585	0.3209	0.0001	0.0878	**1.15E-10**
0.7836	0.6169	0.3476	NA	NA	0.8407	0.8054	0.0022
0.3168	0.4077	0.5327	NA	NA	1.31E-05	0.6598	0.2000
0.4339	0.0204	0.0055	0.9687	0.8777	**2.03E-15**	0.1315	0.0152
0.4081	0.0263	0.0162	0.8994	0.9844	**2.55E-17**	0.1273	0.0142
NA	0.3359	0.1484	NA	NA	0.0002	0.8522	0.1202
NA	0.4252	0.2074	NA	NA	0.2873	0.3410	0.0005
0.5130	0.0032	0.1220	NA	NA	0.0044	0.0452	0.0105
0.1206	0.6294	0.4610	NA	NA	0.2147	0.4399	0.0016
0.4879	0.7614	0.4665	NA	NA	0.3232	0.3592	0.0002
0.6303	0.5991	0.3967	NA	NA	0.0006	0.4516	0.0012
0.6178	0.1919	0.2832	0.0420	0.7817	**1.86E-15**	0.2464	4.98E-06
0.1388	0.0206	0.4268	0.9586	0.6817	**5.05E-18**	0.0106	**3.00E-25**
NA	0.3665	0.5489	NA	NA	0.3406	0.4957	0.0100
0.6877	0.0396	0.0133	NA	NA	0.2574	0.5443	0.0074
NA	0.6597	0.6042	NA	NA	1.14E-07	0.1533	0.0402
0.3075	0.2218	0.2004	NA	NA	0.1140	0.8200	0.7857
0.3803	0.0004	0.4263	0.8515	0.8064	**4.98E-15**	0.7041	0.0003
0.2055	0.2312	0.1786	NA	NA	0.0279	0.0721	0.2327
0.3440	0.4015	0.2294	NA	NA	3.89E-06	0.8500	0.1828
NA	NA	NA	NA	NA	NA	NA	NA
0.4770	0.1032	0.4182	NA	NA	0.0052	0.3193	0.0015
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
NA	0.0697	0.5419	0.0357	0.5302	**4.02E-32**	0.0093	0.0008
0.3915	0.4435	0.4714	NA	NA	0.0029	0.6944	0.6622

0.2214	0.3186	0.3522	NA	NA	0.0003	0.4627	0.0107
0.3079	0.0205	0.7017	0.8414	0.9557	**1.67E-15**	0.4325	0.0249
0.2941	0.3256	0.2088	NA	NA	0.0002	0.0585	0.2879
0.5129	0.2172	0.2270	0.5088	0.3633	0.0031	0.0193	**1.07E-96**
0.6809	0.0755	0.0489	0.5534	0.3720	0.0122	0.0246	**2.29E-107**
0.0498	0.7050	0.4487	NA	NA	0.3695	0.2119	0.0062
0.4694	0.5451	0.7961	0.3753	0.9101	0.7325	0.5590	**3.45E-28**
0.8783	0.8850	0.7222	0.7707	0.8045	0.2960	0.4683	**2.01E-24**
0.5011	0.8677	0.6768	0.0811	0.1343	0.0261	0.1994	**2.05E-20**
NA	0.1511	0.1681	NA	NA	0.6756	0.1215	3.17E-05
0.3763	0.1902	0.1923	NA	NA	0.0008	0.9338	3.87E-07
NA	NA	NA	NA	NA	0.0213	0.1570	0.0004
0.0937	0.5193	0.2696	NA	NA	8.65E-05	0.5498	0.0100
0.4764	0.7281	0.4243	NA	NA	0.0002	0.3594	0.1115
NA	0.1233	0.2476	NA	NA	0.3589	0.7078	0.0281
0.0138	0.7786	0.6778	NA	NA	0.0041	0.4707	0.0100
0.1512	7.34E-06	0.1230	0.5745	0.3974	**8.33E-25**	0.0507	0.0036
0.0219	0.4414	0.3477	NA	NA	0.1680	0.0609	0.0001
0.0278	0.4614	0.4819	NA	NA	0.0999	0.0344	0.0003
0.0212	0.3276	0.2185	0.9022	0.8172	0.2999	0.0535	**3.74E-10**
0.3687	0.6188	0.3368	NA	NA	0.0073	0.3174	5.50E-06
0.1942	0.2563	0.2577	0.7027	0.9938	1.67E-05	0.0124	**7.64E-13**
0.1323	0.2315	0.5315	0.0103	0.1943	**6.39E-13**	0.4543	0.0564
0.4841	0.0186	0.0063	0.0021	0.9787	**1.33E-13**	0.0152	0.0437
0.2129	0.0010	0.0061	0.0060	0.4849	**1.17E-12**	0.0150	0.0369
0.1042	0.3680	0.6235	NA	NA	1.79E-05	0.0270	0.0202
0.3572	0.0396	0.5334	0.8054	0.9311	**5.58E-16**	0.0644	0.0292
0.4360	0.0420	0.5497	0.7641	0.9206	**4.98E-15**	0.0680	0.0345
0.1840	0.1899	0.0830	NA	NA	0.0032	0.2326	0.1443
0.4199	0.0241	0.0050	0.8693	0.7286	0.0958	0.3762	**3.40E-24**
0.5425	0.0149	0.0671	0.8486	0.9492	0.0995	0.1185	**2.94E-23**
NA	0.3165	0.4430	NA	NA	0.0001	0.3478	0.0098
0.5438	0.0058	0.5217	NA	NA	0.0004	0.1500	0.3700
0.4221	0.6838	0.8827	NA	NA	0.0059	0.8940	0.4271
0.5546	0.5832	0.7833	0.4312	0.7264	**9.71E-28**	0.4202	0.1504
0.7900	0.3939	0.6640	0.5808	0.7336	**5.12E-28**	0.5673	0.2038
0.2380	0.7248	0.4313	NA	NA	0.5698	0.6636	1.94E-06
0.4020	0.1884	0.1656	0.7172	0.6191	0.0236	0.1338	**7.30E-13**
0.5521	0.8264	0.7463	0.2047	0.1128	0.2254	0.3108	**1.02E-22**
0.5553	0.7047	0.6413	0.4539	0.0358	0.1764	0.4402	**5.10E-22**
0.0961	0.2405	0.1403	0.0579	0.5189	0.0900	0.3782	**6.08E-35**
0.3608	0.2007	0.3936	NA	NA	0.0002	0.5187	0.0649
0.6895	0.4821	0.9132	NA	NA	0.6667	0.8341	0.6357
0.3129	0.6605	0.5129	NA	NA	0.1575	0.0991	0.7373
NA	NA	NA	NA	NA	0.1692	0.2265	0.4087
0.8073	0.0346	0.7150	0.3116	0.4014	**2.94E-25**	0.5107	0.8801
0.2021	0.0003	0.0789	0.6921	0.4074	**1.79E-13**	0.2572	0.5076

NA	0.0166	0.1848	0.0277	0.0952	**1.60E-26**	0.2626	NA
0.3165	0.6059	0.5524	NA	NA	0.0292	0.2272	0.1957
0.6533	4.65E-05	0.2471	0.0917	0.7217	**1.14E-33**	0.1591	0.0032
0.2007	8.97E-05	0.3817	0.0996	0.7946	**2.45E-35**	0.1181	0.0013
NA	0.9781	0.8964	NA	NA	0.0029	0.0646	0.8300
0.5776	**5.38E-23**	0.0009	0.0803	0.0528	**3.65E-108**	0.0505	**1.45E-37**
0.5604	**6.84E-23**	0.0008	0.1185	0.0643	**4.99E-111**	0.0368	**2.09E-38**
NA	0.2106	0.3893	NA	NA	0.6229	0.6970	0.0998
0.7949	0.0366	0.1329	NA	NA	0.1208	0.0120	0.0827
0.0388	0.2352	0.0969	NA	NA	0.2898	0.3062	NA
0.0188	0.3506	0.3361	0.7159	0.4706	0.0177	0.5402	2.11E-07
0.0098	0.3307	0.3469	0.6932	0.4637	0.0143	0.3544	2.37E-07
0.7242	**1.37E-15**	0.6901	0.0015	0.4561	**0**	0.5405	0.1170
0.6779	**1.73E-11**	0.3275	0.1299	0.6390	**1.61E-172**	0.4915	0.0278
0.0228	0.4317	0.2308	0.0627	0.0744	0.0614	0.1869	**8.58E-19**
0.1843	0.6808	0.7698	0.5877	0.1465	0.7212	0.2249	**2.61E-25**
0.2282	0.6901	0.7876	0.5926	0.1544	0.7049	0.2264	**5.57E-24**
0.1241	0.1282	0.0649	NA	NA	0.0534	0.5784	0.6809
0.1212	0.7512	0.5117	NA	NA	0.0104	0.4022	0.2845
0.0282	0.1269	0.0434	0.0561	0.5015	**1.37E-29**	0.7527	1.48E-05
0.5912	0.1850	0.0982	NA	NA	0.2472	0.2977	0.0004
0.2112	0.0735	0.0548	0.7938	0.8140	**4.16E-14**	0.3242	0.3914
0.7242	0.0011	0.2650	0.9134	0.7480	**7.10E-24**	0.4093	**4.06E-14**
0.3994	0.1529	0.3280	0.2380	0.3069	**2.63E-36**	0.4186	**2.17E-70**
0.5054	0.1017	0.2405	0.2453	0.3271	**2.26E-36**	0.4491	**1.85E-70**
0.6503	0.7168	0.8183	NA	NA	0.0007	0.3969	0.0596
0.1387	0.4752	0.2153	NA	NA	0.0268	0.0198	5.91E-05
0.0364	0.3949	0.1808	NA	NA	0.0483	0.0245	5.20E-05
0.5797	0.2420	0.2424	NA	NA	0.4373	0.3188	5.52E-05
0.7912	0.1489	0.5529	0.5624	0.4154	**4.38E-40**	0.7749	0.0974
0.5165	0.0658	0.2640	0.8926	0.7780	**1.75E-28**	0.3850	0.0524
0.5451	0.7568	0.4949	NA	NA	0.0360	0.0607	0.0006
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
0.6859	1.67E-06	0.3158	0.0116	0.2527	**5.10E-152**	0.3125	**5.04E-10**
0.1920	0.3932	0.4092	0.6632	0.8085	**7.87E-12**	0.7256	0.0004
0.0346	0.6132	0.7797	0.3517	0.8570	0.1823	0.1418	**1.17E-21**
0.1199	0.4107	0.2843	0.4273	0.5328	6.41E-05	0.6624	**2.37E-67**
0.0348	0.1290	0.0949	0.6081	0.4475	1.35E-05	0.6842	**1.62E-83**
0.3705	0.8755	0.5372	NA	NA	0.2066	0.1541	0.2141
0.3347	0.9427	0.6129	NA	NA	0.3486	0.1795	0.8234
0.7765	0.4453	0.3478	NA	NA	0.1324	0.2513	0.0205
0.7600	0.6228	0.4230	NA	NA	0.0010	0.8275	0.5627
0.5428	0.0072	0.4058	0.3498	0.2382	1.90E-07	0.6648	3.92E-07
0.7657	0.0383	0.5962	0.1946	0.2346	**4.31E-09**	0.1944	9.90E-07
0.6717	0.1069	0.1240	0.7682	0.8712	**3.47E-16**	0.0392	**4.06E-08**
0.6461	8.53E-05	0.3969	0.0013	0.3881	**5.94E-30**	0.3604	**1.38E-10**

0.3062	0.4881	0.2496	NA	NA	0.0689	0.4108	0.2449
NA	NA	NA	NA	NA	NA	NA	NA
0.4135	0.0655	0.5921	NA	NA	0.0002	0.2627	0.1151
0.1152	0.1340	0.0650	NA	NA	0.0015	0.1427	0.5763
0.3786	0.5096	0.6646	NA	NA	0.2021	0.2816	8.78E-06
0.3185	0.5877	0.7229	NA	NA	0.2002	0.1015	2.13E-06
0.0321	0.2191	0.0659	0.2928	0.1326	**2.43E-22**	0.0359	0.2146
0.6274	0.0060	0.0062	0.1863	0.9817	**3.08E-43**	0.1061	0.3161
0.6761	0.0050	0.2579	0.2229	0.9333	**1.09E-27**	0.8716	0.4916
0.0984	0.4748	0.3344	NA	NA	0.0027	0.1734	0.7661
0.4902	0.2193	0.6099	0.5450	0.5187	**1.33E-14**	0.1986	0.3516
NA	NA	NA	NA	NA	NA	NA	NA
0.4439	0.1551	0.6894	NA	NA	0.0002	0.3731	0.1364
0.4100	0.2296	0.2634	0.4443	0.9354	**1.09E-12**	0.4810	0.4377
0.7825	0.0773	0.5402	0.2233	0.8965	**3.92E-10**	0.5611	**4.47E-14**
0.1893	**4.35E-08**	0.2877	0.1736	0.0308	**2.86E-48**	0.1379	**7.18E-46**
0.1660	7.24E-08	0.6107	0.0562	0.0155	**1.54E-48**	0.1422	**8.60E-45**
0.0088	0.0837	0.1209	NA	NA	0.0069	0.3522	0.3455
0.2927	0.8410	0.5850	NA	NA	0.0025	0.1427	0.3064
0.1394	**7.13E-09**	0.6475	0.3297	0.9499	**2.72E-118**	0.1154	**9.82E-37**
0.1242	**4.50E-09**	0.5668	0.5226	0.6044	**1.90E-121**	0.0469	**1.26E-27**
0.1199	**1.62E-23**	0.0121	0.0005	0.5465	**1.51E-237**	0.0023	**5.47E-46**
0.1210	0.0241	0.0258	0.2976	0.1438	2.53E-07	0.0132	0.0008
NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA
0.9112	0.2536	0.2234	NA	NA	0.0046	0.2118	0.1795
0.5801	0.5968	0.3072	NA	NA	0.0001	0.3276	0.0094
0.5011	0.6571	0.3561	NA	NA	0.0001	0.6330	0.0054
0.3804	0.0098	0.1590	0.3263	0.1681	0.0041	0.8549	**1.75E-16**
0.4929	0.1847	0.1254	NA	NA	0.0291	0.4271	0.3525
0.4211	0.4956	0.2909	NA	NA	6.54E-06	0.4012	0.0200
0.0648	0.7267	0.4275	NA	NA	7.78E-05	0.2411	0.1970
0.6046	0.1899	0.2223	NA	NA	0.0011	0.9072	0.1745
0.6900	0.1787	0.1403	NA	NA	0.0005	0.7971	0.1860
0.5560	0.0776	0.1794	0.3568	0.0500	**4.09E-19**	0.3135	**3.68E-20**
0.2915	0.0581	0.1807	0.4363	0.0895	**1.51E-18**	0.2614	0.0014
0.1166	0.1959	0.1197	NA	NA	0.0002	0.2557	0.1953
0.1245	0.0004	0.3810	0.2868	0.8881	**2.62E-28**	0.3027	0.0185
0.1022	0.0005	0.3864	0.3032	0.8392	**1.06E-28**	0.3502	0.0120
NA	0.4552	0.7490	NA	NA	0.0004	0.1454	0.0006
NA	0.6052	0.7996	NA	NA	0.0030	0.1299	0.0040
NA	NA	NA	NA	NA	NA	NA	NA
0.3134	0.2676	0.1433	0.6794	0.9014	0.1653	0.5264	5.38E-06
0.2832	0.0966	0.0259	0.2282	0.6852	0.0052	0.6693	**1.92E-09**
0.5705	0.1068	0.4347	0.1914	0.2281	**3.81E-11**	0.3368	**3.94E-27**
0.0195	0.0114	0.3235	0.2518	0.1717	**1.61E-28**	0.0199	0.0088
0.0637	0.0251	0.4096	0.6482	0.8462	**1.88E-33**	0.2510	0.0052

0.3509	0.5182	0.4738	0.2848	0.8687	**1.96E-22**	0.1473	0.4909
0.3797	0.1581	0.5025	0.0962	0.9083	**4.29E-30**	0.7817	0.4161
0.2024	0.0030	0.7998	0.0363	0.7807	**5.42E-23**	0.7494	0.7051
0.4960	0.3420	0.1745	0.1310	0.9329	0.1241	0.5169	**1.77E-09**
0.7536	0.2441	0.4453	NA	NA	0.3149	0.3590	0.0128
0.3710	0.9581	0.9172	0.9556	0.9119	0.1689	0.0983	**1.56E-12**
0.1352	0.2619	0.1404	NA	NA	0.0053	0.6959	0.9473
0.4500	0.2604	0.2480	NA	NA	4.45E-05	0.5965	0.0246
0.0717	0.0309	0.0745	0.0797	0.3003	6.65E-07	0.1367	0.6938
0.6855	0.0006	0.0170	0.1225	0.6905	**5.55E-13**	0.2501	0.2944
0.1179	0.0009	0.0007	0.5137	0.6431	**5.13E-09**	0.1558	0.1755
0.0308	**3.31E-20**	0.6678	0.0007	0.1118	**0**	0.3532	0.4698
0.1280	**5.49E-12**	0.0154	5.84E-08	0.4096	**3.83E-234**	0.0737	0.0015
0.3173	0.2593	0.4293	0.3117	0.7243	**2.77E-09**	0.6367	0.1489
0.5960	0.3453	0.2536	NA	NA	0.1612	0.2287	0.0947
0.0298	0.4470	0.2269	NA	NA	0.6681	0.5673	0.7747
0.0290	0.4460	0.2082	NA	NA	0.6438	0.4712	0.7669
NA	0.2692	0.3702	NA	NA	0.0013	0.2136	0.1960
0.8009	0.5774	0.2916	NA	NA	0.0224	0.0601	0.5813
0.5311	0.8677	0.8523	NA	NA	0.0229	0.0121	0.1176
0.2849	0.2973	0.4056	NA	NA	0.0003	0.5033	0.0689
0.3898	0.2645	0.7644	NA	NA	0.0004	0.6650	0.0976
0.3269	**3.65E-23**	0.5146	0.0092	0.8040	**0**	0.3994	**3.97E-18**
0.0139	**5.65E-105**	0.1640	**1.69E-16**	0.2983	**0**	0.0051	**2.84E-27**
0.3599	**4.14E-31**	0.4100	0.0057	0.8001	**0**	0.0380	0.0019
0.2820	0.1550	0.3486	0.2284	0.9547	**2.39E-23**	0.0418	0.6572
0.5084	**3.04E-12**	0.3734	1.66E-06	0.1837	**2.00E-86**	0.1060	0.2667
0.0529	0.7987	0.6437	0.3694	0.3822	0.8663	0.6844	**2.50E-15**
0.0105	0.0566	0.0189	0.9595	0.6936	0.2103	0.0551	**4.75E-42**
0.4189	0.0039	0.3091	0.5396	0.5469	**1.00E-44**	0.0366	0.3604
0.2072	0.7096	0.4190	NA	NA	0.6178	0.2175	0.0364
0.5409	0.3059	0.7876	NA	NA	0.2344	0.5968	1.06E-06
NA	NA	NA	NA	NA	NA	NA	NA
0.9512	0.0510	0.1906	0.0256	0.3374	**3.86E-37**	0.3513	0.0023
0.8557	0.0482	0.2381	0.0203	0.3317	**4.49E-36**	0.4364	0.0047
NA	0.2114	0.7826	NA	NA	0.0088	0.0014	0.6147
0.0996	0.3854	0.1626	NA	NA	0.1809	0.2594	4.65E-06
0.5621	0.4677	0.2709	0.5441	0.7172	6.05E-06	0.1485	**7.73E-17**
NA	NA	NA	NA	NA	0.2128	0.4419	2.25E-06
0.4750	0.2835	0.4283	NA	NA	0.0124	0.0619	0.0050
0.1103	0.3858	0.3612	0.8819	0.7086	**2.46E-15**	0.3040	0.0010
0.1396	0.4194	0.3999	0.8786	0.6941	**9.96E-16**	0.4728	0.0017
0.3361	0.0045	0.1631	0.0810	0.1198	**1.72E-28**	0.2381	0.0001
0.0290	0.0261	0.1951	0.2925	0.3576	**3.68E-22**	0.4151	9.99E-07
0.2238	0.0036	0.3262	0.0003	0.0054	**3.55E-101**	0.6480	1.15E-05
0.6140	4.95E-06	0.0391	9.35E-06	0.0006	**4.32E-115**	0.3521	1.21E-05
0.1198	0.0397	0.3294	0.1239	0.3811	**8.87E-53**	0.5363	0.0002

0.0337	0.4764	0.7133	NA	NA	1.42E-06	0.3782	0.7991
0.3252	0.0019	0.0003	0.0856	0.8446	**3.10E-14**	0.0614	0.2714
0.1797	0.1344	0.3418	NA	NA	0.2611	0.2254	0.0201
0.1955	0.1073	0.6670	0.8096	0.6401	1.98E-05	0.0590	0.6635
0.2106	0.0595	0.0732	0.6734	0.4645	**7.29E-21**	0.5578	0.0277
0.2717	0.0156	0.0583	0.5686	0.4996	**1.38E-22**	0.5319	0.0334
0.1972	0.3976	0.6565	0.6173	0.4340	1.24E-05	0.7908	**0**
0.5360	0.0743	0.0389	0.2269	0.7388	0.0004	0.0108	**2.14E-61**
0.0240	**2.07E-18**	0.1274	0.0724	0.9129	**1.35E-62**	0.0065	0.5383
NA	NA	NA	NA	NA	NA	NA	NA
0.0150	0.2312	0.1674	0.8353	0.4900	1.25E-06	0.0010	**5.12E-58**
0.0986	0.0890	0.1161	NA	NA	0.0020	0.4940	0.6727
0.5526	0.2187	0.4011	NA	NA	0.1250	0.1113	0.1145
0.1760	0.0006	0.2353	0.0547	0.0801	**2.06E-18**	0.0285	**4.67E-125**
0.5925	0.0052	0.1497	0.3933	0.6026	**1.47E-23**	0.3211	**0**
0.1442	4.51E-05	0.0677	0.0405	0.1391	**1.67E-90**	0.1308	**1.01E-289**
0.0719	0.9423	0.7933	0.0578	0.1580	0.0046	0.5101	**1.10E-18**
0.1084	0.0555	0.1077	0.1776	0.0380	**3.48E-17**	0.5706	0.5832
0.6343	0.0150	0.4083	0.1100	0.7891	**5.11E-50**	0.3485	0.0993
0.6580	3.91E-06	0.8286	0.1890	0.4554	**9.23E-61**	0.4229	0.1530
0.0917	0.0724	0.0247	NA	NA	0.9592	0.5588	0.0003
0.3782	0.7644	0.9317	0.6286	0.5913	0.0851	0.4243	**2.67E-85**
0.4441	0.4471	0.5006	NA	NA	0.0062	0.5340	0.0005
0.2976	0.5686	0.2913	NA	NA	0.0177	0.5370	0.0002
0.8810	0.3296	0.6385	NA	NA	0.5382	0.1201	1.10E-05
0.2762	0.6540	0.4873	0.5978	0.6170	0.3483	0.5880	**1.03E-22**
0.2613	0.2185	0.1638	0.0854	0.0682	0.0617	0.2021	**2.83E-27**
0.3463	0.4952	0.5198	0.0743	0.0568	0.0947	0.1238	**1.26E-26**
0.7821	**3.68E-17**	0.0404	0.0001	0.5482	**1.07E-71**	0.1166	**9.73E-10**
0.4220	0.1022	0.2875	0.3965	0.9641	**2.18E-64**	0.0972	0.0912
0.3878	0.0369	0.3290	0.3559	0.6811	**6.99E-62**	0.0734	0.0835
NA	NA	NA	NA	NA	0.0073	0.1826	NA
0.7006	0.0006	0.3032	0.6184	0.4379	**4.95E-26**	0.3975	0.0004
0.6221	0.7335	0.4497	NA	NA	0.0481	0.3477	0.1161
0.5930	0.6823	0.4863	NA	NA	0.0058	0.1119	0.0092
0.5206	0.2135	0.0971	NA	NA	0.0005	0.2961	0.0436
0.7050	0.0596	0.1369	0.8433	0.7117	**1.56E-08**	0.4080	0.1114
NA	0.1010	0.0792	NA	NA	0.5346	0.2470	0.0150
NA	0.1890	0.6169	NA	NA	0.4852	0.1314	0.0100

LDL-C								
JR	AFR		ASN		HIS		BRA	
P.Int	P.2df	P.Int	P.2df	P.Int	P.2df	P.Int	P.2df	P.Int
0.6993	0.3552	0.4566	0.0014	0.0002	0.5337	0.6487	NA	NA
0.3558	0.0141	0.0765	0.0007	0.2653	0.0014	0.1885	0.0233	0.0753
0.3371	0.3191	0.3089	0.0007	0.2093	0.0072	0.1388	0.0045	0.1030
0.0804	0.2790	0.3699	0.3005	0.9311	0.0543	0.0508	0.4970	0.9620
0.2440	0.8237	0.6440	0.0964	0.6580	0.0497	0.1294	0.5219	0.8931
0.0828	0.0725	0.4542	0.0067	0.2270	0.0003	0.0075	0.0670	0.4236
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.3591	0.1412	0.7284	0.3784	0.2957	0.0386	0.0491	NA	NA
0.4830	2.40E-07	0.0799	0.0005	0.1880	0.0003	0.3797	0.1242	0.1526
0.6228	0.0029	0.3663	0.0126	0.6489	0.0012	0.6782	0.1326	0.3612
0.3275	0.0170	0.4101	0.6016	0.4706	0.3708	0.1726	NA	NA
0.4083	0.0167	0.4757	0.6546	0.5305	0.3679	0.1689	NA	NA
0.2514	0.9548	0.4891	0.0082	0.6001	0.2255	0.4441	0.5007	0.4931
0.3330	**7.69E-26**	0.6759	**2.97E-48**	0.0138	**1.76E-45**	0.4112	**5.51E-11**	0.8426
0.5013	**1.81E-26**	0.7621	**4.03E-50**	0.0156	**1.34E-45**	0.4091	**3.78E-11**	0.8990
0.2624	0.0074	0.3597	0.1297	0.1216	0.2089	0.1064	0.3336	0.4538
0.6539	0.1093	0.3821	0.7165	0.4786	0.6926	0.3794	NA	NA
0.0362	0.1836	0.1731	0.5290	0.3951	0.1038	0.3102	NA	NA
0.4687	0.1884	0.0433	0.3233	0.7783	0.0976	0.0322	NA	NA
0.0745	0.5452	0.7984	0.2042	0.4810	0.0841	0.0202	0.7532	0.8625
0.0632	0.4023	0.5443	0.4097	0.5630	0.0954	0.0224	0.9910	0.7138
0.7117	0.2528	0.2241	7.45E-06	0.0377	0.0002	0.5528	0.1437	0.8009
0.4863	0.1078	0.2800	0.0002	0.0602	0.0002	0.7932	0.0090	0.7942
0.3168	0.0730	0.5236	0.0116	0.0203	0.4313	0.7326	NA	NA
0.1707	0.1155	0.2203	0.0405	0.3207	0.4587	0.4961	0.6010	0.9621
0.1334	0.8004	0.5040	0.1752	0.1757	0.0230	0.0068	NA	NA
0.0728	0.0008	0.0194	4.88E-06	0.7028	0.0155	0.0475	0.1575	0.0429
0.0817	0.0470	0.3193	1.35E-05	0.4193	0.0300	0.0329	0.0723	0.0099
0.3336	0.0001	0.5270	**1.08E-16**	0.7671	**8.14E-28**	0.3176	0.1952	0.4687
0.4939	0.0004	0.7191	2.76E-07	0.2617	**4.70E-15**	0.2915	0.0007	0.2212
0.0955	0.0138	0.4846	0.0062	0.0689	0.0103	0.2832	0.0679	0.0478
0.0941	0.0632	0.6165	0.1519	0.8908	0.4656	0.3776	0.3533	0.8285
0.0358	0.1346	0.7761	0.0065	0.0203	0.0045	0.2184	0.0180	0.0219
0.3638	2.73E-07	0.4676	0.0007	0.2303	**2.33E-10**	0.0336	0.2791	0.7515
0.3793	7.74E-08	0.4463	0.0019	0.1289	**8.34E-10**	0.0459	0.4535	0.5709
0.2258	0.1706	0.0757	0.1120	0.8377	0.5867	0.3904	0.4757	0.2915
0.8093	0.9312	0.6053	NA	NA	0.4168	0.3636	NA	NA
0.4534	0.2179	0.2297	6.55E-05	0.1206	0.0006	0.5252	0.8832	0.9328
0.0170	0.2600	0.2137	0.3029	0.7203	0.2615	0.6569	0.0368	0.0970
0.0081	0.1059	0.1012	0.6869	0.4651	0.0745	0.7259	0.0465	0.1312

0.0069	0.1039	0.0829	0.6378	0.2879	0.0573	0.7063	0.0467	0.1335
0.0695	0.4817	0.2769	0.1927	0.6250	0.2698	0.7765	NA	NA
0.1372	0.3653	0.3814	0.0386	0.0557	0.4860	0.3269	NA	NA
0.3466	0.0754	0.6688	0.0015	0.0476	0.0448	0.6129	0.4076	0.8947
0.3886	0.2001	0.1057	0.1382	0.0490	0.1750	0.0507	NA	NA
0.3595	0.1678	0.1930	0.3565	0.2190	0.1714	0.1720	0.4221	0.3958
0.4637	0.0971	0.1673	0.3339	0.2928	0.1560	0.1670	0.3846	0.4941
0.1247	0.0954	0.1117	0.3084	0.1795	0.2995	0.3329	NA	NA
0.3963	0.3622	0.4413	0.0310	0.7685	0.1948	0.5051	0.1124	0.9903
0.3410	0.4239	0.4833	0.2176	0.5608	0.3865	0.6050	NA	NA
0.8180	0.1967	0.2699	0.8275	0.3250	0.5645	0.4871	0.1194	0.0440
0.5590	0.1177	0.1736	0.4768	0.6333	0.3885	0.3238	NA	NA
0.0757	0.7702	0.5190	0.4983	0.2845	0.4417	0.2442	0.8065	0.8387
0.0313	0.6678	0.2504	0.6786	0.4062	0.5892	0.3553	0.6235	0.9540
0.8594	0.0156	0.3068	0.5749	0.7490	0.1982	0.1118	NA	NA
0.3057	0.2309	0.2677	0.3798	0.9444	0.0844	0.3598	NA	NA
0.0711	0.3392	0.3792	0.2997	0.4157	0.0043	0.0731	NA	NA
0.2514	0.3808	0.1043	0.8220	0.6738	0.0297	0.0093	0.1418	0.0907
0.4462	0.0261	0.0537	0.0783	0.4266	0.2360	0.4779	NA	NA
0.1549	0.5040	0.7619	0.2635	0.2292	0.5885	0.3682	NA	NA
0.0168	0.0191	0.0768	0.2178	0.2454	0.2754	0.1546	0.2958	0.6027
0.0145	0.0908	0.8295	0.2384	0.2726	0.2545	0.1465	0.5824	0.4460
0.0265	0.3323	0.3199	NA	NA	0.5655	0.4685	NA	NA
0.2113	0.5349	0.8164	NA	NA	0.6229	0.3144	NA	NA
0.0780	0.3069	0.0384	0.1135	0.3943	0.7068	0.5455	NA	NA
0.4619	0.1393	0.7880	0.3492	0.8152	0.0964	0.7086	NA	NA
0.1250	0.2465	0.5393	0.5689	0.7548	0.1380	0.6165	NA	NA
0.0227	0.4816	0.1546	0.1856	0.0855	0.0776	0.4148	NA	NA
0.5898	0.2152	0.0815	0.5305	0.1593	0.2297	0.2746	0.5817	0.4097
0.6772	0.2154	0.0781	0.0523	0.7352	0.2457	0.1106	0.4652	0.1802
0.0121	0.6062	0.5805	NA	NA	0.1842	0.1217	NA	NA
0.3965	0.6462	0.4303	0.0613	0.3088	0.0150	0.0139	NA	NA
0.1195	0.2004	0.1518	NA	NA	0.8101	0.6873	NA	NA
0.5237	0.5077	0.2191	0.6090	0.6662	0.1227	0.3632	NA	NA
0.4724	0.2730	0.7589	0.0004	0.0411	0.5852	0.5994	0.0437	0.1987
0.6165	0.0220	0.1710	0.4054	0.8195	0.4912	0.2917	NA	NA
0.6325	0.4090	0.1825	0.1895	0.1396	0.4059	0.2794	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.0006	0.6422	0.5119	0.0841	0.0245	0.0975	0.1013	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.4614	0.1528	0.1913	NA	NA	0.0055	0.0772	0.6722	0.5089
0.4442	0.0344	0.6287	0.4645	0.2560	0.6009	0.3930	NA	NA

0.3086	0.1999	0.3033	0.8352	0.6053	0.4398	0.4769	NA	NA
0.0451	0.0432	0.0272	0.2388	0.3804	0.1527	0.7995	0.0745	0.0416
0.0779	0.5056	0.2989	0.5796	0.0450	0.1333	0.0592	NA	NA
0.0742	0.0007	0.4314	**7.02E-28**	0.7127	**3.05E-14**	0.2354	0.1206	0.8946
0.0679	7.57E-05	0.5747	**2.53E-32**	0.5922	**2.79E-15**	0.0266	0.0147	0.7392
0.4021	0.0433	0.0788	0.0141	0.0742	0.2660	0.1902	NA	NA
0.4833	0.0004	0.3319	2.89E-06	0.1113	0.0001	0.1712	0.0017	0.2962
0.1279	0.0361	0.0403	0.3623	0.1740	0.1052	0.2743	0.0766	0.0636
0.8740	0.0023	0.0129	0.1756	0.2501	0.0030	0.3315	0.9020	0.7374
0.5388	0.6529	0.3645	NA	NA	0.4187	0.2360	NA	NA
0.6138	0.6446	0.4097	0.0114	0.0034	0.0331	0.0410	NA	NA
0.3713	0.0603	0.1425	0.1373	0.3246	NA	NA	NA	NA
0.1080	0.3475	0.1922	0.1230	0.0543	0.7483	0.2772	NA	NA
0.1794	0.0170	0.0036	0.7884	0.9494	0.8347	0.5938	NA	NA
0.3185	0.0640	0.0786	NA	NA	0.8044	0.7596	NA	NA
0.8585	0.3172	0.3356	0.4568	0.2615	0.7217	0.5807	NA	NA
0.0884	0.3079	0.2051	0.0144	0.1154	0.1142	0.2740	0.6106	0.3884
0.0351	0.0184	0.3591	0.7533	0.4004	0.1807	0.3893	NA	NA
0.0419	0.0015	0.3450	0.2925	0.0683	0.2740	0.2372	NA	NA
0.2126	0.4429	0.1380	0.5530	0.2863	0.2806	0.4944	0.9387	0.9071
0.3325	0.1744	0.3432	0.4322	0.2371	0.0589	0.5813	NA	NA
0.9700	0.1509	0.0937	0.1000	0.8543	0.1641	0.3575	0.0266	0.0107
0.2195	0.0484	0.0256	0.1663	0.7454	0.2330	0.1346	0.3599	0.3959
0.5175	0.2165	0.1674	0.2256	0.0732	0.5540	0.2705	0.2579	0.3697
0.7546	0.6234	0.6881	0.2213	0.0396	0.7769	0.5478	0.5057	0.9478
0.4123	0.7145	0.4270	0.0333	0.3173	0.4628	0.5873	NA	NA
0.3239	0.9668	0.9282	0.2557	0.6987	0.6414	0.4655	0.6686	0.8034
0.2786	0.9175	0.7157	0.2422	0.6707	0.6246	0.4454	0.6838	0.8187
0.0447	0.0423	0.0151	0.1178	0.2067	0.7562	0.5477	NA	NA
0.2139	0.1014	0.2703	0.5402	0.8631	0.0124	0.0254	0.3242	0.9276
0.4338	0.0055	0.1911	0.0279	0.6860	1.39E-05	0.1459	0.1001	0.0564
0.3189	0.6473	0.2623	NA	NA	0.7110	0.5257	NA	NA
0.2638	0.1542	0.0163	0.7174	0.7467	0.8050	0.5502	NA	NA
0.2153	0.9159	0.6208	0.6199	0.4530	0.5658	0.3278	NA	NA
0.2708	0.0913	0.5522	0.0879	0.3656	0.7966	0.6250	0.6176	0.7635
0.3807	0.1902	0.4902	0.0841	0.3247	0.8859	0.7709	0.3891	0.7376
0.1734	0.4763	0.3048	0.3885	0.4906	0.3611	0.3410	NA	NA
0.5326	0.1902	0.3435	0.0100	0.7891	0.0050	0.1721	0.0003	0.3806
0.2908	0.0708	0.0090	0.2246	0.8031	0.7393	0.4530	0.3602	0.1803
0.0581	0.0164	0.0268	0.1726	0.8277	0.1032	0.9451	0.7527	0.3812
0.2151	0.0135	0.1938	0.0515	0.5724	0.0144	0.0148	0.1320	0.3588
0.0166	0.0611	0.0166	0.7378	0.6622	0.5364	0.3503	NA	NA
0.1401	0.9042	0.7647	0.0369	0.4482	0.1325	0.0675	NA	NA
0.4570	0.4508	0.2278	0.2732	0.5711	0.7881	0.4946	NA	NA
0.1740	NA	NA	NA	NA	NA	NA	NA	NA
0.7812	0.6194	0.4786	0.0006	0.1681	0.1526	0.0961	0.5551	0.5484
0.5519	0.1039	0.6895	0.1231	0.6410	0.4528	0.6242	0.1210	0.0699

NA	0.6584	0.3807	NA	NA	0.1687	0.0889	0.2655	0.1243
0.3354	0.4832	0.2022	0.0978	0.1820	0.0860	0.1865	NA	NA
0.6903	0.7769	0.6339	0.0999	0.1673	0.8470	0.6995	0.2826	0.4336
0.4384	0.6691	0.6068	0.0821	0.2081	0.8246	0.7429	0.2345	0.4591
0.4736	0.0445	0.0044	NA	NA	0.8566	0.6396	NA	NA
0.5490	3.61E-06	0.4341	**1.55E-08**	0.6550	0.0327	0.3392	0.1296	0.3577
0.4611	2.08E-06	0.4083	**1.24E-08**	0.6708	0.0323	0.2831	0.1109	0.3026
0.4832	0.3748	0.3555	NA	NA	0.4585	0.2184	NA	NA
0.0840	0.6808	0.4413	0.6863	0.5710	0.4892	0.6256	NA	NA
NA	0.1923	0.0827	0.2604	0.2129	0.8542	0.7022	NA	NA
0.6006	0.0972	0.2207	0.2002	0.6487	0.0905	0.2809	0.4872	0.5110
0.6494	0.0854	0.3610	0.1920	0.6244	0.0877	0.2496	0.5496	0.6376
0.0781	0.4618	0.5148	0.4007	0.6523	0.8649	0.5609	0.5486	0.5075
0.0895	0.1311	0.0437	0.7335	0.4989	0.4775	0.3519	0.5311	0.2486
0.0170	0.0071	0.6558	0.0445	0.0908	0.4004	0.2282	0.0255	0.3871
0.3208	0.8638	0.8869	2.45E-06	0.0253	0.2161	0.4107	0.5496	0.6049
0.6047	0.9208	0.8547	6.99E-06	0.0327	0.2044	0.4244	0.5338	0.5786
0.5616	0.0839	0.3732	0.6006	0.4879	0.3604	0.2330	NA	NA
0.4840	0.0371	0.0258	0.6290	0.3993	0.5187	0.6144	NA	NA
0.6357	0.0196	0.2345	0.0120	0.1775	0.8231	0.5929	0.4218	0.3818
0.8392	0.4780	0.2686	0.0159	0.2803	0.3552	0.1983	NA	NA
0.2179	0.6643	0.5208	0.5736	0.4230	0.7369	0.4363	0.1218	0.8203
0.4317	0.5638	0.2763	5.01E-05	0.3319	0.2433	0.7497	0.7025	0.2793
0.1341	0.5577	0.6922	**1.41E-11**	0.5387	9.27E-06	0.1289	0.1395	0.0585
0.1340	0.1565	0.5847	**5.18E-11**	0.4963	7.13E-06	0.1438	0.2446	0.1110
0.1357	0.6024	0.5637	0.5060	0.6502	0.3814	0.5931	NA	NA
0.5718	0.1350	0.1835	0.4379	0.2107	0.2961	0.3087	NA	NA
0.6538	0.0955	0.2463	0.4377	0.1864	0.2995	0.4987	NA	NA
0.1277	0.2799	0.6255	0.2432	0.7436	0.3014	0.1753	NA	NA
0.2885	0.0014	0.1610	0.4897	0.8293	0.1420	0.0741	0.0365	0.0179
0.0424	0.1316	0.6585	0.5234	0.4421	0.2114	0.0677	0.0239	0.0090
0.6002	0.6222	0.4973	0.4738	0.2986	0.1946	0.8224	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.5833	0.5661	0.4832	0.0181	0.2363	0.0006	0.0506	0.1761	0.7055
0.1893	0.4955	0.4332	0.7584	0.9432	0.0913	0.4244	0.6308	0.5428
0.4701	0.0578	0.0656	0.0038	0.1212	0.2920	0.3547	0.6213	0.6949
0.3123	0.0001	0.1668	**1.16E-10**	0.2302	**1.84E-08**	0.7912	0.0129	0.9618
0.2818	0.0003	0.2511	**1.96E-08**	0.3893	**4.68E-10**	0.7675	0.0025	0.9138
0.2709	0.2931	0.1739	0.0070	0.2330	0.5519	0.2666	NA	NA
0.6694	0.7768	0.6626	0.5077	0.7436	0.9368	0.7449	NA	NA
0.6724	0.0642	0.1308	0.5437	0.6362	0.4570	0.2149	NA	NA
0.4920	0.3216	0.1186	0.2373	0.1670	0.4708	0.4582	NA	NA
0.1635	0.1644	0.1853	0.0605	0.8556	0.5887	0.3733	0.4579	0.4879
0.0802	0.1067	0.2275	0.0021	0.9215	0.5613	0.4433	0.5602	0.4998
0.0934	0.0020	0.0683	0.1574	0.7619	0.1490	0.2132	0.4013	0.4091
0.4914	0.7217	0.6654	0.0004	0.1891	0.0097	0.7873	0.2834	0.3007

0.1067	0.0131	0.0050	0.3906	0.1079	0.0433	0.2626	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.0133	0.0330	0.2070	0.1656	0.1033	0.9074	0.7578	NA	NA
0.7170	0.4307	0.1567	0.1720	0.1126	0.2828	0.1537	NA	NA
0.3478	0.6770	0.4555	0.0158	0.1785	0.4935	0.3495	NA	NA
0.2732	0.8169	0.6522	0.0678	0.2747	0.4879	0.3444	NA	NA
0.1634	0.0435	0.1866	0.7612	0.7048	0.0434	0.0340	0.6261	0.5928
0.8521	0.5173	0.8992	0.7535	0.7866	0.5587	0.2910	0.2588	0.6119
0.4813	0.5298	0.7313	0.9732	0.6799	0.0133	0.0285	0.9819	0.9402
0.7104	0.2143	0.0465	0.0794	0.3256	0.3150	0.1313	NA	NA
0.6388	0.2678	0.1084	0.6921	0.9366	0.2947	0.4245	0.5531	0.2745
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.1056	0.8802	0.7964	0.2735	0.3531	0.4042	0.1514	NA	NA
0.4975	0.6918	0.5149	0.2633	0.5118	0.6924	0.4900	0.3651	0.4413
0.2278	0.9090	0.5157	0.4044	0.7383	0.0309	0.4737	0.7532	0.3860
0.0301	0.0831	0.1542	0.0001	0.1086	**2.31E-11**	0.0036	0.2117	0.8498
0.0498	0.1200	0.1257	0.0002	0.0917	**2.51E-10**	0.0050	0.2193	0.8672
0.5217	0.0287	0.0335	0.6707	0.5876	0.0158	0.0029	NA	NA
0.1603	0.3448	0.5465	0.2275	0.2280	0.3625	0.4052	NA	NA
0.0755	0.0525	0.3586	0.7098	0.4228	0.1443	0.6698	0.4252	0.1956
0.3854	0.0066	0.3957	0.6671	0.3675	0.1496	0.8150	0.1500	0.1779
0.0722	0.0863	0.7217	0.6010	0.3537	0.0053	0.4992	0.0388	0.1095
0.8700	0.3616	0.1312	0.1738	0.3414	0.6270	0.4663	0.1918	0.1251
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.2947	0.5510	0.7370	0.7544	0.4831	0.7194	0.4515	NA	NA
0.3677	0.2269	0.7554	0.2683	0.8855	0.0301	0.3740	NA	NA
0.2224	0.1959	0.4813	0.3646	0.8039	0.0364	0.4312	NA	NA
0.1211	0.0197	0.6574	0.0040	0.4785	0.0010	0.5236	0.4777	0.2875
0.1285	0.2077	0.2200	0.0080	0.0043	0.4742	0.2456	NA	NA
0.6112	0.2149	0.5741	0.2656	0.4861	0.2333	0.2155	NA	NA
0.2965	0.7944	0.6393	0.2368	0.6090	0.0919	0.1534	NA	NA
0.1295	0.1726	0.2282	0.3763	0.8979	0.3780	0.7033	NA	NA
0.1158	0.2073	0.1383	0.3464	0.8323	0.2076	0.5781	NA	NA
0.0573	0.2486	0.3953	0.5554	0.9180	0.2841	0.4069	0.1941	0.7744
0.0466	0.5112	0.3749	0.3127	0.8850	0.3836	0.4916	0.5960	0.9392
0.1539	0.0931	0.2967	0.0880	0.4470	0.5741	0.5280	NA	NA
0.4537	0.3047	0.6309	0.2079	0.1739	0.9301	0.7280	0.4179	0.7242
0.3018	0.2556	0.3241	0.3345	0.3242	0.9503	0.8419	0.3822	0.7034
0.1310	0.0045	0.1047	NA	NA	0.0135	0.2334	NA	NA
0.1182	7.99E-05	0.0564	NA	NA	0.0647	0.3130	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.4298	0.0071	0.3828	0.2139	0.3797	0.2009	0.2916	0.1979	0.2141
0.6179	0.6051	0.3330	0.1983	0.7840	0.4583	0.1602	0.5114	0.2589
0.0985	0.2716	0.1677	0.0325	0.6335	0.0573	0.4723	0.3906	0.2676
0.1803	0.2041	0.6144	0.1231	0.6506	0.0563	0.0693	0.0502	0.2628
0.0732	0.1248	0.4386	0.5080	0.4199	0.5029	0.7062	0.7849	0.7563

0.2938	0.1399	0.0419	0.0236	0.3658	0.7809	0.5738	0.0177	0.0282
0.2142	0.0765	0.0622	0.3073	0.4471	0.1562	0.2200	0.0725	0.1149
0.3420	0.3552	0.2217	0.4336	0.0894	0.8170	0.5498	0.4609	0.2458
0.3168	0.1057	0.1723	0.0002	0.4120	0.2463	0.2530	0.9419	0.9077
0.2945	0.3029	0.1630	0.0919	0.8300	0.7406	0.4470	NA	NA
0.6313	0.0132	0.0039	2.32E-06	0.6950	0.0030	0.0196	0.0253	0.6741
0.6523	0.7426	0.6773	0.2787	0.1768	0.4798	0.2079	NA	NA
0.0039	0.4202	0.2747	0.1461	0.3930	0.0100	0.1620	NA	NA
0.3438	0.0405	0.0271	0.4322	0.4548	0.0702	0.0454	0.1021	0.0921
0.0665	0.9091	0.4739	0.0624	0.4293	0.1113	0.1931	0.1205	0.2031
0.0243	0.6454	0.3378	0.0971	0.2252	0.1286	0.3595	0.3228	0.2393
0.5762	0.2098	0.6528	0.0026	0.1905	0.4825	0.6057	0.7917	0.8244
0.0215	0.2377	0.0895	0.0346	0.1416	0.7296	0.4628	0.2233	0.3403
0.9430	0.2711	0.0852	0.1429	0.1548	0.0718	0.1122	0.6495	0.4121
0.3047	0.6200	0.7919	0.1121	0.4314	0.3885	0.2378	NA	NA
0.4160	0.5271	0.3361	0.8853	0.6857	0.0341	0.0113	NA	NA
0.4069	0.3513	0.2362	0.8835	0.6732	0.0382	0.0125	NA	NA
0.2544	0.7511	0.8361	NA	NA	0.6893	0.4343	NA	NA
0.3905	0.1174	0.1369	0.5354	0.1699	0.4222	0.5851	NA	NA
0.0503	0.7103	0.5042	0.5510	0.6796	0.2673	0.1858	NA	NA
0.0234	0.3809	0.5301	0.5238	0.2316	0.4091	0.3295	NA	NA
0.0332	0.1416	0.7635	0.4716	0.2398	0.2089	0.2513	NA	NA
0.0649	0.6338	0.4141	0.5892	0.8714	0.4390	0.6197	0.0437	0.5183
0.5294	0.0419	0.4331	0.7122	0.4765	0.1751	0.1208	0.2656	0.8880
0.2845	0.0817	0.0303	0.1918	0.5818	0.5868	0.3269	0.9295	0.7067
0.3100	0.5079	0.4050	0.0192	0.0066	0.6212	0.6428	0.3884	0.4053
0.0308	0.4477	0.3992	0.7989	0.6441	0.0182	0.0043	0.6601	0.7914
0.0051	0.0609	0.0507	5.84E-07	0.6191	3.24E-06	0.3056	0.3095	0.9044
0.3362	0.2774	0.1090	**2.86E-12**	0.2616	3.55E-06	0.8368	0.0112	0.9240
0.5567	0.4560	0.5190	0.2787	0.8471	0.0621	0.0147	0.3004	0.8110
0.6322	0.2246	0.1049	0.2037	0.7291	0.0688	0.4574	NA	NA
0.5375	0.5584	0.8371	0.2848	0.2451	0.0638	0.1472	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.4187	0.5216	0.2707	0.0007	0.5307	0.2314	0.3997	0.5322	0.6682
0.4772	0.3559	0.2275	0.0003	0.4734	0.2090	0.4084	0.5421	0.8916
0.7608	0.0099	0.0056	NA	NA	0.1938	0.1198	NA	NA
0.1491	0.0125	0.0218	0.8104	0.7389	0.2137	0.5459	NA	NA
0.2613	0.0007	0.7230	0.3444	0.3323	0.0122	0.4224	0.3723	0.6134
0.5628	NA	NA	NA	NA	NA	NA	NA	NA
0.6356	0.1397	0.0464	0.5834	0.2820	0.0754	0.2663	NA	NA
0.7481	0.2806	0.7180	0.2706	0.2057	0.5943	0.5910	0.0839	0.4147
0.5229	0.1757	0.7021	0.1452	0.1584	0.6220	0.6534	0.1066	0.4086
0.2640	0.0913	0.1352	0.1560	0.4364	0.0235	0.0174	0.1025	0.5879
0.0991	0.2584	0.3157	0.1887	0.3703	0.0812	0.0759	0.3993	0.6891
0.1664	0.3381	0.1545	0.0255	0.1463	0.0049	0.0188	0.1919	0.3289
0.2246	0.6005	0.3039	0.0024	0.0510	0.0005	0.0121	0.9850	0.8007
0.0438	0.2943	0.1845	0.2305	0.3703	0.0833	0.0640	0.6741	0.9099

0.7502	0.2108	0.2194	0.1757	0.0607	0.9023	0.6868	NA	NA
0.1546	0.8048	0.7798	0.3001	0.1316	0.8057	0.5150	0.0117	0.1988
0.7572	0.7901	0.2887	0.1285	0.0865	0.0020	0.0004	NA	NA
0.4120	0.3913	0.2193	0.1962	0.6024	0.1492	0.1673	0.2550	0.6468
0.0379	0.2009	0.7621	0.3502	0.6461	0.3825	0.3928	0.7882	0.8466
0.0497	0.3306	0.2268	0.3662	0.7072	0.1586	0.2214	0.8893	0.6674
0.6165	**8.75E-11**	0.0436	**2.53E-15**	0.5721	**1.23E-19**	0.4496	1.84E-07	0.8833
0.2037	0.0001	0.1374	**6.89E-18**	0.1423	1.05E-05	0.4615	0.0227	0.9412
0.3988	0.0015	0.2033	6.54E-08	0.3800	0.0002	0.4327	0.6066	0.6116
NA	NA	NA	NA	NA	NA	NA	NA	NA
0.3804	0.0073	0.0692	0.3130	0.9694	0.0227	0.5052	0.0032	0.9424
0.6583	0.2211	0.0707	0.1983	0.0875	0.1845	0.0564	NA	NA
0.2429	0.4885	0.3780	0.0844	0.2624	0.1600	0.0226	NA	NA
0.2203	0.0002	0.3984	4.48E-05	0.7671	0.0038	0.1697	0.1465	0.9270
0.1237	**4.33E-31**	0.4193	**2.94E-96**	0.2302	**1.00E-37**	0.2456	**7.46E-16**	0.2408
0.0008	0.5641	0.3832	**1.28E-27**	0.6650	**1.65E-08**	0.2709	0.0001	0.4758
0.3468	0.0069	0.1011	1.01E-05	0.7906	6.43E-05	0.0300	0.2761	0.1369
0.8392	0.3255	0.3601	0.7019	0.4073	0.4451	0.2114	0.3676	0.8778
0.0273	0.5183	0.2923	0.7917	0.1953	0.0093	0.0037	0.1843	0.4353
0.0731	0.2815	0.2210	0.8496	0.2328	0.0368	0.0123	0.0449	0.5898
0.3778	0.0644	0.4030	0.0143	0.2583	0.5319	0.3577	NA	NA
0.2750	0.1199	0.3912	0.2628	0.0448	0.0531	0.5706	0.7090	0.3314
0.8288	0.0296	0.8205	0.5227	0.7092	0.2336	0.2063	NA	NA
0.5729	0.8138	0.8061	0.4675	0.2819	0.6375	0.5830	NA	NA
0.2686	0.7628	0.3995	0.7323	0.3475	0.7933	0.7155	NA	NA
0.1527	0.0755	0.2836	0.0007	0.7731	0.0315	0.3714	0.5093	0.9923
0.2886	0.0044	0.6473	1.21E-07	0.1337	0.0166	0.4905	0.0009	0.2100
0.2583	0.0059	0.5386	8.76E-08	0.0934	0.0040	0.5618	0.0014	0.2201
0.1305	NA	NA	0.0003	0.6137	0.2993	0.3206	0.0844	0.8832
0.2764	0.6460	0.3449	0.8953	0.8430	0.7789	0.4920	0.6101	0.4144
0.1976	0.6440	0.4808	0.9874	0.7257	0.6495	0.3319	0.8071	0.5300
NA	0.0405	0.0104	NA	NA	NA	NA	NA	NA
0.0336	0.2516	0.2071	0.0006	0.5094	0.4458	0.2854	0.5262	0.5360
0.8237	0.1007	0.2248	0.3303	0.3735	0.2844	0.8349	NA	NA
0.1364	0.2162	0.4914	0.1980	0.1253	0.3067	0.1648	NA	NA
0.3034	0.1314	0.6160	0.3251	0.2270	0.0623	0.1136	NA	NA
0.3612	0.4517	0.4164	0.3112	0.3986	0.7661	0.4237	0.4732	0.9150
0.5960	0.1626	0.0727	NA	NA	0.0488	0.0189	NA	NA
0.6893	0.0324	0.1543	NA	NA	0.2062	0.3547	NA	NA

								TG	
META		**EUR**		**AFR**		**ASN**		**HIS**	
P.2df	**P.Int**	**P.2df**	**P.Int**	**P.2df**	**P.Int**	**P.2df**	**P.Int**	**P.2df**	**P.Int**
5.97E-05	0.1163	0.0618	0.8439	0.0927	0.1131	0.0996	0.0860	0.0110	0.0048
4.78E-20	0.5721	0.1854	0.0460	0.2914	0.2240	0.0583	0.0269	0.0620	0.1005
3.64E-18	0.7109	0.1642	0.0445	0.2333	0.0971	0.0637	0.0285	0.0575	0.1944
1.58E-07	0.1507	1.55E-06	0.1464	0.3218	0.1774	0.1850	0.6270	0.1929	0.5382
0.2460	0.2795	0.0003	0.2163	0.3649	0.2725	0.0004	0.1172	0.1988	0.0887
3.31E-42	0.0229	0.7995	0.4422	0.1237	0.0860	0.1299	0.4993	0.0220	0.0072
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
6.92E-06	0.1891	0.0011	0.6336	0.0137	0.0126	0.0777	0.5958	0.4470	0.2396
1.12E-61	0.1932	**2.11E-76**	0.5095	**4.83E-08**	0.0337	**2.41E-25**	0.1690	**2.00E-12**	0.0348
1.10E-58	0.3664	**1.03E-70**	0.6683	6.56E-06	0.0571	**5.76E-38**	0.0012	**4.53E-13**	0.0183
9.16E-06	0.1919	0.5370	0.4470	0.5229	0.8578	0.6542	0.3623	0.1710	0.0978
3.19E-05	0.2469	0.5176	0.2764	0.5208	0.9119	NA	NA	0.1686	0.0952
0.0009	0.3635	0.0345	0.2545	0.0971	0.0461	8.64E-07	0.3644	0.7445	0.6087
0	0.1234	4.80E-05	0.2903	0.1785	0.7654	0.2498	0.2825	0.0222	0.2869
0	0.2013	8.69E-05	0.2041	0.1842	0.7456	0.2039	0.1954	0.0250	0.3172
5.92E-09	0.0411	0.4398	0.1172	0.3945	0.4909	0.1480	0.0845	0.4295	0.6228
2.13E-05	0.5231	0.1101	0.1129	0.2926	0.5081	0.0457	0.0924	0.6253	0.5404
0.0880	0.0300	0.0669	0.9024	0.7410	0.3407	0.2644	0.2323	0.9922	0.8459
0.4822	0.3802	0.0680	0.0145	0.9044	0.8302	0.8429	0.5347	0.0342	0.0255
7.21E-06	0.0248	0.1100	0.1792	0.7114	0.3022	0.0089	0.1085	0.0537	0.0707
0.0009	0.0379	0.1176	0.1695	0.0396	0.0070	0.0052	0.1253	0.0948	0.0955
1.54E-22	0.2652	0.0003	0.3944	0.3251	0.7101	3.42E-07	0.1791	0.1705	0.5587
2.78E-22	0.2276	0.0009	0.2485	0.0368	0.0088	1.65E-06	0.8097	0.7614	0.8322
4.71E-05	0.7656	0.3293	0.2103	0.3223	0.8112	0.2322	0.1118	0.1172	0.2268
0.7665	0.4648	**9.60E-26**	0.2116	0.0585	0.0783	5.99E-06	0.2214	0.0010	0.4626
0.1322	0.1426	0.0254	0.6185	0.2559	0.2856	0.9199	0.6936	0.6401	0.5176
4.25E-35	0.0189	0.0033	0.0448	0.4346	0.0975	0.4898	0.1646	0.0216	0.3094
7.71E-32	0.0330	0.0015	0.0985	0.6943	0.3738	0.8984	0.3336	0.0490	0.1836
6.18E-227	0.4118	**2.94E-09**	0.1400	0.8960	0.6631	0.1584	0.6572	0.0014	0.9146
1.16E-201	0.3228	0.0004	0.2525	0.3672	0.2050	0.7239	0.6051	0.4297	0.3008
5.27E-21	0.0107	**6.94E-250**	0.0026	**2.89E-12**	0.7022	**3.45E-116**	0.0676	**1.08E-31**	0.7067
3.21E-09	0.1473	**1.51E-59**	0.0742	0.1121	0.0916	**5.22E-71**	0.3183	6.90E-05	0.7291
2.37E-18	0.0017	**1.34E-240**	0.0014	**2.44E-08**	0.3301	**1.64E-104**	0.0875	**5.14E-26**	0.6300
2.48E-89	0.4617	0.0501	0.4334	0.1273	0.3690	0.2290	0.0709	0.0903	0.1741
4.53E-83	0.3333	0.0419	0.3438	0.1216	0.3147	0.2059	0.0552	0.0700	0.1252
2.52E-13	0.3578	0.2622	0.7305	0.2740	0.2376	0.2133	0.0914	0.4112	0.2043
0.4055	0.7648	0.5857	0.4733	0.6199	0.4609	NA	NA	0.2736	0.1114
2.24E-17	0.6135	0.5503	0.7608	0.5471	0.5760	0.5135	0.7055	0.1669	0.0479
2.38E-15	0.0698	0.0582	0.8692	0.1651	0.1844	0.8419	0.8982	0.5556	0.3804
1.70E-14	0.0229	0.0410	0.2831	0.0314	0.0959	0.7236	0.6191	0.5773	0.3829

8.23E-15	0.0167	0.0360	0.3005	0.0332	0.1035	0.6382	0.5443	0.4534	0.3040
0.0008	0.0495	0.3290	0.8326	0.8174	0.8331	0.7149	0.5427	0.5704	0.1723
0.0009	0.2104	0.2837	0.1080	0.4231	0.6819	0.5460	0.6905	0.8600	0.6708
9.56E-14	0.2230	0.7442	0.4372	0.8516	0.4297	0.0054	0.0037	0.2180	0.0945
0.2356	0.5174	0.1365	0.1362	0.0282	0.0090	0.1660	0.6064	0.3440	0.1905
0.0624	0.4109	**6.38E-12**	0.3639	0.0109	0.2344	0.1167	0.3192	0.0457	0.3069
0.0611	0.6255	**7.77E-12**	0.3383	0.0085	0.1144	0.1650	0.2008	0.0499	0.3153
0.1355	0.4639	0.0002	0.7225	0.1742	0.7260	0.9434	0.5431	0.1006	0.2152
1.46E-13	0.4225	0.2820	0.4785	0.0078	0.0706	0.4759	0.1651	0.3528	0.3131
0.0004	0.3922	0.0408	0.4338	0.6610	0.5276	0.7823	0.2801	0.5737	0.4362
0.4851	0.8796	0.0036	0.0038	0.5569	0.8664	0.0175	0.2438	0.2260	0.0812
0.0004	0.4191	0.1417	0.4982	0.0801	0.0372	0.4528	0.2693	0.8300	0.6882
0.0371	0.1300	**4.11E-17**	0.4822	0.7781	0.4899	1.20E-06	0.2995	0.1454	0.5367
0.0127	0.0267	**7.10E-16**	0.3394	0.2012	0.3013	1.93E-06	0.6498	0.4500	0.5637
1.91E-06	0.8467	0.6312	0.2301	0.0399	0.0071	0.0694	0.0534	0.3877	0.1620
0.4067	0.2316	0.3043	0.3864	0.1340	0.0843	0.5558	0.3157	0.2977	0.2360
1.17E-06	0.0381	0.0750	0.3064	0.3221	0.2457	0.6400	0.6289	0.1402	0.0631
2.26E-10	0.0356	0.0129	0.1936	0.4770	0.2623	0.0150	0.0635	0.5578	0.4603
2.24E-05	0.1404	0.2211	0.7182	0.4369	0.5803	0.6926	0.2922	0.1081	0.7041
0.1714	0.1205	0.0171	0.1755	0.3496	0.2060	0.3598	0.1571	0.1960	0.4087
0.0408	0.1032	0.0482	0.6086	0.0607	0.7805	0.0440	0.0236	0.7009	0.4231
0.1345	0.2117	0.0457	0.7055	0.1584	0.4242	0.0321	0.0221	0.9010	0.7244
0.0975	0.0455	0.0037	0.4326	0.9042	0.5150	NA	NA	0.1840	0.0887
0.0003	0.1759	0.5790	0.2267	0.1705	0.1913	NA	NA	0.2154	0.1591
0.0056	0.0403	0.8310	0.7361	0.6079	0.4547	0.7005	0.2853	0.1335	0.8689
0.0011	0.5104	0.3677	0.3089	0.0169	0.1734	0.9624	0.7864	0.1269	0.1006
0.0004	0.1614	0.1809	0.2751	0.0932	0.1118	0.8197	0.5397	0.1680	0.1555
0.0015	0.0908	1.63E-05	0.2629	0.7573	0.6460	0.2792	0.1527	0.1542	0.0817
0.0001	0.2242	**1.16E-12**	0.6634	0.8140	0.6449	0.0017	0.0438	0.2276	0.2550
3.28E-20	0.5835	0.0279	0.1623	0.1674	0.0931	0.1814	0.3276	0.0318	0.0213
0.0075	0.0077	0.1702	0.1464	0.0046	0.0561	NA	NA	0.9547	0.8200
0.0058	0.5068	0.0007	0.1665	0.7132	0.5538	0.7196	0.3950	0.0539	0.1623
0.0330	0.2724	4.71E-06	0.0078	0.2278	0.3463	NA	NA	0.6373	0.6094
0.5159	0.2551	0.0095	0.1287	0.1446	0.0517	0.9392	0.5709	0.4955	0.3263
0.0026	0.2027	**2.43E-19**	0.0612	0.0062	0.0495	**7.18E-12**	0.0495	0.0007	0.4128
0.8589	0.5756	1.00E-05	0.3487	0.4685	0.2551	0.0951	0.1959	0.6184	0.7717
0.1349	0.2031	0.0382	0.8261	0.0866	0.3131	0.4715	0.3436	0.7677	0.4896
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
0.0180	0.0023	7.63E-05	0.1341	0.4535	0.2495	0.2155	0.1043	0.5963	0.7926
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
5.04E-05	0.3279	0.0027	0.2468	0.5598	0.8362	NA	NA	0.3669	0.4293
0.3901	0.2770	0.0062	0.7901	0.1197	0.0518	0.0684	0.0410	0.0488	0.0141

0.0095	0.5744	0.0001	0.3532	0.0393	0.0363	0.3088	0.2144	0.0003	0.0025
0.0073	0.0765	**5.57E-13**	0.5363	0.0138	0.6472	0.3817	0.6203	0.0003	0.7590
0.1788	0.0282	0.0025	0.1240	0.0003	0.4220	0.3447	0.2335	0.1854	0.2959
8.25E-135	0.2684	0.1412	0.1460	0.5097	0.2787	0.0233	0.0983	0.0721	0.0647
6.99E-153	0.4057	0.2028	0.2326	0.0426	0.0103	0.0247	0.1386	0.0171	0.0433
0.0003	0.5234	0.0457	0.0024	0.5615	0.6643	0.0476	0.2594	0.5341	0.2407
1.05E-40	0.7454	**1.22E-16**	0.3626	0.1903	0.2067	**1.50E-11**	0.0100	0.0031	0.6815
4.63E-21	0.2257	0.7891	0.7751	0.1233	0.0702	0.0731	0.0411	0.3164	0.1984
4.64E-18	0.7047	0.4620	0.2110	0.0385	0.0105	0.6350	0.7334	0.0598	0.0167
5.53E-05	0.5100	0.1454	0.6492	0.5447	0.2892	NA	NA	0.1748	0.1047
5.27E-08	0.2323	**1.98E-12**	0.0691	0.2475	0.1684	0.7030	0.4492	0.0019	0.8988
0.0236	0.4615	0.2469	0.1473	0.8246	0.6362	NA	NA	NA	NA
0.0601	0.0883	0.1713	0.2147	0.6983	0.4250	0.7027	0.2339	0.5471	0.6166
0.5121	0.8856	0.0480	0.0124	0.2117	0.1575	0.8045	0.6791	0.1220	0.4379
0.0222	0.2318	0.0362	0.3319	0.4332	0.2207	NA	NA	0.0422	0.1368
0.0051	0.4911	0.2988	0.4899	0.3883	0.2098	0.7656	0.4696	0.0326	0.2783
0.0011	0.2815	**1.65E-19**	0.3427	0.0018	0.7147	**4.05E-09**	0.0784	0.0001	0.4175
3.44E-05	0.1108	0.6610	0.3262	0.0638	0.0781	0.3121	0.0503	0.0356	0.0176
1.97E-05	0.2004	0.7211	0.5078	0.3118	0.2755	0.2966	0.0504	0.1751	0.0571
1.98E-09	0.2749	0.0433	0.8086	0.3969	0.2938	0.5765	0.6060	0.1428	0.8179
1.25E-06	0.4374	0.2034	0.0987	0.1727	0.4554	0.9761	0.6299	0.1461	0.1173
4.10E-14	0.6106	0.0015	0.5098	0.1049	0.5328	0.0415	0.3705	0.0890	0.0350
0.0548	0.2095	**3.53E-09**	0.2816	0.0027	0.0494	0.0037	0.0895	0.3544	0.2256
0.4072	0.4484	6.60E-08	0.3056	0.1090	0.0308	0.0303	0.0667	0.1805	0.0802
0.2320	0.4747	**1.64E-08**	0.2628	0.5464	0.2910	**4.72E-31**	0.1506	0.0741	0.0807
0.0070	0.5348	0.0197	0.0333	0.6361	0.2398	0.6819	0.3107	0.1686	0.4250
0.0178	0.3551	**5.09E-18**	0.2841	0.1760	0.5405	1.15E-05	0.0120	0.0008	0.1591
0.0192	0.3096	**4.39E-16**	0.2629	0.2415	0.7720	1.83E-05	0.0112	0.0009	0.1687
0.4867	0.2872	0.1108	0.0564	0.5828	0.1567	0.5637	0.2101	0.7160	0.8792
1.64E-22	0.7400	0.1524	0.3005	0.8848	0.5511	0.0684	0.0192	0.2360	0.1402
4.09E-29	0.5089	0.0116	0.1357	0.4643	0.3795	0.6077	0.6744	0.0098	0.0940
0.0175	0.3480	0.0501	0.5275	0.1805	0.0748	NA	NA	0.6150	0.3377
0.3742	0.1082	0.3158	0.2201	0.8195	0.6711	0.2034	0.4366	0.0720	0.1552
0.3706	0.1400	0.0063	0.0429	0.0569	0.1242	0.5142	0.2401	0.7347	0.4330
0.0546	0.2787	0.0019	0.4547	0.0005	0.0023	0.0093	0.0278	0.5970	0.6143
0.1015	0.3444	0.0014	0.4483	0.0008	0.0015	0.0070	0.0148	0.7074	0.9150
6.93E-06	0.1352	0.1273	0.3019	0.1964	0.0579	0.3111	0.4586	0.1592	0.1530
2.22E-18	0.5693	**2.25E-09**	0.1272	0.0150	0.5505	0.1981	0.8240	0.0145	0.7254
1.69E-18	0.1474	0.0009	0.0139	0.4227	0.8186	0.5325	0.3082	0.8083	0.7959
3.63E-19	0.1639	0.0001	0.0028	0.7782	0.5205	0.3841	0.4333	0.6841	0.3998
1.25E-36	0.0458	0.0460	0.0840	0.0411	0.0773	0.2303	0.2170	0.0977	0.0410
0.1000	0.0216	0.1270	0.0321	0.2003	0.2261	0.3577	0.1016	0.1018	0.0371
0.7448	0.2701	0.5847	0.5073	0.4574	0.5725	0.3349	0.3705	0.4745	0.3836
0.7293	0.7773	0.2141	0.8064	0.4537	0.1025	0.3420	0.5953	0.4677	0.5645
0.4350	0.1780	0.0545	0.0487	NA	NA	NA	NA	NA	NA
0.2168	0.6280	**2.57E-118**	0.0935	2.36E-07	0.1748	**5.30E-57**	0.0492	**8.71E-12**	0.3842
0.3923	0.6143	**1.08E-33**	0.6351	0.1671	0.2234	**2.21E-21**	0.0678	0.0066	0.1212

0.6200	0.3606	NA	NA	0.0002	0.4362	NA	NA	0.5455	0.3387
0.0616	0.3442	0.0002	0.3767	0.0809	0.0622	0.7114	0.5869	0.0385	0.0056
0.0021	0.8434	**1.52E-16**	0.0125	0.3671	0.4488	0.0001	0.0149	1.74E-06	0.7523
0.0011	0.6261	**3.88E-18**	0.0127	0.3359	0.3983	1.61E-05	0.0161	3.21E-06	0.6810
0.6022	0.2331	0.7135	0.8071	0.1081	0.0794	NA	NA	0.5031	0.2517
1.31E-48	0.5678	2.47E-06	0.0514	0.0003	0.3845	0.0011	0.0135	0.0116	0.2681
1.19E-49	0.4626	3.80E-07	0.0649	0.0003	0.4461	0.0012	0.0130	0.0171	0.2661
0.2872	0.7341	0.0009	0.7776	0.0107	0.4655	NA	NA	0.9651	0.8264
0.0615	0.1678	2.76E-05	0.1808	0.7520	0.4857	0.2661	0.8440	0.0202	0.0039
0.3956	0.4584	0.3365	0.2538	0.1335	0.0780	0.0805	0.0142	0.3830	0.2186
1.05E-07	0.4142	**3.78E-15**	0.2736	0.0318	0.6392	**4.57E-11**	0.3842	0.0123	0.0654
9.76E-08	0.4276	**1.83E-16**	0.2790	0.0435	0.6524	**3.05E-11**	0.3836	0.0131	0.0557
0.3878	0.4192	**2.07E-226**	0.3416	**1.95E-10**	0.3532	**1.87E-158**	0.4948	**8.30E-26**	0.5175
0.0400	0.1479	**8.35E-84**	0.3655	0.0001	0.0456	**2.54E-89**	0.6437	**2.80E-12**	0.0714
2.63E-18	0.1636	0.0156	0.6038	0.2187	0.0949	0.3100	0.2247	0.9269	0.7562
2.51E-29	0.5917	6.45E-07	0.0272	0.0976	0.4553	0.0029	0.0752	0.0767	0.1540
8.72E-28	0.4119	9.49E-07	0.0289	0.0799	0.5549	0.0035	0.1544	0.0868	0.1613
0.7005	0.5708	0.5213	0.2515	0.4702	0.7022	0.1350	0.1593	0.4886	0.5740
0.3850	0.2687	0.4192	0.8026	0.0632	0.0165	0.0127	0.1206	0.7387	0.4962
1.64E-07	0.8362	0.0016	0.0452	0.8925	0.4446	0.0126	0.0445	0.3217	0.4350
0.0001	0.4125	0.2827	0.2598	0.3783	0.1517	0.0550	0.0196	0.0848	0.4700
0.3964	0.1609	0.3126	0.3038	0.6849	0.1838	0.7125	0.8207	0.0474	0.0875
8.76E-18	0.4152	**3.85E-42**	0.5456	0.3849	0.2371	**5.33E-22**	0.0567	1.47E-07	0.3365
2.50E-77	0.1144	**2.79E-117**	0.6569	0.1711	0.3927	**4.87E-35**	0.1367	**1.81E-09**	0.6614
1.22E-75	0.1227	**1.09E-118**	0.7025	0.5590	0.5822	**5.95E-36**	0.1123	**1.06E-09**	0.6123
0.0971	0.1249	0.3131	0.4408	0.1232	0.1551	0.8501	0.5180	0.9841	0.7296
1.67E-05	0.8148	0.2781	0.0897	0.5388	0.5063	0.2741	0.2267	0.6909	0.7069
1.29E-05	0.8087	0.1411	0.0346	0.1101	0.2001	0.2288	0.1594	0.7481	0.6985
2.13E-05	0.2672	0.5251	0.2558	0.2301	0.0718	0.5468	0.2148	0.4134	0.2006
0.3457	0.7138	0.0003	0.0969	0.2827	0.5762	0.0753	0.0571	0.0884	0.1439
0.1052	0.0853	0.0007	0.1998	0.2257	0.1446	0.1470	0.0864	0.2831	0.2409
0.0003	0.3138	0.0003	0.5307	0.2355	0.1483	0.6490	0.5608	0.3638	0.5363
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
8.17E-12	0.8267	7.17E-08	0.2693	0.6330	0.8208	0.0144	0.3058	0.2451	0.5792
0.0006	0.1636	0.5940	0.5149	0.4062	0.2028	0.2538	0.0623	0.9936	0.8660
3.40E-19	0.2640	0.2451	0.2855	0.4668	0.1872	8.64E-08	0.2937	0.3550	0.2283
8.68E-87	0.1504	0.0013	0.0224	0.0007	0.0168	1.53E-07	0.3847	0.4602	0.2593
8.67E-100	0.1877	0.0002	0.0063	0.0236	0.0493	1.38E-07	0.3908	0.6327	0.4136
0.1081	0.2073	6.40E-06	0.4981	0.2758	0.3433	0.0864	0.0105	0.8421	0.6531
0.7101	0.7522	1.13E-05	0.2119	0.0166	0.0537	0.0036	0.0005	0.6248	0.3387
0.0293	0.3548	0.5445	0.2404	0.3432	0.3724	0.5174	0.1702	0.5894	0.3365
0.6676	0.8296	0.5511	0.1899	0.0220	0.0769	0.4973	0.3084	0.1092	0.0688
8.48E-08	0.0931	**4.78E-16**	0.4075	0.0018	0.8010	1.07E-06	0.0838	0.0112	0.3971
1.23E-08	0.0536	**2.53E-16**	0.7576	0.0014	0.2767	8.27E-07	0.0704	0.0272	0.6549
1.29E-10	0.1571	**1.01E-09**	0.3822	0.0485	0.7969	**5.09E-13**	0.0995	0.0208	0.0991
1.12E-14	0.5069	2.17E-06	0.3870	0.2011	0.1060	2.92E-06	0.0628	0.2184	0.2937

0.0060	0.0009	0.0008	0.1946	0.4930	0.5767	0.1626	0.1988	0.9247	0.7983
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
0.2013	0.4456	0.0059	0.6112	0.0153	0.0454	0.2948	0.0049	0.0073	0.0197
0.4418	0.4636	0.0119	0.0942	0.5749	0.1889	0.9667	0.9986	0.5533	0.3169
0.0001	0.2506	0.0016	0.0731	0.6006	0.4360	0.8338	0.7115	0.6719	0.5382
2.84E-05	0.2233	0.0012	0.1664	0.4630	0.5391	0.4751	0.4141	0.7078	0.5599
0.7247	0.4793	**9.20E-11**	0.9043	0.0051	0.0173	0.0078	0.7533	0.1498	0.0837
0.1905	0.7268	2.37E-07	0.4578	0.0168	0.7796	0.0003	0.1488	0.0206	0.0062
0.3056	0.3306	0.0336	0.3979	0.0024	0.0428	0.0092	0.4963	0.1203	0.3683
0.8520	0.7425	0.2386	0.1168	0.6461	0.5949	0.2665	0.3232	0.9007	0.6007
0.2914	0.5095	0.0615	0.7805	0.0129	0.0501	0.8737	0.5142	0.1678	0.0588
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
0.1363	0.0784	0.1787	0.4331	0.1593	0.4417	0.7310	0.0521	0.1939	0.2524
0.3493	0.4587	0.0363	0.2343	0.1206	0.5490	0.3941	0.8064	0.5088	0.3218
6.37E-15	0.3102	4.67E-05	0.2260	0.2669	0.1078	0.2774	0.4467	0.1363	0.4723
2.11E-52	0.0040	**4.84E-38**	0.2840	3.87E-07	0.1213	**3.70E-16**	0.4918	**2.33E-09**	0.3408
3.41E-50	0.0060	**1.79E-38**	0.2214	6.48E-08	0.1709	**4.25E-16**	0.6327	**9.00E-10**	0.3707
0.5608	0.4663	0.0005	0.3229	0.3754	0.4421	0.0755	0.0958	0.6181	0.3779
0.7899	0.2483	0.0191	0.1248	0.1265	0.9274	0.6706	0.2807	0.3294	0.3625
1.77E-27	0.0835	**7.25E-255**	0.7089	2.61E-07	0.1269	**6.26E-271**	0.0654	**3.85E-50**	0.7794
1.31E-21	0.3483	**2.41E-262**	0.6966	5.30E-07	0.6013	**3.77E-273**	0.0528	**8.16E-48**	0.7338
7.72E-39	0.1084	**0**	0.8682	0.0821	0.5398	**3.33E-274**	0.0474	**1.15E-102**	0.1505
0.0009	0.3525	**4.36E-51**	0.3416	0.4914	0.6123	**4.74E-189**	0.0420	**3.64E-11**	0.0817
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
0.2070	0.3461	0.7898	0.8118	0.0927	0.1251	0.5910	0.2905	0.0620	0.8478
0.0006	0.3615	0.7575	0.4658	0.5155	0.3796	0.6114	0.6787	0.1354	0.7043
0.0003	0.2730	0.6304	0.5319	0.4312	0.2047	0.6403	0.7751	0.1416	0.6915
7.37E-20	0.0719	0.3073	0.1175	0.8668	0.5939	0.1197	0.1511	0.0016	0.0077
0.0828	0.0190	0.8838	0.6124	0.1565	0.1264	0.9629	0.6645	0.2202	0.1021
0.0013	0.5152	0.0798	0.3958	0.2121	0.7243	0.4725	0.1490	0.2014	0.3692
0.0686	0.1732	0.1592	0.4597	0.0068	0.6845	0.4076	0.2647	0.1004	0.0329
0.0616	0.0714	0.0023	0.0475	0.4139	0.6049	0.0438	0.0981	0.4988	0.4575
0.0357	0.0502	0.0041	0.1049	0.3249	0.4412	0.0274	0.1452	0.3270	0.3697
6.87E-21	0.0719	**5.37E-10**	0.0043	0.0547	0.3785	0.1029	0.7184	0.2139	0.2513
0.0005	0.0575	**1.81E-11**	0.0051	0.0602	0.3711	0.0708	0.4440	0.3207	0.3526
0.1030	0.3290	8.76E-06	0.2802	0.3711	0.5791	0.3347	0.0926	0.0957	0.3582
0.0591	0.5529	0.1963	0.3010	0.2994	0.1152	0.6462	0.2699	0.8613	0.8003
0.0466	0.4381	0.3467	0.3864	0.3603	0.1307	0.6270	0.3043	0.9190	0.8942
1.90E-05	0.0619	0.1074	0.1480	0.0890	0.0866	NA	NA	0.0144	0.2738
0.0001	0.0571	0.3483	0.3587	0.0666	0.0869	NA	NA	0.0336	0.2216
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
4.68E-08	0.1215	0.1479	0.1775	0.0040	0.4620	0.3056	0.2759	0.4201	0.3736
1.84E-07	0.2787	0.4493	0.2868	0.6224	0.5368	0.5282	0.4777	0.5140	0.2322
1.44E-25	0.1025	0.5278	0.2534	0.5432	0.3098	0.7176	0.4013	0.5488	0.3933
0.0009	0.3127	0.0746	0.0421	0.3016	0.6352	0.0851	0.7102	0.1815	0.0746
0.0097	0.1272	**5.71E-14**	0.3172	0.0017	0.4194	0.0535	0.4310	0.0497	0.4768

0.8541	0.9032	0.7959	0.5074	0.4403	0.1627	0.0749	0.0095	0.0335	0.0507
0.7717	0.6438	0.7767	0.7909	0.1022	0.2122	0.6620	0.4925	0.0040	0.0017
0.9206	0.6611	0.0546	0.6485	0.2179	0.5963	0.1579	0.1813	0.1017	0.1091
2.67E-12	0.4162	0.0008	0.1965	0.0054	0.0009	0.3205	0.2373	0.8033	0.5901
0.0072	0.1994	0.0647	0.4507	0.1994	0.6579	0.4943	0.2319	0.5219	0.4255
9.05E-19	0.7096	0.1564	0.3901	0.0375	0.6278	0.2840	0.7776	0.3179	0.3406
0.9298	0.6783	0.5779	0.3999	0.0398	0.5258	0.4202	0.2532	0.1182	0.1899
0.0940	0.0071	0.2478	0.5782	0.6422	0.4549	0.4175	0.2100	0.6821	0.3867
0.1253	0.0238	**1.99E-10**	0.0002	0.0041	0.3868	0.2923	0.1459	0.2147	0.3080
0.0436	0.0164	**3.48E-16**	0.0069	0.8270	0.6555	0.0941	0.0900	0.0003	0.2299
0.0543	0.0491	**5.69E-18**	0.0196	0.6159	0.7315	0.7270	0.4198	0.0025	0.1438
0.1697	0.6018	**5.09E-14**	0.2206	1.32E-05	0.1381	**3.92E-20**	0.0473	0.0217	0.6511
0.0058	0.0252	**1.22E-35**	0.7902	0.2806	0.6571	**1.10E-13**	0.6197	0.1670	0.1456
0.2164	0.3264	0.0002	0.2457	0.3717	0.5957	0.3131	0.7350	0.9297	0.6725
0.0520	0.5969	0.0270	0.2611	0.6991	0.3947	0.6712	0.6522	0.0253	0.2575
0.8781	0.5702	0.4799	0.4256	0.1073	0.0444	0.0028	0.0502	0.2385	0.2881
0.8856	0.5724	0.4611	0.4078	0.1282	0.0451	0.0029	0.0505	0.2537	0.2611
0.2324	0.2382	0.0003	0.6751	0.6520	0.4348	NA	NA	0.5081	0.4455
0.3593	0.2010	0.0006	0.4834	0.1998	0.2117	0.4164	0.2673	0.0490	0.0233
0.1927	0.0587	0.0007	0.4079	0.2892	0.2360	0.6617	0.5182	0.0444	0.0171
0.1878	0.0489	0.1403	0.2529	0.2173	0.0740	0.1213	0.0627	0.1348	0.6812
0.3516	0.1275	0.1561	0.3044	0.2415	0.1000	0.5407	0.2568	0.1075	0.6177
6.46E-15	0.1356	**1.32E-09**	0.7830	0.3382	0.2947	0.5238	0.6190	0.0003	0.0244
2.11E-21	0.3059	**1.23E-19**	0.6105	0.0158	0.0987	**1.77E-09**	0.8591	0.0009	0.1087
0.0659	0.3826	5.07E-08	0.2696	0.7402	0.5387	0.6211	0.3079	0.1358	0.4140
0.4405	0.0747	0.5138	0.7235	0.1744	0.1432	0.1650	0.9502	0.2394	0.1018
0.1663	0.0247	0.0895	0.0816	0.2799	0.7440	7.49E-05	0.0337	0.1662	0.6581
8.64E-22	0.0293	0.0016	0.0928	0.1680	0.1433	0.0223	0.6535	0.0265	0.1691
1.50E-56	0.7061	**9.54E-10**	0.0446	0.0548	0.5563	0.0127	0.9465	0.1168	0.2213
0.5435	0.6764	**6.83E-12**	0.0170	0.0079	0.7081	**4.34E-08**	0.7126	0.0347	0.2321
0.0037	0.3607	0.6258	0.7292	0.0960	0.2243	0.4015	0.6191	0.0829	0.1254
1.67E-06	0.5309	0.3018	0.1844	0.0966	0.0244	0.0145	0.0799	0.0758	0.0256
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
0.0009	0.4420	0.0002	0.0121	0.8025	0.5897	0.0102	0.0084	0.0067	0.0037
0.0003	0.4398	0.0002	0.0182	0.3458	0.7043	0.0096	0.0068	0.0048	0.0032
0.1700	0.2263	0.0321	0.5479	0.1049	0.0592	NA	NA	0.5436	0.7523
2.40E-06	0.0929	0.2158	0.4326	0.5878	0.4882	0.6227	0.2804	0.3813	0.5735
1.44E-19	0.1228	2.48E-06	0.1719	0.2710	0.4249	0.0012	0.0207	0.7040	0.3747
4.28E-06	0.7767	0.0842	0.3815	NA	NA	NA	NA	NA	NA
0.0015	0.4204	0.0041	0.0680	0.6131	0.1797	0.7294	0.5083	0.1433	0.1519
0.0011	0.4784	0.0173	0.3965	0.0167	0.4053	0.6375	0.7182	0.8266	0.6539
0.0005	0.2901	0.0045	0.2087	0.0136	0.2851	0.5916	0.4753	0.8304	0.6980
3.23E-06	0.4208	0.0002	0.3885	0.2939	0.3128	3.74E-05	0.8582	0.0434	0.1428
1.09E-07	0.3912	0.0023	0.6886	0.3714	0.8679	0.0001	0.3692	0.3774	0.2433
5.64E-08	0.3723	0.3565	0.1020	0.4891	0.4356	0.1308	0.0685	0.0279	0.0295
2.15E-07	0.3112	0.7524	0.2999	0.8440	0.6447	0.3244	0.1124	0.2537	0.2438
8.55E-05	0.0579	0.9513	0.6371	0.2142	0.5613	0.8235	0.5094	0.4954	0.2647

0.3336	0.3452	0.0164	0.3876	0.0463	0.6004	0.6619	0.6810	0.4651	0.1115
0.7153	0.4574	3.25E-05	0.2727	0.1088	0.3338	0.0046	0.2434	0.0132	0.0182
0.0046	0.1020	0.3795	0.4833	0.4782	0.4633	0.4849	0.2340	0.0010	0.0009
0.4278	0.6935	**3.74E-09**	0.5648	0.0947	0.1658	0.7862	0.4938	0.4199	0.3971
0.0040	0.0295	0.0001	0.6485	0.1181	0.1508	0.8468	0.7537	0.6500	0.5652
0.0146	0.0622	8.21E-05	0.7514	0.0077	0.7883	0.5460	0.7159	0.4804	0.9348
0	0.9222	0.0057	0.6022	0.0355	0.0051	0.4621	0.1847	0.6461	0.3581
1.25E-85	0.1432	0.1055	0.0654	0.4252	0.1726	0.0802	0.3118	0.0938	0.4017
5.93E-10	0.3242	0.0004	0.0970	0.0912	0.0505	**2.97E-10**	0.8256	0.2987	0.1351
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
4.24E-42	0.5296	**2.17E-63**	0.1313	0.1257	0.1692	**5.46E-17**	0.7368	1.21E-05	0.7004
0.6739	0.9538	0.0007	0.4475	0.6400	0.6097	0.1533	0.0418	0.1352	0.1639
0.0186	0.1390	0.0530	0.1607	0.0098	0.4403	0.0743	0.5897	0.3381	0.5393
4.90E-117	0.4813	0.1206	0.0774	0.0012	0.3362	**2.18E-10**	0.1661	0.0074	0.1703
0	0.1570	**5.08E-31**	0.5551	0.2013	0.4760	**3.44E-35**	0.3454	0.0006	0.0649
7.16E-286	0.0170	**5.77E-32**	0.2484	**1.39E-20**	0.1665	**2.16E-12**	0.4443	0.1475	0.3844
6.55E-26	0.1536	2.35E-07	0.3508	0.3157	0.2538	0.0024	0.5200	0.0453	0.0194
0.4934	0.3414	0.0279	0.7479	0.6805	0.3884	0.1608	0.2924	0.1791	0.1664
0.4600	0.3797	0.0017	0.0374	0.2310	0.2014	0.2286	0.1391	0.1720	0.0559
0.6459	0.6291	0.0058	0.1048	0.0238	0.4204	0.3786	0.1613	0.1467	0.0713
4.23E-06	0.5241	0.9681	0.8751	0.0075	0.0062	0.3445	0.0779	0.6743	0.4383
7.02E-77	0.0305	0.8293	0.6507	0.4873	0.3339	0.0010	0.0656	0.1249	0.3151
3.12E-05	0.8061	0.0562	0.2216	0.7447	0.2978	0.1809	0.1425	0.1807	0.0731
0.0004	0.6355	0.1337	0.8004	0.7708	0.2956	0.0598	0.1429	0.0064	0.0036
6.87E-05	0.2313	0.1733	0.5261	0.3354	0.3124	0.6638	0.4383	0.4002	0.1443
6.28E-27	0.3105	0.0003	0.0453	0.3622	0.8011	0.0143	0.0262	0.2428	0.4911
1.47E-38	0.1974	0.0005	0.5239	0.3148	0.8550	0.8990	0.4960	0.3845	0.3544
7.82E-38	0.1648	0.0002	0.4293	0.1425	0.3891	0.9081	0.5069	0.6839	0.7573
1.94E-12	0.2106	0.8265	0.9067	NA	NA	0.2093	0.6582	0.0049	0.0416
0.0529	0.1574	**9.12E-31**	0.1949	0.0027	0.1104	0.0658	0.4215	0.0987	0.1154
0.0728	0.1698	**4.45E-29**	0.2628	0.1065	0.2116	0.0485	0.4208	0.0741	0.2573
0.0481	0.0116	NA	NA	**6.87E-10**	0.1310	NA	NA	NA	NA
0.0001	0.1353	0.0064	0.8338	0.4364	0.3660	0.0129	0.6280	0.6742	0.6582
0.1448	0.5912	0.3083	0.1691	0.3543	0.6227	0.2049	0.1448	0.1369	0.0361
0.0014	0.2061	0.6225	0.3692	0.3246	0.1489	0.5310	0.5364	0.5744	0.3338
0.0141	0.3327	0.0004	0.7091	0.1130	0.2912	0.0536	0.3677	0.1257	0.0404
0.0945	0.7867	2.69E-07	0.7565	0.1754	0.6689	0.0017	0.1729	0.0519	0.3334
0.0186	0.3575	0.0210	0.4661	0.1130	0.0636	NA	NA	0.1729	0.1134
0.1406	0.2477	0.0212	0.4040	0.5311	0.7104	NA	NA	0.2993	0.1766

BRA		META	
P.2df	P.Int	P.2df	P.Int
NA	NA	0.0058	0.2194
0.2726	0.1099	0.0110	0.0025
0.4482	0.3154	0.0043	0.0010
0.9518	0.7560	4.14E-07	0.2140
0.7764	0.6264	4.65E-06	0.1659
0.9138	0.9214	0.2886	0.1452
NA	NA	NA	NA
NA	NA	7.98E-05	0.3306
0.3079	0.7486	**9.10E-111**	0.8225
0.4502	0.7517	**2.99E-116**	0.2652
NA	NA	0.3411	0.6779
NA	NA	0.3797	0.4809
0.1820	0.0887	2.14E-06	0.4964
0.5931	0.3747	0.0002	0.5762
0.6300	0.4032	0.0003	0.6558
0.5377	0.4437	0.3905	0.1493
NA	NA	0.1653	0.1491
NA	NA	0.1043	0.7732
NA	NA	0.1112	0.0110
0.7282	0.9619	0.0004	0.0376
0.9513	0.8926	0.0007	0.1106
0.5422	0.3282	**3.13E-10**	0.2036
0.6055	0.3801	1.23E-07	0.3530
NA	NA	0.1443	0.1689
0.8841	0.6198	**2.11E-32**	0.6856
NA	NA	0.0224	0.5653
0.8929	0.8114	0.0079	0.2324
0.9503	0.7596	0.0048	0.3400
0.0928	0.0536	**6.77E-11**	0.1706
0.7653	0.5065	0.0068	0.0796
0.0191	0.3558	**0**	0.0030
0.5663	0.4387	**6.45E-130**	0.0896
0.0241	0.1742	**0**	0.0012
0.4860	0.4582	0.0123	0.4123
0.5265	0.4908	0.0096	0.2911
0.3550	0.5830	0.3858	0.2384
NA	NA	0.6475	0.2821
0.7053	0.4186	0.3318	0.4304
0.4083	0.4163	0.1041	0.6953
0.1785	0.6408	0.0825	0.4612

0.1782	0.6441	0.0647	0.5232
NA	NA	0.4852	0.9489
NA	NA	0.5160	0.2230
0.6783	0.3804	0.6768	0.3215
NA	NA	0.0300	0.0184
0.0106	0.0026	**5.51E-15**	0.3421
0.0069	0.0017	**7.70E-15**	0.2186
NA	NA	8.74E-05	0.9354
0.9953	0.9881	0.4470	0.2492
NA	NA	0.0744	0.5470
0.0704	0.1977	0.0003	0.0018
NA	NA	0.0657	0.1294
0.0446	0.1657	**1.02E-20**	0.7419
0.0277	0.2201	**9.61E-20**	0.4261
NA	NA	0.1392	0.0211
NA	NA	0.6632	0.4854
NA	NA	0.2743	0.4877
0.0654	0.5604	0.0050	0.1247
NA	NA	0.1033	0.6713
NA	NA	0.0160	0.2049
0.3653	0.5452	0.3383	0.5034
0.3812	0.1870	0.3482	0.5034
NA	NA	0.0212	0.4154
NA	NA	0.5536	0.4353
NA	NA	0.8172	0.8550
NA	NA	0.8717	0.3505
NA	NA	0.5884	0.4137
NA	NA	0.0003	0.2247
0.0522	0.7895	**2.95E-13**	0.1483
0.0219	0.2806	0.0028	0.1407
NA	NA	0.0035	0.0474
NA	NA	0.0005	0.1605
NA	NA	1.40E-05	0.0244
NA	NA	0.0032	0.0276
0.8361	0.6203	**2.28E-31**	0.3958
NA	NA	0.0001	0.1449
NA	NA	0.0081	0.7190
NA	NA	NA	NA
NA	NA	0.0028	0.1254
NA	NA	NA	NA
NA	NA	NA	NA
NA	NA	NA	NA
NA	NA	NA	NA
NA	NA	NA	NA
NA	NA	NA	NA
0.6123	0.5972	0.0024	0.1994
NA	NA	0.0115	0.2575

NA	NA	1.12E-05	0.0342
0.4668	0.3494	**1.89E-15**	0.7608
NA	NA	1.95E-05	0.1974
0.4568	0.2186	0.0342	0.0524
0.5448	0.2794	0.0455	0.0426
NA	NA	0.1278	0.0016
0.0773	0.3505	**7.84E-28**	0.2583
0.4579	0.3495	0.6201	0.6516
0.0155	0.5398	0.3649	0.0926
NA	NA	0.1709	0.6496
NA	NA	**1.73E-08**	0.1479
NA	NA	0.2602	0.1467
NA	NA	0.3026	0.6459
NA	NA	0.1256	0.0340
NA	NA	0.0199	0.2955
NA	NA	0.1741	0.3351
0.3636	0.8145	**4.67E-33**	0.0994
NA	NA	0.6504	0.8147
NA	NA	0.8928	0.8014
0.5918	0.9493	0.0544	0.6480
NA	NA	0.6079	0.1213
0.6464	0.3513	0.0040	0.9816
0.0770	0.0538	**2.44E-12**	0.6479
0.5997	0.5266	6.87E-08	0.6597
0.2201	0.9243	**3.77E-28**	0.6636
NA	NA	0.0661	0.0261
0.9907	0.8964	**1.67E-23**	0.0214
0.9914	0.9776	**1.54E-21**	0.0190
NA	NA	0.2774	0.2024
0.4799	0.7317	0.0876	0.1118
0.4861	0.3838	0.0009	0.0411
NA	NA	0.0906	0.6617
NA	NA	0.5078	0.3441
NA	NA	0.0135	0.1509
0.4847	0.7183	1.87E-05	0.1672
0.6110	0.7997	1.44E-05	0.1129
NA	NA	0.0651	0.1382
0.6278	0.3800	**4.36E-12**	0.2160
NA	NA	0.0160	0.0183
0.4824	0.9012	0.0070	0.0070
0.3781	0.2041	0.0115	0.0262
NA	NA	0.7639	0.3771
NA	NA	0.9789	0.7822
NA	NA	0.2542	0.3227
NA	NA	0.0694	0.0499
0.0495	0.7010	**4.65E-182**	0.0109
NA	NA	**3.58E-48**	0.1060

NA	NA	0.0003	0.6017
NA	NA	0.0007	0.2685
0.0260	0.0520	**2.72E-22**	0.0007
0.0064	0.0301	**2.12E-24**	0.0007
NA	NA	0.9505	0.6666
0.5782	0.9357	**1.95E-12**	0.0120
0.5555	0.9218	**2.98E-13**	0.0174
NA	NA	0.0475	0.6707
NA	NA	0.0009	0.0830
NA	NA	0.7632	0.5209
0.0831	0.1257	**4.88E-27**	0.6514
0.0823	0.1253	**4.11E-28**	0.7652
0.1094	0.5951	**0**	0.5620
0.2388	0.5484	**8.61E-179**	0.8171
0.2367	0.0911	0.0268	0.2947
0.1311	0.9325	**1.07E-09**	0.0038
0.1356	0.9276	**4.15E-10**	0.0069
NA	NA	0.2814	0.3694
NA	NA	0.8599	0.5010
0.0113	0.0048	0.0012	0.0278
NA	NA	0.8336	0.4737
0.4436	0.2118	0.1513	0.3450
0.1240	0.7982	**5.45E-66**	0.2792
0.0033	0.4273	**8.65E-148**	0.1640
0.0029	0.4954	**1.42E-148**	0.1413
NA	NA	0.2571	0.4200
NA	NA	0.3166	0.1537
NA	NA	0.0678	0.0771
NA	NA	0.4716	0.1362
0.6623	0.9497	1.43E-05	0.0198
0.8114	0.6738	0.0006	0.1058
NA	NA	0.0002	0.6329
NA	NA	NA	NA
NA	NA	NA	NA
0.5219	0.5428	**3.46E-09**	0.2345
0.0265	0.0188	0.4621	0.2416
0.2173	0.0832	0.0007	0.3594
0.2569	0.1021	3.09E-07	0.0074
0.4017	0.1903	**1.48E-08**	0.0065
NA	NA	2.65E-05	0.6730
NA	NA	5.41E-06	0.2475
NA	NA	0.4664	0.1786
NA	NA	0.2269	0.2785
0.7228	0.4221	**3.87E-24**	0.1057
0.6420	0.6221	**9.78E-24**	0.4038
0.1439	0.7918	**5.28E-24**	0.1270
0.5091	0.3489	**1.03E-11**	0.4572

NA	NA	0.0391	0.4627
NA	NA	NA	NA
NA	NA	0.0017	0.0251
NA	NA	0.0775	0.1947
NA	NA	0.0209	0.1564
NA	NA	0.0243	0.3663
0.4023	0.1935	**4.49E-10**	0.5892
0.2394	0.8207	**3.64E-11**	0.0716
0.8587	0.6544	7.37E-05	0.8059
NA	NA	0.2506	0.0934
0.0304	0.9645	0.0276	0.0738
NA	NA	NA	NA
NA	NA	0.0377	0.3191
0.7154	0.6951	0.1132	0.3543
0.9334	0.7917	2.46E-05	0.2685
0.2252	0.9837	**5.19E-62**	0.3812
0.2123	0.9318	**1.37E-63**	0.2551
NA	NA	0.0005	0.1201
NA	NA	0.0027	0.1524
0.0004	0.0025	**0**	0.1123
0.0367	0.0847	**0**	0.1367
0.1193	0.7896	**0**	0.0369
0.0183	0.5749	**2.19E-189**	0.0673
NA	NA	NA	NA
NA	NA	NA	NA
NA	NA	0.1861	0.2921
NA	NA	0.4233	0.2646
NA	NA	0.2858	0.2189
0.3674	0.1809	0.2118	0.5710
NA	NA	0.5756	0.3416
NA	NA	0.0346	0.8295
NA	NA	0.0612	0.6713
NA	NA	0.0271	0.0456
NA	NA	0.0416	0.0813
0.4835	0.2731	**1.32E-11**	0.0083
0.5078	0.2445	**1.47E-12**	0.0202
NA	NA	4.26E-06	0.5512
0.8549	0.8097	0.3970	0.2414
0.8797	0.8745	0.4756	0.3129
NA	NA	0.0963	0.0611
NA	NA	0.2149	0.1777
NA	NA	NA	NA
0.8578	0.6581	0.0810	0.1261
0.2800	0.2432	0.7086	0.1598
0.8968	0.6529	0.8983	0.8012
0.4583	0.2503	0.0517	0.0831
0.4242	0.4414	**2.05E-16**	0.2136

0.6915	0.7623	0.4778	0.1078
0.8855	0.9523	0.5914	0.4836
0.3173	0.2919	0.1310	0.3055
0.8864	0.9816	0.0053	0.3458
NA	NA	0.0255	0.3079
0.8373	0.5512	0.2860	0.7236
NA	NA	0.2520	0.7124
NA	NA	0.2565	0.4942
0.7313	0.5314	**6.18E-10**	0.0033
0.0003	0.0001	**1.92E-09**	0.0074
0.0353	0.0116	**2.00E-10**	0.0246
0.6082	0.6716	**9.11E-38**	0.1555
0.3953	0.4609	**8.20E-44**	0.4203
0.6846	0.9525	0.0002	0.2987
NA	NA	0.0196	0.3694
NA	NA	0.1738	0.1498
NA	NA	0.1260	0.1247
NA	NA	0.0004	0.7204
NA	NA	0.0052	0.5153
NA	NA	0.0104	0.4988
NA	NA	0.1679	0.5438
NA	NA	0.0633	0.3974
0.8639	0.7362	**2.40E-10**	0.4897
0.7095	0.4150	**1.83E-30**	0.3396
NA	NA	1.04E-07	0.7358
0.6178	0.7979	0.0947	0.1411
0.3603	0.2453	7.08E-06	0.0192
0.9023	0.6504	0.0005	0.3043
0.4732	0.7605	**1.63E-11**	0.1915
0.9959	0.9950	**4.77E-21**	0.0496
NA	NA	0.0871	0.4727
NA	NA	0.5896	0.2561
NA	NA	NA	NA
0.8354	0.5649	0.0003	0.0055
0.6404	0.4349	0.0007	0.0075
NA	NA	0.0342	0.1926
NA	NA	0.4845	0.6934
0.2312	0.4690	**2.55E-08**	0.0281
NA	NA	0.0476	0.2485
NA	NA	0.0200	0.2970
0.9440	0.8457	0.0222	0.4264
0.9382	0.9566	0.0039	0.3377
0.9076	0.8509	**3.00E-09**	0.3906
0.5580	0.4907	2.29E-07	0.5416
0.9345	0.8921	0.9288	0.4040
0.8590	0.8179	0.9034	0.7858
0.8540	0.5743	0.8157	0.3482

NA	NA	0.0029	0.5570
0.8176	0.8097	6.15E-08	0.7931
NA	NA	0.6659	0.7422
0.0601	0.2493	1.79E-06	0.4970
0.7111	0.5617	0.0003	0.7410
0.3171	0.3597	3.83E-06	0.6416
NA	NA	0.0154	0.8064
0.0427	0.0321	0.4017	0.4327
0.2632	0.1060	8.86E-05	0.1138
NA	NA	NA	NA
0.0657	0.2504	**4.01E-70**	0.5471
NA	NA	0.0146	0.4321
NA	NA	0.0001	0.0888
NA	NA	**1.44E-08**	0.0660
NA	NA	**6.86E-58**	0.2326
NA	NA	**3.53E-23**	0.2464
0.0101	0.1961	**4.03E-08**	0.6572
0.1990	0.0862	0.0065	0.1852
0.7600	0.4652	0.0023	0.0759
0.2629	0.1158	0.0064	0.0552
NA	NA	0.3398	0.1161
0.9646	0.8059	0.0170	0.2571
NA	NA	0.0546	0.1435
NA	NA	0.1111	0.5115
NA	NA	0.6110	0.6649
0.0114	0.0384	8.71E-05	0.8077
0.0831	0.0412	0.0111	0.2965
0.0328	0.0214	0.0025	0.5438
0.5022	0.3439	0.4125	0.3596
0.8681	0.7299	**7.33E-31**	0.4318
0.9967	0.9983	**9.12E-30**	0.5857
NA	NA	**1.94E-09**	0.1348
0.5890	0.3492	0.0003	0.4725
NA	NA	0.3600	0.4952
NA	NA	0.5880	0.2509
NA	NA	0.0001	0.6308
0.4130	0.9890	**3.41E-11**	0.5380
NA	NA	0.0106	0.2461
NA	NA	0.2403	0.3703

Web Table 9: Percent variance explained by known and novel lipid index vari

Trait	Ancestry	Study	N	Lifestyle Exposure	Known Lipid Variants
HDL-C	European	Airwaves Study	14113	2.95%	9.59%
		ARIC	9045	3.98%	7.77%
		WGHS	23155	5.31%	9.28%
		Weighted Average	***46313***	***4.33%***	***9.08%***
	African	ARIC	2461	2.20%	8.07%
		JHS	1988	2.10%	4.83%
		Weighted Average	***4449***	***2.16%***	***6.62%***
	Asian	GenSALT	1813	1.86%	7.21%
		SCES	1853	0.54%	9.75%
		SiMES	2541	0.23%	8.56%
		SINDI	2496	1.63%	9.07%
		Weighted Average	***8703***	***1.04%***	***8.68%***
	Hispanic	***SOL***	***10088***	***1.80%***	***10.51%***
	Total	***Weighted Average***	***69553***	***3.41%***	***9.08%***
LDL-C	European	Airwaves Study	NA		
		ARIC	9045	0.14%	10.62%
		WGHS	23155	0.46%	12.63%
		Weighted Average	***32200***	***0.37%***	***12.07%***
	African	ARIC	2461	0.28%	5.41%
		JHS	1966	0.08%	4.23%
		Weighted Average	***4427***	***0.19%***	***4.89%***
	Asian	GenSALT	1790	0.19%	7.10%
		SCES	1853	0.19%	11.19%
		SiMES	2540	0.03%	8.46%
		SINDI	2495	0.05%	9.49%
		Weighted Average	***8678***	***0.10%***	***9.06%***
	Hispanic	SOL	***9864***	***0.08%***	***8.49%***
	Total	***Weighted Average***	***55169***	***0.26%***	***10.38%***
TG	European	Airwaves Study	NA		
		ARIC	9045	0.23%	8.25%
		WGHS	16705	1.70%	8.32%
		Weighted Average	***25750***	***1.18%***	***8.30%***
	African	ARIC	2461	0.25%	6.16%
		JHS	1988	0.18%	5.14%
		Weighted Average	***4449***	***0.22%***	***5.70%***
	Asian	GenSALT	1813	0.06%	7.35%
		SCES	NA		
		SiMES	NA		
		SINDI	NA		
		Weighted Average	***1813***	***0.06%***	***7.35%***
	Hispanic	SOL	***10089***	***0.04%***	***6.08%***
	Total	***Weighted Average***	***42101***	***0.76%***	***7.45%***

ants across multiple studies and ancestries.

Novel variants		
From novel variants	**From novel interactions**	**Total novel**
0.11%	0.02%	0.13%
0.00%	0.08%	0.08%
0.16%	0.01%	0.17%
0.11%	***0.03%***	***0.14%***
0.13%	0.20%	0.33%
0.00%	0.00%	0.00%
0.07%	***0.11%***	***0.18%***
0.00%	0.21%	0.21%
0.33%	0.00%	0.33%
0.00%	0.13%	0.13%
0.00%	0.34%	0.34%
0.07%	***0.18%***	***0.25%***
0.28%	***0.07%***	***0.35%***
0.13%	***0.06%***	***0.19%***
0.04%	0.00%	0.04%
0.21%	0.05%	0.26%
0.16%	***0.04%***	***0.20%***
0.53%	0.24%	0.77%
0.51%	0.00%	0.51%
0.52%	***0.13%***	***0.65%***
0.00%	0.17%	0.17%
0.40%	0.00%	0.40%
0.24%	0.00%	0.24%
0.19%	0.00%	0.19%
0.21%	***0.04%***	***0.25%***
0.25%	***0.18%***	***0.43%***
0.21%	***0.07%***	***0.29%***
0.32%	0.11%	0.42%
0.24%	0.00%	0.24%
0.27%	***0.04%***	***0.30%***
0.00%	0.16%	0.16%
0.21%	0.21%	0.42%
0.09%	***0.18%***	***0.28%***
0.00%	0.58%	0.58%
0.00%	***0.58%***	***0.58%***
0.36%	***0.11%***	***0.47%***
0.26%	***0.09%***	***0.35%***

Web Table 10: Regulatory information obtained from HaploReg and RegulomeDB for available var
Joint *P* -value). Any significant variant within +/- 1 Mbp of the index variant is shown here. Novel ir

rsID	CHR	BP (hg19)	BP (hg38)	Index Variant	Ref	Alt	AFR freq	AMR freq	ASN freq	EUR freq	GERP cons	SiPhy cons
rs9645452	1	25668326	25341835		C	T	0.21	0.49	0.73	0.45		
rs926438	1	25753638	25427147		C	T	0.78	0.49	0.25	0.54		
rs9438905	1	25764177	25437686	Y	A	G	0.8	0.49	0.25	0.54		
rs190737	1	26899444	26572953		C	A	0.52	0.67	0.98	0.53		
rs12759594	1	27002991	26676500		G	A	0.02	0.07	0.03	0.08		
rs35738294	1	27020133	26693642		C	T	0.02	0.06	0.03	0.07		
rs114165349	1	27021913	26695422	Y	G	C	0	0.03	0.02	0.03		
rs35615194	1	27118171	26791680		T	C	0.04	0.06	0.03	0.07		
rs35583548	1	27140149	26813658		G	A	0.04	0.06	0.03	0.07		
rs12753968	1	27197363	26870872		C	T	0.01	0.06	0.01	0.07		
rs34353981	1	27213362	26886871		T	C	0.01	0.06	0.01	0.07		
rs34339345	1	27226089	26899598		G	A	0	0.06	0.01	0.07		
rs6659176	1	27239920	26913429		C	G	0.05	0.06	0.01	0.07		
rs12728150	1	27268737	26942246		A	G	0.24	0.09	0.01	0.07		
rs6656815	1	27292462	26965971		G	A	0.23	0.09	0.01	0.07		
rs17343193	1	39881468	39415796		T	A	0.02	0.21	0.16	0.2		
rs61779313	1	39944249	39478577		T	C	0.02	0.22	0.13	0.23		
rs60069508	1	39964912	39499240		G	C	0.05	0.25	0.14	0.25		
rs61779359	1	40010235	39544563		T	C	0.02	0.16	0.12	0.23		
rs2068663	1	40038571	39572899		C	T	0.02	0.16	0.12	0.23		
rs4660303	1	40060473	39594801	Y	G	A	0.01	0.17	0.11	0.23		
rs61781390	1	40075894	39610222		G	A	0.01	0.16	0.11	0.22		
rs114337524	1	55446970	54981297		C	T	0.09	0.01	0	0		
rs12117661	1	55487346	55021673		C	G	0.42	0.25	0.11	0.22		
rs11591147	1	55505647	55039974	Y	G	T	0	0.02	0	0.02		
rs72660594	1	55636240	55170567		T	C	0	0.02	0	0.02		
rs67722862	1	55679666	55213993		T	A	0.08	0.02	0.06	0.04		
rs66679331	1	55691689	55226016		G	T	0.1	0.02	0.06	0.04		
rs60500353	1	62898984	62433313		C	T	0.27	0.1	0.17	0.13		
rs10493322	1	62905893	62440222		C	T	0.38	0.31	0.17	0.31		
rs10789117	1	63072265	62606594		A	C	0.69	0.34	0.22	0.31		
rs4495740	1	63124465	62658794	Y	T	G	0.41	0.3	0.17	0.31		
rs61775963	1	63202258	62736587		G	A,C	0.05	0.2	0.01	0.19		
rs7532549	1	93539656	93074099		G	T	0.16	0.61	0.65	0.67		
rs10874762	1	93639101	93173544		T	G	0.16	0.61	0.66	0.66		
rs35940311	1	93663604	93198047		G	A	0.2	0.61	0.64	0.66		
rs10874772	1	93787770	93322213		G	A	0.16	0.61	0.66	0.66		
rs4847240	1	93817946	93352389	Y	A	G	0.17	0.58	0.65	0.65		

rs2162276	1	93875371	93409814		G	T	0.59	0.71	0.72	0.82		
rs4970824	1	109715950	109173328		G	A	0	0.02	0	0.07		
rs35271870	1	109776285	109233663		T	C	0.01	0.04	0	0.07		
rs12740374	1	109817590	109274968		G	T	0.3	0.19	0.05	0.21		
rs1277930	1	109822143	109279521		G	A	0.2	0.77	0.94	0.78		
rs115967373	1	109831225	109288603		G	A	0.09	0.04	0.03	0.08		
rs115984459	1	109905778	109363156		G	A	0	0.02	0	0.06		
rs17586966	1	109955569	109412947		T	C	0.04	0.02	0	0.06		
rs62623713	1	110019439	109476817		A	G	0.02	0.02	0	0.06		
rs41279732	1	110032431	109489809		T	G	0.02	0.02	0	0.07		
rs115823613	1	110036634	109494012		C	T	0.04	0.01	0	0.06		
rs41301283	1	110049457	109506835		G	A	0.01	0.02	0	0.06		
rs114382843	1	110067787	109525165		T	C	0	0.02	0	0.03		
rs501163	1	110078434	109535812		A	G	0.83	0.18	0.34	0.19		
rs114003685	1	110122950	109580328		C	T	0	0	0	0.01		
rs116586116	1	110152069	109609447		A	G	0	0.01	0	0.02		
rs56079255	1	110162190	109619568		C	T	0	0.02	0	0.04		
rs650985	1	110201580	109658958		C	T	0.99	0.96	1	0.96		
rs1537234	1	110279821	109737199		C	A	0.16	0.48	0.85	0.43		
rs12753251	1	178529898	178560763	Y	G	A	0.19	0.39	0.51	0.48		
rs1689788	1	182144422	182175287	Y	T	C	0.18	0.3	0.27	0.3		
rs1779820	1	182176923	182207788		C	G	0.3	0.25	0.31	0.21		
rs2642438	1	220970028	220796686	Y	A	G	0.93	0.77	0.81	0.75		
rs1335920	1	221018288	220844946		C	T	0.05	0.14	0.03	0.15		
rs3738182	1	221057662	220884320		G	A	0.22	0.15	0.1	0.17		
rs10127775	1	230295789	230160042	Y	A	T	0.09	0.52	0.22	0.58		
rs74147717	1	234743676	234607930		C	G	0.2	0.03	0	0		
rs487738	1	234840803	234705056		A	G	0.71	0.78	0.85	0.68		
rs486142	1	234848609	234712862	Y	G	A	0.92	0.67	0.75	0.53		
rs11580878	1	234876434	234740687		A	G	0.06	0.31	0.28	0.48		
rs201445483	2	17890087	17708820	Y	T	TTG	0.38	0.07	0.04	0.05		
rs907866	2	20371380	20171619		G	A	0.46	0.44	0.33	0.43		
rs79800183	2	20978615	20778855		T	C	0.01	0.01	0	0.03		
rs6711016	2	21123352	20923592		C	A	0.05	0.22	0.57	0.25		
rs581411	2	21289432	21066560	Y	G	A	0.32	0.82	0.99	0.78		
rs28562532	2	21309122	21086250		C	T	0.33	0.14	0.01	0.18		
rs10221768	2	21417431	21194559		C	A	0.27	0.13	0	0.19		
rs78620068	2	21524000	21301128		G	A	0.01	0.06	0	0.1		
rs62129551	2	26940912	26718044		C	T	0.01	0.06	0	0.06		
rs72804857	2	27161476	26938608		G	C	0.02	0.13	0.2	0.13		
rs72808908	2	27242761	27019893		C	T	0.02	0.09	0	0.14		
rs186879900	2	27273641	27050773		G	A	0.01	0	0	0		
rs7588926	2	27342894	27120026		C	T	0.02	0.09	0	0.17		
rs41288799	2	27353630	27130762		G	C	0	0.02	0	0.04		
rs11695641	2	27354419	27131551		C	T	0.01	0.05	0	0.16		
rs2580754	2	27398196	27175328		T	A	0.2	0.58	0.89	0.71		
rs1275504	2	27416702	27193834		A	T	0.24	0.57	0.87	0.7		

rs1275535	2	27437496	27214628		C	T	0.19	0.57	0.88	0.71		
rs3769143	2	27450724	27227856		G	A	0.89	0.42	0.11	0.28		
rs11693052	2	27484620	27261752		A	G	0.88	0.42	0.12	0.28		
rs4665961	2	27500381	27277513		T	C	0.82	0.41	0.12	0.24		
rs4665963	2	27528692	27305824		T	C	0.87	0.41	0.13	0.24		
rs6731600	2	27531665	27308797		T	C	0.07	0.04	0	0.02		
rs4665378	2	27548038	27325171		A	C	0.73	0.42	0.13	0.39		
rs10205592	2	27568871	27346004		T	C	0.83	0.47	0.13	0.41		
rs6729709	2	27583156	27360289		G	A	0.75	0.43	0.14	0.37		
rs7586601	2	27584666	27361799		A	G	0.84	0.47	0.13	0.42		
rs4665972	2	27598097	27375230	Y	T	C	0.94	0.59	0.42	0.58		
rs1271144	2	27615294	27392427		C	T	0.74	0.43	0.14	0.38		
rs1728918	2	27635463	27412596		A	G	0.95	0.71	0.73	0.73		
rs4665978	2	27648726	27425859		T	A,C,G	0.87	0.48	0.14	0.41		
rs1260342	2	27663416	27440549		G	T	0.71	0.42	0.14	0.39		
rs780108	2	27684957	27462090		T	C	0.92	0.47	0.14	0.42		
rs8395	2	27715207	27492340		T	A	0.51	0.41	0.14	0.38		
rs1260326	2	27730940	27508073		T	C	0.88	0.59	0.44	0.59		
rs12995461	2	27778167	27555300		A	C	0.04	0.46	0.56	0.27		
rs12467476	2	27825715	27602848		T	C	0.03	0.46	0.56	0.27		
rs3749147	2	27851918	27629051		G	A	0.03	0.25	0.35	0.26		
rs34502053	2	27854524	27631657		G	A	0.03	0.25	0.35	0.26		
rs4666010	2	27878686	27655819		T	C	0.13	0.34	0.55	0.22		
rs13021208	2	27901728	27678861		C	T	0.02	0.19	0.36	0.23		
rs4616435	2	27933642	27710775		C	T	0.02	0.19	0.35	0.22		
rs10432705	2	27950837	27727970		G	A	0.02	0.2	0.35	0.23		
rs13030345	2	28003174	27780307		G	T	0.02	0.18	0.31	0.2		
rs77353560	2	28085544	27862677		C	A	0.01	0.19	0.27	0.2		
rs2305929	2	28113911	27891044		A	G	0.02	0.2	0.13	0.2		
rs4666074	2	28652023	28429156		C	G	0.35	0.73	0.34	0.79		
rs1111336	2	28657896	28435029	Y	A	C	0.15	0.23	0.62	0.22		
rs11887534	2	44066247	43839108		G	A,C	0.06	0.11	0.01	0.09		
rs4299376	2	44072576	43845437	Y	G	T	0.85	0.78	1	0.7		
rs2111622	2	53984823	53757686	Y	A	G	0.61	0.32	0.56	0.26		
rs4671046	2	62842243	62615108		A	T	0.06	0.15	0.21	0.13		
rs360804	2	62939397	62712262	Y	G	A	0.17	0.31	0.29	0.35		
rs10206947	2	63425505	63198370		G	A	0.38	0.28	0.62	0.19		
rs17508045	2	118576719	117819143		T	C	0	0.04	0	0.07		
rs72834335	2	118611529	117853953		G	A	0	0.02	0	0.03		
rs72834351	2	118638336	117880760		T	C	0	0.04	0	0.07		
rs56145894	2	118812449	118054873		C	T	0	0.04	0	0.08		
rs55809639	2	118842801	118085225	Y	T	A	0	0.06	0	0.09		
rs72839616	2	118846970	118089394		T	G	0	0.06	0	0.09		
rs7570971	2	135837906	135080336	Y	C	A	0.97	0.73	1	0.49		
rs13391980	2	165504841	164648331		G	A	0.21	0.09	0	0.15		
rs1128249	2	165528624	164672114	Y	G	T	0.79	0.29	0.1	0.41		
rs10176901	2	169830661	168974151	Y	G	A	0.54	0.5	0.7	0.59		

rs1047891	2	211540507	210675783	Y	C	A	0.31	0.34	0.14	0.3		
rs2972143	2	227116365	226251649	Y	A	G	0.68	0.72	0.94	0.63		
rs1584063	3	12266855	12225355	Y	G	A	0.64	0.39	0.38	0.46		
rs17819602	3	12507119	12465620		A	G	0.02	0.08	0	0.07		
rs111973309	3	12561138	12519639		G	A	0.02	0.08	0	0.09		
rs113760078	3	12585073	12543574		G	A	0.01	0.08	0	0.09		
rs113671109	3	12620885	12579386		T	C	0.33	0.23	0.03	0.23		
rs11711419	3	12667784	12626285		A	T	0.3	0.22	0.04	0.2		
rs113026294	3	12748879	12707380		G	A	0.03	0.06	0	0.06		
rs6771546	3	49968572	49931139		T	C	0.5	0.36	0.14	0.51		
rs34831713	3	50118748	50081315		T	C	0.51	0.64	0.86	0.51		
rs2013208	3	50129399	50091966	Y	C	A,G,T	0.61	0.65	0.86	0.51		
rs2856236	3	50161717	50124284		A	C	0.64	0.59	0.83	0.48		
rs4431046	3	135849123	136130281		A	C	0.57	0.76	0.82	0.73		
rs1154988	3	135925191	136206349	Y	T	A	0.71	0.8	0.86	0.77		
rs3821445	3	136002809	136283967		T	C	0.06	0.16	0.01	0.21		
rs610860	3	136052816	136333974		A	G	0.88	0.85	0.99	0.79		
rs17451107	3	156797609	157079820	Y	T	C	0.35	0.42	0.52	0.38		
rs80080062	3	185812169	186094380	Y	C	G	0.15	0.1	0.05	0.14		
rs34311866	4	951947	958159	Y	T	C	0.01	0.07	0.12	0.2		
rs3129320	4	3265130	3263403		G	C	0.56	0.4	0.38	0.45		
rs13116176	4	3436588	3434861		G	A	0.22	0.41	0.45	0.42		
rs13108218	4	3443931	3442204	Y	A	G	0.45	0.57	0.53	0.61		
rs59950280	4	3452345	3450618		G	A	0.66	0.35	0.39	0.32		
rs9884830	4	26027797	26026175		C	T	0.17	0.14	0	0.16		
rs7661844	4	87468625	86547472		C	T	0.16	0.43	0.57	0.56		
rs60695258	4	88022709	87101557	Y	C	T	0.2	0.37	0.37	0.36		
rs7656630	4	88173692	87252540		T	C	0.65	0.36	0.43	0.39		
rs13141053	4	88212545	87291393		G	A	0.28	0.34	0.35	0.4		
rs11735092	4	88226231	87305079		T	C	0.14	0.33	0.34	0.39		
rs13135092	4	103198082	102276925	Y	A	G	0	0.05	0	0.08		
rs71621626	4	103345983	102424826		C	T	0.01	0.05	0	0.09		
rs143528679	4	124558378	123637223	Y	A	G	0.87	0.97	0.99	0.99		
rs72729610	4	154190965	153269813	Y	A	G	0.03	0.09	0.04	0.15		
rs465002	5	55808475	56512648	Y	C	T	0.41	0.72	0.52	0.71		
rs10069709	5	74269562	74973737		A	T	0.07	0.22	0.39	0.26		
rs6897082	5	74330957	75035132		T	C	0.16	0.08	0.03	0.12		
rs7700965	5	74356857	75061032		T	C	0.88	0.42	0.47	0.41		
rs4704200	5	74569856	75274031		G	T	0.76	0.51	0.56	0.45		
rs12916	5	74656539	75360714		T	C	0.26	0.39	0.52	0.43		
rs4704220	5	74757556	75461731		G	A	0.94	0.45	0.51	0.42		
rs5744672	5	74877803	75581978		T	C	0.94	0.44	0.51	0.42		
rs984976	5	74910870	75615045		A	G	0.94	0.44	0.54	0.42		
rs34361	5	74971846	75676021		A	G	0.47	0.63	0.34	0.62		
rs2112347	5	75015242	75719417		T	G	0.51	0.38	0.53	0.38		
rs10056543	5	75143624	75847799		A	C	0.19	0.25	0.52	0.36		
rs56076449	5	132442190	133106498	Y	T	G	0.26	0.14	0.1	0.26		

rs79605869	5	156168529	156741518		C	T	0.01	0.01	0	0.01		
rs77643868	5	156219046	156792035		T	C	0.06	0.02	0	0		
rs17053943	5	156250595	156823584		T	C	0.24	0.02	0	0.01		
rs6882345	5	156397673	156970662		G	A	0.33	0.69	0.74	0.67		
rs10066168	5	156484218	157057207	Y	C	T	0.86	0.89	0.98	0.84		
rs31223	5	156625279	157198268		T	C	0.45	0.39	0.38	0.37		
rs2963472	5	157999022	158572014	Y	G	A	0.38	0.29	0.25	0.21		
rs2235215	6	16131156	16130925	Y	T	C	0.7	0.52	0.78	0.33		
rs4716048	6	16140827	16140596		C	G	0.46	0.38	0.46	0.29		
rs57977865	6	16189618	16189387		C	T	0.3	0.23	0.49	0.26		
rs13201341	6	25822661	25822433		C	T	0	0.02	0	0.07		
rs13198474	6	25874423	25874195		G	A	0.01	0.02	0	0.06		
rs17526722	6	25918855	25918627		G	A	0.01	0.04	0	0.07		
rs36012762	6	25980523	25980295		A	C	0.11	0.07	0.02	0.1		
rs116201501	6	25999149	25998921		C	T	0.11	0.07	0.02	0.1		
rs13191445	6	26015489	26015261		G	A	0.05	0.05	0	0.07		
rs41266779	6	26021872	26021644	Y	C	T	0	0.02	0	0.07		
rs35249036	6	26026163	26025935		C	G	0.1	0.07	0.02	0.1		
rs10484433	6	26030492	26030264		C	A	0.1	0.07	0.02	0.1		
rs13210041	6	26037601	26037373		G	A	0	0.02	0	0.07		
rs35506517	6	26044864	26044636		T	C	0.05	0.04	0	0.07		
rs67296946	6	26048559	26048331		T	G	0.17	0.08	0.02	0.1		
rs35050608	6	26067360	26067132		A	G	0.05	0.04	0	0.07		
rs34197618	6	26083519	26083291		T	C	0	0.02	0	0.07		
rs13200888	6	26100198	26099970		G	A	0.1	0.07	0.02	0.1		
rs13206501	6	26110148	26109920		T	C	0.17	0.08	0.02	0.1		
rs13197334	6	26122648	26122420		G	C	0.17	0.08	0.02	0.1		
rs36109883	6	26133070	26132842		G	A	0.02	0.04	0	0.08		
rs55706012	6	26266311	26266083		A	C	0.03	0.02	0	0.07		
rs34637389	6	26377991	26377763		C	G	0.01	0.04	0.01	0.12		
rs66757203	6	26454956	26454728		C	T	0.04	0.03	0.01	0.09		
rs2523569	6	31329921	31362144		T	G	0.07	0.07	0.13	0.18		
rs3130923	6	31462135	31494358		G	A	0.1	0.02	0.05	0.08		
rs3130616	6	31473746	31505969		G	A	0.1	0.03	0.05	0.08		
rs114060326	6	31492016	31524239		G	C	0	0.02	0	0.05		
rs115225594	6	31504805	31537028		G	A	0.03	0.03	0.01	0.06		
rs9267488	6	31514247	31546470		A	G	0.09	0.03	0.05	0.08		
rs2229094	6	31540556	31572779		T	C	0.28	0.3	0.19	0.3		
rs1800628	6	31546850	31579073		G	A	0.03	0.02	0	0.08		
rs139139829	6	31563571	31595794		C	T	0	0.03	0.01	0.06		
rs138719004	6	31576508	31608731		A	G	0.03	0.03	0	0.06		
rs114276434	6	31669585	31701808		T	C	0	0.02	0	0.06		
rs28745895	6	31709969	31742192		C	A	0.01	0.03	0	0.06		
rs187911831	6	31732942	31765165		C	T	0	0.02	0	0.06		
rs114936741	6	31744148	31776371		C	T	0	0.03	0	0.06		
rs142006308	6	31757791	31790014		G	A	0	0.04	0	0.06		
rs146752130	6	31768538	31800761		C	A	0	0.03	0	0.06		

rs115302857	6	31818719	31850942		G	C	0	0.03	0	0.06		
rs2763981	6	31840021	31872244	Y	T	A	0.89	0.89	0.82	0.74		
rs605203	6	31847012	31879235		C	A	0.89	0.91	0.83	0.7		
rs570263	6	31847196	31879419		T	C	0.89	0.91	0.83	0.7		
rs389883	6	31947460	31979683		G	T	0.94	0.87	0.69	0.78		
rs1150754	6	32050758	32082981		C	T	0.05	0.04	0.02	0.11		
rs6907508	6	34592090	34624313	Y	A	G	0.01	0.06	0.01	0.11		
rs2764203	6	34708901	34741124		A	G	0.34	0.12	0.01	0.13		
rs112563428	6	34800435	34832658		C	T	0.01	0.06	0.01	0.11		
rs56144648	6	41988742	42021004	Y	G	A	0.02	0.14	0.06	0.26		
rs6458314	6	42922215	42954477		C	A	0.95	0.59	0.33	0.59		
rs2395943	6	42940673	42972935		A	G	0.96	0.59	0.33	0.6		
rs998584	6	43757896	43790159		C	A	0.17	0.51	0.58	0.51		
rs11967262	6	43760327	43792590	Y	C	G	0.15	0.51	0.59	0.52		
rs2749008	6	52626120	52761322	Y	C	T	0.97	0.76	0.86	0.64		
rs9496567	6	100602753	100154877	Y	G	A	0.3	0.18	0	0.23		
rs13210143	6	116389636	116068473	Y	G	A	0.32	0.48	0.06	0.39		
rs9491694	6	127437100	127115955	Y	T	A	0.4	0.35	0.46	0.25		
rs2908522	6	139835399	139514262	Y	C	G	0.29	0.57	0.31	0.54		
rs146203232	6	160521885	160100853		C	T	0.01	0.04	0	0.05		
rs662138	6	160564476	160143444		C	G	0.04	0.3	0	0.18		
rs77881708	6	160685047	160264015		G	A	0.01	0.04	0.18	0.04		
rs10080815	6	160687412	160266380		T	G	0.01	0.16	0.07	0.01		
rs3120137	6	160771192	160350160		G	A	0	0.06	0	0.14		
rs9457927	6	160910282	160489250		A	G	0.01	0.15	0.03	0.01		
rs5014650	6	161099503	160678471	Y	G	A	0.13	0.13	0	0.17		
rs2315065	6	161108144	160687112		C	A	0	0.05	0	0.09		
rs3729790	7	6426954	6387323		G	A	0.06	0.19	0.22	0.22		
rs836546	7	6479668	6440037	Y	G	A	0.05	0.17	0.26	0.21		
rs6461354	7	17914600	17874977	Y	C	T	0.82	0.49	0.48	0.38		
rs6952559	7	18030170	17990547		T	C	0.1	0.52	0.27	0.58		
rs66476925	7	21611399	21571781	Y	G	C	0.06	0.13	0.21	0.2		
rs4722551	7	25991826	25952206	Y	T	C	0.02	0.14	0.02	0.17		
rs10260606	7	44584551	44544952		G	C	0.31	0.27	0.41	0.19		
rs217381	7	44606217	44566618	Y	C	G	0.45	0.36	0.02	0.41		
rs10271770	7	44627398	44587799		C	G	0.12	0.23	0	0.29		
rs732797	7	44646763	44607164		G	A	0.55	0.62	0.98	0.57		
rs42132	7	72809618	73395288		C	T	0.03	0.09	0.11	0.16		
rs1178947	7	72850178	73435848		T	C	0.46	0.14	0.11	0.2		
rs79862839	7	72921609	73507279		T	C	0.04	0.06	0.11	0.12		
rs34594435	7	72977249	73562919		C	T	0.05	0.1	0.1	0.2		
rs9638182	7	72999105	73584775		T	G	0.16	0.1	0.1	0.19		
rs79624003	7	73012785	73598455	Y	A	G	0.07	0.06	0.1	0.12		
rs799160	7	73060006	73645676		C	T	0.38	0.64	0.76	0.52		
rs8891	7	73096993	73682663		T	C	0.21	0.3	0.35	0.45		
rs13234498	7	73104905	73690575		T	G	0.22	0.3	0.35	0.45		
rs35459363	7	73118033	73703703		G	A	0.34	0.33	0.32	0.45		

rs13245286	7	73122508	73708178		C	T	0.22	0.31	0.32	0.44		
rs74708934	7	80089656	80460340		G	A	0.09	0	0	0		
rs58737329	7	80188082	80558766		A	G	0.1	0	0	0		
rs139906208	7	80322438	80693122		T	G	0.15	0	0	0		
rs4470970	7	80344361	80715045	Y	A	G	0.65	0.93	0.9	0.89		
rs11762784	7	130424646	130739885	Y	G	A	0.16	0.41	0.31	0.46		
rs73729083	7	137559799	137875053	Y	T	C	0.11	0.04	0.02	0		
rs2911971	8	6607634	6750113	Y	C	G	0.97	0.72	0.7	0.62		
rs2921097	8	8281142	8423632		T	C	0.52	0.65	0.88	0.5		
rs4841132	8	9183596	9326086	Y	A	G	0.9	0.81	0.99	0.92		
rs35899262	8	9210559	9353049		C	A	0.02	0.23	0.01	0.1		
rs11783641	8	9221207	9363697		G	A	0.01	0.23	0.01	0.1		
rs71516504	8	9224410	9366900		C	T	0.03	0.22	0.01	0.09		
rs6995541	8	10671260	10813750		A	G	0.26	0.36	0.34	0.32		
rs7841093	8	10683333	10825823		C	A	0.36	0.32	0.17	0.34		
rs73201442	8	11516594	11659085		T	C	0.02	0.12	0	0.14		
rs804281	8	11611865	11754356		A	G	0.84	0.68	0.98	0.56		
rs1004712	8	11622293	11764784		C	T	0.5	0.39	0.53	0.36		
rs1090107	8	11632528	11775019	Y	A	G	0.23	0.58	0.97	0.41		
rs2686187	8	11654796	11797287		G	A	0.39	0.55	0.67	0.4		
rs6601616	8	11703652	11846143		A	G	0.2	0.23	0.49	0.19		
rs1495743	8	18273300	18415790	Y	G	C	0.64	0.65	0.43	0.75		
rs4921675	8	19616581	19759070		C	G	0.77	0.76	0.68	0.72		
rs6981571	8	19651457	19793946		C	G	0.15	0.18	0.06	0.15		
rs11986182	8	19727447	19869936		A	T	0.21	0.1	0.17	0.16		
rs12550077	8	19751399	19893888		G	A	0.1	0.11	0.09	0.16		
rs3988301	8	19770379	19912868		T	G	0.12	0.11	0.16	0.13		
rs10096633	8	19830921	19973410		C	T	0.46	0.12	0.1	0.16		
rs114650503	8	19884257	20026746		G	A	0.04	0.07	0.11	0.13		
rs16842	8	19968929	20111418		T	C	0.48	0.27	0.36	0.25		
rs56204645	8	55421769	54509209	Y	T	C	0.21	0.15	0.22	0.17		
rs10957054	8	59336556	58423997	Y	C	T	0.93	0.77	0.83	0.65		
rs2326077	8	59385919	58473360		C	T	0.75	0.76	0.82	0.65		
rs2737216	8	116630079	115617852	Y	A	T	0.73	0.66	0.83	0.58		
rs148079817	8	116781554	115769328		C	T	0	0	0	0.02		
rs10955992	8	121872464	120860224	Y	A	C	0.4	0.7	0.67	0.65		
rs2954021	8	126482077	125469835		A	G	0.66	0.51	0.58	0.51		
rs2954038	8	126507389	125495147	Y	C	A	0.92	0.76	0.71	0.69		
rs9650459	8	144280215	143198753		C	T	0.36	0.46	0.35	0.47		
rs56960668	8	144300760	143218568	Y	G	A	0.3	0.32	0.49	0.32		
rs1215112	9	15303583	15303585	Y	G	A	0.91	0.87	0.98	0.87		
rs7035578	9	78745177	76130261	Y	G	A	0.09	0.14	0	0.14		
rs144592826	9	107489026	104726745		A	T	0.09	0.01	0	0		
rs2575876	9	107665739	104903458	Y	G	A	0.25	0.28	0.25	0.24		
rs1125873	9	107721423	104959142		A	T	0.74	0.58	0.5	0.5		
rs2027399	9	107743287	104981006		G	A	0.59	0.44	0.48	0.42		
rs13284665	9	131513370	128751091	Y	A	G	0.03	0.1	0.08	0.12		

rs35434910	9	136042324	133166937		T	A	0.03	0.24	0	0.22		
rs11795370	9	136059193	133183806		G	T	0.15	0.29	0.01	0.27		
rs11794634	9	136090813	133215426		T	C	0.17	0.23	0	0.32		
rs8176757	9	136130012	133254625		A	C	0.49	0.43	0.48	0.31		
rs495828	9	136154867	133279294	Y	G	T	0.15	0.13	0.22	0.22		
rs9650778	9	136184798	133317963		C	T	0.05	0.03	0.02	0.09		
rs28658542	9	136214276	133347421		C	A	0.07	0.08	0.01	0.11		
rs56343119	9	136237672	133370796		C	A	0.08	0.09	0.01	0.14		
rs17474001	9	136267149	133402020		C	T	0.08	0.07	0.02	0.14		
rs3802548	10	45952745	45457297	Y	T	A	0.18	0.26	0.05	0.27		
rs41274050	10	52573772	50814012	Y	C	T	0	0.01	0	0.01		
rs10761716	10	64882300	63122540	Y	C	G	0.25	0.34	0.41	0.43		
rs13095	10	64914372	63154612		G	C	0.27	0.37	0.39	0.47		
rs10822164	10	65127258	63367498		G	A	0.27	0.37	0.36	0.46		
rs7085018	10	65286667	63526907		T	C	0.26	0.36	0.41	0.47		
rs7895549	10	65357438	63597678		G	A	0.43	0.51	0.44	0.48		
rs10740138	10	65395133	63635373		A	C	0.4	0.58	0.55	0.54		
rs7068500	10	94795705	93035948		C	T	0.44	0.27	0.74	0.3		
rs4919594	10	94823596	93063839		G	C	0.29	0.28	0.75	0.31		
rs4418728	10	94839724	93079967	Y	G	T	0.26	0.44	0.74	0.49		
rs7096937	10	113950418	112190660	Y	T	C	0.78	0.67	0.74	0.68		
rs4573621	10	113987548	112227790		A	G	0.16	0.26	0.32	0.17		
rs12412743	10	114045333	112285575		C	T	0.15	0.27	0.3	0.15		
rs7076205	10	124629253	122869737		G	C	0.09	0.22	0.23	0.32		
rs7910726	10	124662143	122902627		A	G	0.57	0.46	0.51	0.57		
rs7082181	10	124680468	122920952		C	A	0.4	0.44	0.51	0.57		
rs7904973	10	124693587	122934071	Y	G	T	0.45	0.48	0.54	0.59		
rs2896635	11	13359745	13338198	Y	T	A	0.86	0.62	0.35	0.7		
rs10832961	11	18653957	18632410	Y	C	G	0.4	0.71	0.47	0.73		
rs150757221	11	46612511	46590961		C	G	0	0.08	0	0.02		
rs76533702	11	46692689	46671139		C	T	0.01	0.19	0.57	0.11		
rs4491174	11	46721605	46700055		A	C	0.01	0.28	0.57	0.14		
rs58922799	11	46725196	46703646		C	T	0.01	0.27	0.57	0.14		
rs3136449	11	46744470	46722920		G	A	0.01	0.27	0.57	0.14		
rs7941964	11	46805575	46784025		G	A	0.88	0.7	0.42	0.86		
rs898604	11	46917983	46896432		G	A	0.68	0.68	0.41	0.85		
rs4576779	11	47121547	47099996		C	G	0.01	0.27	0.65	0.15		
rs4752968	11	47185457	47163906		A	G	0.02	0.26	0.62	0.16		
rs11039122	11	47213117	47191566		G	A	0.06	0.43	0.21	0.42		
rs901746	11	47260319	47238768		A	G	0.57	0.39	0.74	0.31		
rs2167079	11	47270255	47248704		C	T	0.57	0.38	0.74	0.31		
rs3758673	11	47278917	47257366		C	T	0.44	0.36	0.74	0.3		
rs10501321	11	47294626	47273075		T	C	0.58	0.39	0.69	0.31		
rs326214	11	47298360	47276809		G	A	0.39	0.6	0.31	0.69		
rs10769254	11	47362465	47340914	Y	G	C	0.35	0.29	0.55	0.18		
rs12146565	11	47398963	47377412		G	A	0.07	0.36	0.34	0.32		
rs74206205	11	47422772	47401221		T	C	0.01	0.19	0.32	0.13		

rs11820650	11	47424963	47403412		A	G	0.37	0.23	0.32	0.15		
rs7130693	11	47452321	47430770		T	C	0.55	0.33	0.35	0.3		
rs35184771	11	47475189	47453637		G	T	0.06	0.36	0.32	0.36		
rs12798346	11	47583121	47561569		C	T	0.06	0.36	0.33	0.36		
rs7945473	11	47589707	47568155		C	T	0.14	0.37	0.32	0.34		
rs59837204	11	47596783	47575231		G	A	0.2	0.18	0.25	0.14		
rs2030166	11	47602729	47581177		C	T	0.14	0.38	0.33	0.36		
rs11605348	11	47606483	47584931		G	A	0.07	0.37	0.31	0.35		
rs12799623	11	47622139	47600587		G	A	0.06	0.36	0.32	0.36		
rs12419692	11	47624714	47603162		C	A	0.06	0.36	0.33	0.36		
rs10838747	11	47716324	47694772		G	C	0.05	0.36	0.33	0.36		
rs7927771	11	47781306	47759754		A	G	0.05	0.36	0.32	0.35		
rs12798109	11	47889850	47868298		C	T	0.06	0.36	0.32	0.35		
rs2930191	11	47946836	47925284		G	A	0.25	0.44	0.33	0.37		
rs1503190	11	48117873	48096321		A	G	0.47	0.81	0.81	0.8		
rs11529374	11	48223758	48202206		A	G	0	0.09	0.16	0.11		
rs11039603	11	48256786	48235234		G	A	0	0.09	0.16	0.12		
rs16905753	11	48285906	48264354		C	T	0.27	0.12	0.16	0.13		
rs11039666	11	48324841	48303289		C	G	0	0.1	0.16	0.12		
rs10838873	11	48337765	48316213		T	C	0.26	0.13	0.17	0.15		
rs4351844	11	48437221	48415669		C	A	0.25	0.13	0.16	0.13		
rs11530224	11	48552070	48530518		T	C	0	0.09	0.16	0.11		
rs10769562	11	49066148	49044596		G	A	0.46	0.15	0.16	0.14		
rs11040242	11	49096981	49075429		G	A	0.45	0.14	0.16	0.13		
rs658118	11	49255042	49233490	Y	C	T	0.25	0.1	0.12	0.07		
rs11040387	11	49493736	49472184		G	A	0.04	0.09	0.21	0.12		
rs11246533	11	51377255	54742025	Y	C	T	0.08	0.09	0.15	0.13		
rs72486173	11	55084997	55317521		T	C	0.06	0.09	0.15	0.13		
rs141250596	11	55104771	55337295		C	A	0.04	0.09	0.15	0.13		
rs11229777	11	55227708	55460232		C	T	0.09	0.11	0.16	0.14		
rs72472105	11	55235199	55467723		G	A	0.06	0.09	0.15	0.13		
rs1459102	11	55339287	55571811		A	G	0.06	0.09	0.15	0.13		
rs11230302	11	55362569	55595093		C	T	0	0.09	0.15	0.13		
rs12225322	11	55392438	55624962		C	T	0.06	0.12	0.23	0.18		
rs11230523	11	55415618	55648142		C	T	0.06	0.12	0.25	0.18		
rs11230661	11	55451313	55683837	Y	G	A	0.07	0.14	0.24	0.18		
rs140655242	11	55515459	55747983		C	A	0.06	0.09	0.15	0.13		
rs10897279	11	55565572	55798096		T	A	0.07	0.09	0.15	0.14		
rs11231127	11	55572895	55805419		A	T	0.06	0.09	0.15	0.13		
rs1396622	11	55598039	55830563		A	T	0.07	0.09	0.15	0.13		
rs11231228	11	55601978	55834502		C	T	0.06	0.09	0.15	0.13		
rs11231378	11	55634086	55866610		C	T	0.06	0.09	0.15	0.13		
rs12419022	11	55681865	55914389		T	C	0.06	0.09	0.15	0.13		
rs79426455	11	55697591	55930115		C	T	0.06	0.09	0.15	0.13		
rs4628693	11	55740226	55972750		C	T	0.06	0.09	0.15	0.13		
rs12417606	11	55750479	55983003		C	T	0.07	0.09	0.15	0.13		
rs11231821	11	55777052	56009576		C	G	0.07	0.09	0.15	0.14		

rs1552151	11	55780951	56013475		C	T	0.06	0.09	0.15	0.13		
rs11559557	11	55844685	56077209		G	A	0.07	0.09	0.15	0.13		
rs61751933	11	55889895	56122419		C	T	0.07	0.09	0.15	0.13		
rs17150102	11	55904382	56136906		A	C	0.07	0.09	0.15	0.13		
rs12282595	11	55933084	56165608		C	T	0.14	0.1	0.13	0.13		
rs10896123	11	55968854	56201378		G	A	0.07	0.09	0.13	0.13		
rs74707325	11	56005562	56238086		T	A	0.08	0.08	0.13	0.12		
rs10501349	11	56021284	56253808		G	A	0.08	0.09	0.13	0.13		
rs7933691	11	56046900	56279424		G	A	0.08	0.09	0.13	0.13		
rs11227810	11	56071851	56304375		A	G	0.17	0.11	0.13	0.13		
rs1842675	11	56080824	56313348		G	C	0.08	0.09	0.13	0.12		
rs60446066	11	56102442	56334966		A	G	0.08	0.09	0.13	0.13		
rs971758	11	56126967	56359491		A	C	0.92	0.9	0.87	0.87		
rs7124724	11	56151135	56383659		T	C	0.92	0.91	0.87	0.87		
rs6591323	11	56180753	56413277		A	G	0.92	0.91	0.87	0.88		
rs7109453	11	56182514	56415038		G	A	0.92	0.91	0.87	0.88		
rs618889	11	56308536	56541060		T	G	0.83	0.9	0.87	0.87		
rs1945263	11	56340201	56572725		G	A	0.68	0.89	0.87	0.87		
rs4939081	11	56394288	56626812		G	A	0.7	0.89	0.87	0.87		
rs174536	11	61551927	61784455		A	C	0.04	0.55	0.41	0.36		
rs102274	11	61557826	61790354		T	C	0.04	0.55	0.41	0.36		
rs4246215	11	61564299	61796827		G	T	0.04	0.55	0.41	0.38		
rs174551	11	61573684	61806212		T	C	0.04	0.48	0.38	0.34		
rs174566	11	61592362	61824890	Y	A	G	0.2	0.57	0.41	0.36		
rs174449	11	61640379	61872907		G	A	0.35	0.4	0.74	0.63		
rs174469	11	61667443	61899971		C	T	0.08	0.22	0.32	0.16		
rs11231698	11	63877163	64109691		C	T	0.17	0.07	0.39	0.07		
rs190528931	11	63911273	64143801	Y	C	A	0	0.02	0	0.05		
rs56271783	11	64004723	64237251		G	C	0	0.02	0	0.05		
rs35169799	11	64031241	64263769		C	T	0	0.04	0	0.07		
rs73502335	11	64100401	64332929		G	A	0.29	0.15	0.47	0.08		
rs11236519	11	75459015	75747970		C	T	0.23	0.14	0.2	0.09		
rs1806895	11	75473715	75762670	Y	T	C	0.39	0.16	0.25	0.1		
rs11501918	11	75521196	75810151		G	A	0.37	0.14	0.2	0.08		
rs10899135	11	75533949	75822904		C	T	0.38	0.14	0.21	0.08		
rs61270867	11	116499500	116628783		A	G	0.26	0.14	0.2	0.19		
rs509728	11	116533167	116662450	Y	G	C	0	0.01	0	0.05		
rs1558860	11	116607368	116736652		A	C	1	0.89	0.76	0.91		
rs10750096	11	116656788	116786072		C	A	0.94	0.88	0.76	0.91		
rs2072560	11	116661826	116791110		T	C	1	0.89	0.76	0.92		
rs6589572	11	116681563	116810847		G	A	0.88	0.81	0.65	0.83		
rs5141	11	116702123	116831407		T	C	0.9	0.85	0.65	0.87		
rs10750098	11	116705568	116834852		G	T	0.9	0.85	0.66	0.88		
rs2070665	11	116707684	116836968		A	G	0.9	0.86	0.63	0.89		
rs6589574	11	116730638	116859922		A	G	0.95	0.87	0.62	0.88		
rs7925256	11	117045335	117174619		T	C	0.91	0.89	0.7	0.88		
rs1242229	11	117062370	117191654		T	C	0.91	0.83	0.51	0.87		

rs641620	11	117074229	117203513		T	C	0.47	0.32	0.56	0.16		
rs659955	11	117080379	117209663		T	A	0.11	0.17	0.48	0.13		
rs187929675	11	117111368	117240652		C	T	0.01	0.01	0	0.01		
rs116987336	11	117175658	117304942		G	A	0	0.01	0	0.03		
rs670712	11	126060666	126190771		G	A	0.11	0.24	0.08	0.41		
rs580145	11	126079939	126210044		C	T	0.39	0.66	0.87	0.58		
rs75757016	11	126212022	126342127		G	A	0.02	0.04	0.1	0.05		
rs78471630	11	126221298	126351403		G	T	0.01	0.05	0.1	0.07		
rs76970536	11	126250680	126380785	Y	G	A	0.01	0.06	0.17	0.08		
rs78459082	12	20442785	20289851	Y	G	C	0.07	0.23	0.08	0.2		
rs74484931	12	49611304	49217521		A	G	0.01	0.02	0	0.03		
rs4898521	12	49755162	49361379	Y	T	A	1	0.98	1	0.96		
rs11172134	12	57645789	57252006		T	A	0.07	0.27	0.11	0.16		
rs540730	12	57807114	57413331	Y	T	C	0.51	0.68	0.9	0.79		
rs73119306	12	57826982	57433199		A	G	0.07	0.28	0.08	0.19		
rs507562	12	57849768	57455985		C	G	0.53	0.28	0.32	0.23		
rs6606717	12	109873227	109435422		A	C	0.77	0.52	0.47	0.56		
rs2058804	12	109909011	109471206		A	G	0.74	0.5	0.33	0.55		
rs10744826	12	109965512	109527707	Y	C	G	0.71	0.51	0.29	0.55		
rs7134594	12	110000193	109562388		C	T	0.71	0.51	0.29	0.56		
rs7954144	12	110015893	109578088		A	G	0.72	0.51	0.29	0.56		
rs7310615	12	111865049	111427245	Y	C	G	0.97	0.7	0.99	0.53		
rs10849948	12	111875410	111437606		A	G	0.77	0.36	0.88	0.2		
rs7137828	12	111932800	111494996		C	T	0.97	0.7	0.99	0.53		
rs12579287	12	112090814	111653010		A	G	0.77	0.35	0.9	0.17		
rs594570	12	112164622	111726818		A	G	0.77	0.34	0.89	0.17		
rs6489793	12	112249884	111812080		T	G	0.76	0.35	0.86	0.16		
rs2269803	12	112326145	111888341		T	C	0.77	0.36	0.86	0.16		
rs3742000	12	112338539	111900735		T	C	0.76	0.36	0.86	0.16		
rs61670030	12	112351854	111914050		C	T	0.76	0.36	0.86	0.16		
rs7972112	12	112505182	112067378		T	A	0.76	0.35	0.86	0.16		
rs2004910	12	121374727	120936924		A	G	0.12	0.5	0.49	0.37		
rs7954331	12	121398657	120960854		G	T	0.92	0.65	0.52	0.64		
rs2244608	12	121416988	120979185	Y	A	G	0.11	0.34	0.42	0.34		
rs1169314	12	121443116	121005313		A	G	0.13	0.36	0.52	0.31		
rs3213545	12	121471337	121033534		G	A	0.13	0.3	0.49	0.3		
rs7956284	12	123183017	122698470		G	A	0.29	0.23	0.47	0.14		
rs545234	12	123188076	122703529		G	T	0.29	0.22	0.46	0.14		
rs2262194	12	123198921	122714374		T	G	0.33	0.25	0.48	0.18		
rs2454702	12	123209159	122724612		C	T	0.33	0.24	0.49	0.18		
rs10444449	12	123764271	123279724		A	G	0.1	0.13	0.3	0.09		
rs7298909	12	123830939	123346392	Y	C	T	0.9	0.87	0.7	0.9		
rs28786830	12	123860472	123375925		C	G	0.91	0.87	0.7	0.91		
rs12298484	12	124418674	123934127		C	T	0.31	0.33	0.14	0.36		
rs4765219	12	124440110	123955563		C	A	0.31	0.32	0.09	0.36		
rs11057413	12	124489162	124004615		A	G	0.36	0.33	0.09	0.36		
rs825452	12	124509177	124024630		G	A	0.43	0.55	0.45	0.58		

rs10773112	12	125338529	124853983		C	T	0.43	0.59	0.6	0.71		
rs67053123	12	125353810	124869264		T	A	0.03	0.13	0.22	0.13		
rs57276302	12	125363987	124879441	Y	C	A	0.01	0.12	0.23	0.12		
rs12832859	12	125372916	124888370		C	T	0.02	0.12	0.23	0.12		
rs9534323	13	32950257	32376120		A	G	0.5	0.53	0.55	0.54		
rs10492397	13	32976358	32402221		G	A	0.15	0.17	0.35	0.16		
rs7140110	13	114544024	113841051	Y	T	C	0.24	0.29	0.24	0.31		
rs6573778	14	24872209	24403003	Y	T	C	0.76	0.71	0.93	0.53		
rs2498786	14	105262368	104796031		C	G	0.28	0.47	0.22	0.63		
rs45490496	14	105272678	104806341	Y	A	T	0.1	0.46	0.22	0.63		
rs28364406	15	42679423	42387225	Y	C	T	0	0.04	0	0.02		
rs184334219	15	42721845	42429647		G	A	0	0.04	0	0.02		
rs62020665	15	43020324	42728126		C	G	0	0.08	0	0.09		
rs149492745	15	43099550	42807352		C	T	0	0.01	0	0.02		
rs143875230	15	43278726	42986528		G	A	0	0.02	0	0.02		
rs62019362	15	43414115	43121917		C	T	0	0.11	0	0.13		
rs117578063	15	43580645	43288447		C	T	0	0.03	0	0.03		
rs528517	15	43612925	43320727		A	G	0.75	0.23	0.5	0.11		
rs45617141	15	43623397	43331199		T	G	0	0.02	0	0.01		
rs2278860	15	43659046	43366848		A	G	0.69	0.22	0.5	0.1		
rs149181595	15	43685807	43393609		A	C	0	0.02	0	0.02		
rs150844304	15	43726625	43434427	Y	A	C	0	0.02	0	0.02		
rs55707100	15	43820717	43528519		C	T	0	0.02	0	0.02		
rs2470130	15	43829615	43537417		G	A	0.7	0.21	0.48	0.09		
rs56397895	15	43891235	43599037		G	C	0.74	0.22	0.45	0.1		
rs2260160	15	43895643	43603445		C	A,G,T	0.56	0.19	0.33	0.08		
rs141866277	15	43950699	43658501		A	T	0	0.02	0	0.02		
rs2467426	15	43989518	43697320		A	G	0.5	0.2	0.37	0.09		
rs147233090	15	44028047	43735849		C	T	0	0.02	0	0.02		
rs117519814	15	44052248	43760050		G	A	0	0.05	0.15	0.05		
rs2788	15	44064886	43772688		A	G	0.34	0.19	0.31	0.09		
rs28546844	15	44082088	43789890		C	A	0.33	0.18	0.29	0.09		
rs3759791	15	44090798	43798600		T	C	0.33	0.19	0.31	0.09		
rs28509275	15	44098105	43805907		C	G,T	0.1	0.18	0.3	0.09		
rs13329084	15	44151063	43858865		G	A	0.02	0.14	0.24	0.08		
rs138570705	15	44266730	43974532		G	A	0	0.01	0	0.02		
rs144972973	15	44564692	44272494		A	G	0	0.01	0	0.02		
rs28487964	15	44784375	44492177	Y	T	A	0	0.02	0	0.02		
rs1532085	15	58683366	58391167		A	G	0.49	0.59	0.48	0.63		
rs1077834	15	58723479	58431280		T	C	0.54	0.39	0.43	0.21		
rs7174174	15	63372327	63080128		T	C	0.49	0.22	0.02	0.27		
rs76127683	15	63391362	63099163	Y	G	C	0.62	0.81	0.97	0.73		
rs7193144	16	53810686	53776774		T	C	0.45	0.26	0.16	0.42		
rs147056003	16	56388396	56354484		T	G	0.1	0.1	0.13	0.1		
rs117262820	16	56437620	56403708		A	G	0	0.01	0	0.04		
rs282225	16	56583042	56549130		A	G	0.91	0.93	0.92	0.92		
rs45540935	16	56627641	56593729		G	A	0.1	0.09	0.25	0.1		

rs11863743	16	56633321	56599409		C	T	0.07	0.07	0.2	0.1		
rs59238099	16	56651160	56617248		A	T	0.29	0.09	0.26	0.09		
rs112792569	16	56658745	56624833		G	C	0.09	0.01	0	0.02		
rs1846692	16	56671696	56637784		T	C	0.52	0.72	0.52	0.76		
rs72824235	16	56676399	56642487		T	A	0	0.06	0	0.08		
rs3859113	16	56699967	56666055		C	T	0.86	0.98	1	0.94		
rs55994220	16	56702883	56668971		C	G	0.01	0.06	0	0.1		
rs2062545	16	56704125	56670213		G	A	0.65	0.96	1	0.96		
rs4784709	16	56711375	56677463		T	A	0.82	0.98	1	0.97		
rs4783953	16	56721262	56687350		A	T	0.01	0.07	0	0.11		
rs74023363	16	56736490	56702578		G	A	0.19	0.19	0.23	0.12		
rs4583235	16	56758596	56724684		G	A	0.14	0.1	0.13	0.1		
rs77050717	16	56767381	56733469		G	A	0	0.01	0	0.02		
rs77850047	16	56885915	56852003		C	T	0.13	0.1	0.13	0.1		
rs11648751	16	56937262	56903350		C	T	0.17	0.19	0.09	0.13		
rs59515242	16	56945049	56911137		C	A	0.13	0.12	0.23	0.23		
rs12448528	16	56985555	56951643		A	G	0.85	0.8	0.93	0.77		
rs11076175	16	57006378	56972466		A	G	0.27	0.17	0.11	0.21		
rs75911530	16	57049137	57015225		G	A	0	0.01	0	0.03		
rs111843362	16	57139069	57105157		C	T	0	0.03	0	0.05		
rs7186799	16	57220016	57186104		A	C	0.3	0.48	0.38	0.45		
rs13336686	16	57256949	57223037		T	C	0.38	0.5	0.38	0.49		
rs2046532	16	57283085	57249173		C	T	0.03	0.36	0.37	0.36		
rs8058985	16	57293282	57259370		G	A	0.08	0.36	0.37	0.36		
rs2232722	16	66585611	66551708		T	C	0.1	0.01	0	0		
rs57912912	16	66668592	66634689		T	C	0.09	0.01	0	0		
rs363199	16	66835391	66801488		G	A	0.08	0.01	0	0		
rs191201199	16	66911321	66877418		G	T	0.09	0.01	0	0		
rs34621310	16	66944180	66910277	Y	C	T	0.09	0.01	0	0		
rs66645535	16	66996156	66962253		G	A	0.18	0.01	0	0		
rs7185839	16	67052047	67018144		T	G	0.6	0.11	0.04	0.07		
rs66907233	16	67079680	67045777		C	T	0.59	0.1	0.04	0.07		
rs7184692	16	67180171	67146268		T	C	0.82	0.12	0.04	0.07		
rs1106304	16	67197138	67163235		C	T	0.18	0.01	0	0		
rs61684153	16	67202206	67168303		G	C	0.22	0.04	0	0.03		
rs2233455	16	67207933	67174030		C	G,T	0.32	0.08	0.02	0.06		
rs13339140	16	67213923	67180020		C	T	0.3	0.06	0.01	0.06		
rs9939768	16	67219107	67185204		G	C	0.47	0.09	0.02	0.06		
rs9932087	16	67232360	67198457		T	C	0.3	0.06	0.01	0.06		
rs73586989	16	67234741	67200838		A	G	0.28	0.06	0.01	0.06		
rs12051247	16	67241282	67207379		C	T	0.29	0.06	0.01	0.06		
rs13338688	16	67248831	67214928		G	A	0.3	0.06	0.01	0.06		
rs6499118	16	67265360	67231457		C	A	0.71	0.1	0.02	0.06		
rs9940665	16	67289841	67255938		C	T	0.5	0.09	0.02	0.07		
rs8044843	16	67318242	67284339		A	G	0.76	0.14	0.03	0.1		
rs16957291	16	67326102	67292199		T	A	0.76	0.14	0.03	0.1		
rs114089132	16	67378461	67344558		C	T	0.04	0.01	0	0.03		

rs145348547	16	67428096	67394193		G	A	0.04	0.01	0	0.03		
rs8052687	16	67446037	67412134		T	G	0.75	0.14	0.02	0.1		
rs12935253	16	67466430	67432527		T	A,C	0.75	0.12	0.01	0.1		
rs55877766	16	67473389	67439486		G	A	0.74	0.1	0.01	0.09		
rs77576274	16	67519266	67485363		C	G	0.18	0.02	0	0		
rs13338499	16	67520123	67486220		A	G	0.72	0.12	0.01	0.1		
rs34697097	16	67555339	67521436		A	C	0.03	0.01	0	0.03		
rs13334205	16	67581883	67547980		A	G	0.76	0.14	0.01	0.13		
rs8046907	16	67591389	67557486		A	G	0.36	0.1	0.01	0.12		
rs111893345	16	67607848	67573945		C	T	0.17	0.04	0.01	0.09		
rs60990105	16	67680956	67647053		T	A	0.31	0.15	0.03	0.12		
rs67114979	16	67691645	67657742		G	T	0.21	0.14	0.03	0.11		
rs7187476	16	67699948	67666045		T	C	0.72	0.24	0.03	0.16		
rs56047901	16	67742326	67708423		G	A	0.23	0.15	0.03	0.12		
rs55661503	16	67836552	67802649		T	A	0.23	0.17	0.03	0.13		
rs2292316	16	67861134	67827231		C	G	0.23	0.16	0.03	0.13		
rs8060967	16	67871501	67837598		C	T	0.24	0.16	0.03	0.13		
rs1124324	16	67897487	67863584		C	T	0.23	0.16	0.03	0.13		
rs56374641	16	67908713	67874810		G	T	0.23	0.16	0.03	0.13		
rs73594554	16	67920049	67886146		G	A	0.23	0.16	0.03	0.13		
rs55781197	16	67940350	67906447		A	G	0.23	0.16	0.03	0.13		
rs1134760	16	67964203	67930300		T	C	0.52	0.23	0.12	0.18		
rs20549	16	67969930	67936027		A	G,T	0.69	0.25	0.12	0.18		
rs1109166	16	67977382	67943479		T	C	0.74	0.25	0.12	0.18		
rs2292318	16	67985706	67951803		C	T	0.23	0.16	0.12	0.14		
rs255056	16	68016185	67982282	Y	G	C	0.18	0.18	0.12	0.15		
rs255052	16	68024995	67991092		G	A	0.22	0.18	0.12	0.15		
rs112358753	16	68046052	68012149		C	T	0.06	0.16	0.12	0.14		
rs55682260	16	68057880	68023977		G	A	0.07	0.16	0.12	0.15		
rs79323429	16	68084594	68050691		A	G	0.07	0.16	0.12	0.14		
rs55857142	16	68236741	68202838		A	T	0.06	0.15	0.12	0.14		
rs8057119	16	68268836	68234933		C	T	0.31	0.14	0.12	0.12		
rs7189155	16	68277882	68243979		G	C	0.04	0.13	0.12	0.13		
rs12447119	16	68297928	68264025		G	A	0.03	0.12	0.11	0.11		
rs8060690	16	68340085	68306182		G	T	0.14	0.1	0.08	0.13		
rs73613962	16	68361974	68328071		T	G	0.13	0.09	0.08	0.13		
rs57434514	16	68402649	68368746		G	A	0.14	0.1	0.09	0.13		
rs72801761	16	71859690	71825787		G	A	0.09	0.14	0.19	0.15		
rs4788561	16	71878255	71844352		G	A	0.38	0.61	0.93	0.44		
rs2288030	16	71914107	71880204		G	A	0.38	0.61	0.93	0.44		
rs4788450	16	71955400	71921497		T	G	0.55	0.63	0.93	0.46		
rs117844066	16	72001521	71967622		G	C	0.02	0.32	0.24	0.13		
rs11648003	16	72052348	72018449		A	G	0.06	0.2	0.26	0.23		
rs12924886	16	72075593	72041694		A	T	0.06	0.18	0.32	0.18		
rs4788458	16	72088675	72054776		T	C	0.66	0.43	0.4	0.53		
rs3794695	16	72097827	72063928	Y	C	T	0.1	0.18	0.33	0.19		
rs2287997	16	72140553	72106654		G	A	0.09	0.17	0.32	0.18		

rs57186116	16	72198051	72164152		C	T	0.04	0.1	0.31	0.07		
rs2023929	16	72236956	72203057		G	A	0.02	0.29	0.27	0.14		
rs2925979	16	81534790	81501185	Y	T	C	0.67	0.82	0.59	0.7		
rs8076462	17	37400025	39243772		G	C	0.21	0.66	0.75	0.74		
rs8076494	17	37516722	39360469		T	C	0.51	0.31	0.25	0.25		
rs12948560	17	37570986	39414733		A	G	0.47	0.67	0.72	0.74		
rs34957982	17	37647716	39491463		T	C	0.27	0.68	0.76	0.75		
rs412430	17	37737094	39580841		C	G	0.3	0.69	0.75	0.75		
rs11078917	17	37746359	39590106		A	C	0.21	0.59	0.57	0.72		
rs9915323	17	37770481	39614228		A	T	0.3	0.56	0.51	0.71		
rs1495099	17	37784464	39628211		C	G	0.19	0.55	0.5	0.71		
rs881844	17	37810218	39653965	Y	C	G	0.18	0.52	0.48	0.67		
rs931992	17	37821435	39665182		G	T	0.18	0.52	0.48	0.68		
rs3764351	17	37824339	39668086		G	A	0.34	0.52	0.51	0.66		
rs732083	17	37834367	39678114		G	A	0.17	0.5	0.48	0.67		
rs11653998	17	37877447	39721194		C	G	0.18	0.5	0.48	0.67		
rs4795393	17	37893484	39737231		C	T	0.18	0.46	0.47	0.63		
rs11658993	17	37940808	39784555		C	T	0.18	0.37	0.35	0.48		
rs9908132	17	38042777	39886524		T	A	0.37	0.4	0.31	0.52		
rs62067034	17	38063738	39907485		C	T	0.13	0.37	0.31	0.51		
rs8076131	17	38080912	39924659		G	A	0.85	0.65	0.67	0.52		
rs7221814	17	38089717	39933464		A	G	0.85	0.66	0.64	0.54		
rs4580194	17	38126477	39970224		A	G	0.3	0.52	0.46	0.43		
rs3907022	17	38134889	39978636		T	C	0.29	0.41	0.48	0.46		
rs2227333	17	38174167	40017914		C	G	0.05	0.38	0.41	0.36		
rs2302776	17	38178149	40021896		A	G	0.43	0.5	0.44	0.42		
rs76868109	17	41776943	43699575		A	C	0	0.08	0.01	0.04		
rs77697917	17	41840849	43763481		C	T	0	0.02	0	0.03		
rs72836561	17	41926126	43848758		C	T	0	0.02	0	0.03		
rs35946235	17	42007616	43930248		A	T	0.07	0.28	0.07	0.39		
rs1731897	17	42015818	43938450		G	A	0.08	0.29	0.07	0.42		
rs231473	17	42018471	43941103		T	C	0.54	0.67	0.93	0.56		
rs3809863	17	45385012	47307646		C	T	0.44	0.41	0.27	0.48		
rs12600603	17	45390951	47313585		G	C	0.43	0.41	0.27	0.48		
rs9911944	17	45498937	47421571		G	T	0.43	0.39	0.32	0.46		
rs9895274	17	45539117	47461751		C	T	0.43	0.41	0.28	0.47		
rs8077106	17	45653291	47575925		T	G	0.5	0.6	0.66	0.54		
rs11870935	17	45732605	47655239	Y	G	A	0.46	0.6	0.65	0.53		
rs56325564	17	45766771	47689405		G	A	0.36	0.35	0.33	0.4		
rs9893629	17	45800177	47722811		T	C	0.6	0.35	0.38	0.34		
rs75003668	17	64195431	66199313		A	G	0	0.04	0	0.04		
rs8178824	17	64224775	66228657	Y	C	T	0	0.05	0	0.04		
rs8071366	17	66825940	68829799		G	A	0.28	0.24	0.29	0.19		
rs1373068	17	66901215	68905074		T	G	0.63	0.37	0.42	0.3		
rs76321556	17	66977337	68981196		A	C	0	0.02	0	0.03		
rs117753190	17	67136325	69140184	Y	C	G	0	0.02	0	0.03		
rs72631343	17	67191270	69195129		C	G	0.06	0.12	0.51	0.13		

rs77262773	17	67249711	69253570		C	T	0	0.01	0	0.02		
rs150685018	17	67366944	69370803		C	T	0.09	0.05	0	0.06		
rs75016991	17	67424508	69428367		C	A	0	0.01	0	0.02		
rs181130756	17	67559986	69563845		C	T	0	0.01	0	0.02		
rs62079153	17	76370896	78374815		C	T	0.2	0.51	0.33	0.51		
rs8071884	17	76398058	78401977	Y	C	G	0.59	0.63	0.5	0.64		
rs189595952	18	46458337	48931967		C	A	0	0.01	0	0.01		
rs138215167	18	46486011	48959641		G	A	0	0.02	0	0.01		
rs12969081	18	46994549	49468179		C	T	0.03	0.17	0	0.2		
rs2156499	18	47007234	49480864	Y	G	A	0.08	0.33	0.32	0.29		
rs1943676	18	47017820	49491450		A	G	0.34	0.42	0.42	0.36		
rs6507928	18	47054073	49527703		G	C	0.63	0.61	0.5	0.67		
rs9958734	18	47118398	49592028		T	C	0.16	0.13	0.46	0.07		
rs2156552	18	47181668	49655298		A	T	0.97	0.9	0.83	0.82		
rs6507945	18	47243912	49717542		A	C	0.8	0.53	0.33	0.56		
rs524925	18	47306236	49779866		A	G	0.96	0.94	0.99	0.87		
rs104223	18	47343351	49816981		T	G	0.73	0.82	0.83	0.75		
rs488191	18	47385799	49859429		A	G	1	0.96	1	0.92		
rs6567160	18	57829135	60161902		T	C	0.24	0.15	0.2	0.23		
rs58084604	18	57849429	60182196	Y	C	T	0.29	0.15	0.21	0.23		
rs4804411	19	7222377	7222366	Y	G	C	0.73	0.56	0.51	0.58		
rs146439891	19	8410381	8345497		C	T	0.01	0.02	0	0.02		
rs116843064	19	8429323	8364439	Y	G	A	0	0.02	0	0.03		
rs74377788	19	8453203	8388319		C	A	0.06	0.28	0.08	0.33		
rs10421495	19	8454523	8389639		A	G	0.77	0.48	0.1	0.55		
rs12976739	19	8461663	8396779		G	A	0.52	0.42	0.13	0.42		
rs3815783	19	8503025	8438141		G	A	0.14	0.33	0.43	0.35		
rs1812467	19	8546920	8482036		G	A	0.11	0.33	0.42	0.34		
rs60318332	19	8565131	8500247		A	G	0.19	0.09	0.15	0.11		
rs117162033	19	8627569	8562685		C	T	0	0.01	0	0.02		
rs73007316	19	10640859	10530183		G	A	0.11	0.16	0.09	0.15		
rs113370024	19	10657028	10546352		A	T	0.13	0.09	0.07	0.06		
rs56395932	19	10665530	10554854		A	C	0.11	0.13	0.09	0.15		
rs1465700	19	10680621	10569945		G	A	0.13	0.15	0.15	0.16		
rs11542916	19	10694720	10584044		G	A	0.01	0.06	0	0.07		
rs1811376	19	10751080	10640404		G	A	0.98	0.92	1	0.92		
rs145517816	19	10795968	10685292		C	T	0	0.02	0	0.04		
rs4425006	19	10813364	10702688		T	C	0.99	0.93	1	0.91		
rs2287029	19	10916684	10806008		C	T	0.02	0.14	0.18	0.18		
rs12611335	19	10944040	10833364		A	G	0.37	0.29	0.44	0.28		
rs11881156	19	10950125	10839449		C	T	0.09	0.14	0.19	0.16		
rs17850995	19	11034039	10923363		T	A	0.01	0.08	0	0.05		
rs12978180	19	11041052	10930376		T	C	0.39	0.36	0.62	0.43		
rs12611283	19	11055299	10944623		T	A	0.11	0.27	0.26	0.23		
rs73015007	19	11183837	11073161		G	A	0.02	0.19	0.02	0.24		
rs10402112	19	11191677	11081001		T	A	0.35	0.17	0.04	0.1		
rs11671872	19	11265020	11154344		G	A	0.29	0.3	0.01	0.43		

rs4804573	19	11277232	11166556		G	A,T	0.75	0.38	0.29	0.48		
rs737338	19	11347657	11236981		C	T	0.22	0.15	0.23	0.04		
rs3745683	19	11348521	11237845		G	A	0.22	0.18	0.23	0.07		
rs143729015	19	19130750	19019941		G	A	0	0.01	0	0.05		
rs73008942	19	19155672	19044863		G	A	0	0.02	0	0.05		
rs80341032	19	19207229	19096420		G	A	0	0.04	0.05	0.05		
rs61061000	19	19283268	19172459		C	A,T	0.12	0.07	0.13	0.1		
rs113954889	19	19294392	19183583		T	A	0.13	0.07	0.13	0.1		
rs8100140	19	19314526	19203717		A	G	0.69	0.69	0.66	0.62		
rs2228603	19	19329924	19219115		C	T	0.01	0.02	0.06	0.07		
rs72999033	19	19366632	19255823		C	T	0.01	0.02	0	0.06		
rs58542926	19	19379549	19268740		C	T	0.04	0.07	0.07	0.07		
rs8107974	19	19388500	19277691		A	T	0.19	0.09	0.1	0.07		
rs56255430	19	19477877	19367068		A	C	0.02	0.07	0.09	0.08		
rs3794991	19	19610596	19499787		C	T	0.07	0.08	0.1	0.08		
rs7252888	19	19628037	19517228		G	A	0.16	0.29	0.29	0.16		
rs56397647	19	19642795	19531986		C	T	0.13	0.14	0.16	0.11		
rs17216588	19	19664077	19553268		C	T	0.02	0.08	0.1	0.08		
rs17217098	19	19702384	19591575		G	A	0	0.03	0	0.07		
rs2304128	19	19746151	19635342	Y	G	T	0.22	0.12	0.06	0.08		
rs58434384	19	19786099	19675290		A	G	0.25	0.13	0.14	0.08		
rs17699261	19	19819843	19709034		A	G	0.01	0.06	0.2	0.05		
rs16996277	19	19854296	19743487		C	G	0.01	0.04	0.2	0.06		
rs57457691	19	33911705	33420799	Y	T	C	0.65	0.58	0.44	0.61		
rs8107530	19	44836400	44332247		C	T	0	0.02	0	0.03		
rs17347726	19	44934842	44430667		G	C	0.01	0.11	0.06	0.09		
rs3745148	19	44988716	44484505		G	A	0.04	0.13	0.08	0.1		
rs117999134	19	45012505	44508453		G	A	0.05	0.19	0.19	0.13		
rs144439590	19	45041317	44537330		C	T	0	0.03	0	0.02		
rs62119267	19	45134682	44631381		A	C	0	0.03	0	0.01		
rs76075198	19	45179631	44676359		C	T	0	0.04	0	0.01		
rs62117160	19	45232161	44728895		G	A	0.01	0.04	0	0.02		
rs1531517	19	45242173	44738916	Y	G	A	0.25	0.12	0.19	0.05		
rs148933445	19	45302504	44799247		G	A	0	0.01	0	0.01		
rs118147862	19	45319631	44816374		G	A	0	0.04	0	0.02		
rs283809	19	45387057	44883800		A	G	0.36	0.13	0.08	0.04		
rs111784051	19	45402262	44899005		T	G	0.1	0.02	0.05	0.03		
rs429358	19	45411941	44908684		T	C	0.26	0.11	0.09	0.14		
rs12721046	19	45421254	44917997		G	A	0.02	0.08	0.1	0.16		
rs111789331	19	45427125	44923868		T	A	0.02	0.08	0.1	0.16		
rs12721109	19	45447221	44943964		G	A	0	0	0	0.02		
rs5167	19	45448465	44945208		T	G	0.51	0.47	0.58	0.37		
rs117261169	19	45491032	44987774		C	T	0	0.02	0	0.01		
rs35577563	19	45504349	45001091		C	G	0.73	0.56	0.6	0.4		
rs34827707	19	45541782	45038524		G	A	0	0.01	0	0.02		
rs3178166	19	45594170	45090912		A	G	0.26	0.36	0.1	0.48		
rs7255018	19	45603962	45100704		G	T	0.05	0.23	0.03	0.29		

rs12981729	19	45652193	45148935		G	A	0.09	0.27	0.1	0.3		
rs28469095	19	45655333	45152075		T	C	0.06	0.11	0.07	0.11		
rs149553138	19	45672478	45169220		G	A	0.01	0.01	0	0.04		
rs10402523	19	45687930	45184672		T	G	0.41	0.38	0.21	0.36		
rs181765708	19	45880690	45377432		C	T	0	0.01	0.01	0.03		
rs7255743	19	46018119	45514861		G	A	0	0	0	0.03		
rs2238689	19	46178661	45675403		T	C	0.54	0.4	0.64	0.42		
rs454715	19	49114236	48610979		T	G	0.87	0.73	0.99	0.63		
rs112593985	19	49158532	48655275		A	G	0.2	0.27	0.01	0.38		
rs12462111	19	49171306	48668049		C	T	0.13	0.31	0.01	0.42		
rs681343	19	49206462	48703205		C	T	0.49	0.38	0.01	0.43		
rs35866622	19	49218060	48714803		C	T	0.07	0.3	0.01	0.43		
rs8112983	19	49229525	48726268		T	C	0.16	0.35	0.03	0.47		
rs838145	19	49248730	48745473		G	A	0.97	0.75	0.99	0.58		
rs8103840	19	49254955	48751698		C	T	0.45	0.58	0.65	0.51		
rs28873836	19	52314655	51811402		G	C	0.18	0.28	0.21	0.24		
rs7252805	19	52343422	51840169		T	C	0.58	0.41	0.43	0.41		
rs3848561	19	52379623	51876370		C	T	0.52	0.3	0.31	0.22		
rs62133135	19	54753202	54249344		T	C	0.05	0.33	0.06	0.38		
rs377681	19	54766423	54262573		A	G	0.17	0.23	0.74	0.17		
rs398217	19	54793038	54289184		A	G	0.2	0.38	0.76	0.2		
rs367070	19	54800500	54296648	Y	A	G	0.08	0.27	0.71	0.18		
rs1645783	19	54827401	54316130		T	A,C	0.19	0.37	0.8	0.28		
rs12979085	19	54837165	54325893		G	A	0.18	0.42	0.76	0.29		
rs73106353	20	17837293	17856649		C	T	0.06	0.31	0.24	0.3		
rs2328223	20	17845921	17865277	Y	A	C	0.19	0.26	0.22	0.25		
rs3746427	20	33730464	35142661		A	G	0.9	0.44	0.35	0.54		
rs4911477	20	33780985	35193182	Y	T	C	0.12	0.48	0.63	0.44		
rs6029125	20	39089475	40460835		T	C	0.27	0.17	0	0.14		
rs1012167	20	39159119	40530479		T	C	0.79	0.33	0.57	0.37		
rs6029182	20	39179402	40550762		A	C	0.5	0.27	0.6	0.36		
rs6129730	20	39654545	41025905		A	G	0.03	0.22	0.69	0.13		
rs6072263	20	39705546	41076906		T	C	0.77	0.5	0.81	0.46		
rs6029549	20	39754695	41126055		C	G	0.76	0.49	0.81	0.46		
rs3795128	20	39774163	41145523		T	C	0.77	0.5	0.81	0.47		
rs753381	20	39797465	41168825		T	C	0.97	0.57	0.81	0.54		
rs2050058	20	39906988	41278348	Y	G	A	0.63	0.37	0.63	0.33		
rs6016545	20	39958950	41330310		T	C	0.74	0.49	0.8	0.46		
rs6124342	20	39996771	41368131		T	A	0.01	0.11	0.23	0.09		
rs4810315	20	40014674	41386034		G	A	0.45	0.48	0.88	0.34		
rs116847251	20	42958768	44330128		G	A	0	0.01	0	0.04		
rs1800961	20	43042364	44413724	Y	C	T	0	0.04	0.01	0.03		
rs79833227	20	44446643	45818004		C	A	0.12	0.13	0.03	0.18		
rs6073958	20	44551855	45923216	Y	T	C	0.28	0.15	0.13	0.22		
rs1057208	20	44563007	45934368		C	T	0.03	0.12	0.02	0.2		
rs6065908	20	44569930	45941291		C	T	0.03	0.12	0.02	0.2		
rs6073971	20	44589970	45961331		C	T	0.03	0.12	0.02	0.2		

rs6073985	20	44630804	46002165		A	G	0.01	0.07	0.02	0.09		
rs77547060	20	44661945	46033306		A	C	0.01	0.07	0.03	0.09		
rs6063050	20	45604240	46975601	Y	T	C	0.23	0.24	0	0.24		
rs235314	21	46271452	44851537	Y	C	T	0.32	0.39	0.39	0.54		
rs7445	22	21977047	21622758	Y	C	G,T	0.15	0.34	0.47	0.2		
rs5754426	22	21980638	21626349		T	C	0.11	0.34	0.47	0.2		
rs5754467	22	21985094	21630805		A	G	0.13	0.36	0.47	0.2		
rs5749600	22	21999292	21645003		A	G	0.55	0.44	0.49	0.24		
rs4384	22	38572440	38176433		G	C	0.62	0.51	0.37	0.43		
rs4820323	22	38599767	38203760	Y	C	G	0.58	0.53	0.66	0.6		

iants significant in the combined Stage 1 + 2 analyses (2 DF
ndex variant names are highlighted in green.

Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound
	10 tissues		
	5 tissues		
	BLD		
23 tissues	5 tissues	15 tissues	YY1
24 tissues		48 tissues	8 bound proteins
BLD	7 tissues	BLD,BLD	12 bound proteins
	FAT, BLD		
	BLD		
23 tissues	4 tissues		
6 tissues	4 tissues	GI,LIV	
	LIV		
5 tissues	14 tissues		
	4 tissues	MUS,MUS	
	6 tissues		
	GI, BLD	5 tissues	GATA3
BLD, HRT	16 tissues	BLD	
6 tissues	7 tissues	10 tissues	ZNF263
8 tissues	8 tissues		ERALPHA_A
	6 tissues		
14 tissues	9 tissues	12 tissues	
	BRN, MUS		
24 tissues	GI	9 tissues	
		14 tissues	CTCF,RAD21
	ESDR, LIV		
BLD, SKIN	11 tissues	BLD,SKIN	

			SETDB1
9 tissues	16 tissues	32 tissues	23 bound proteins
	ESDR, BRN, SKIN		
	BRN		
	STRM, BRN, SKIN	SKIN	
	SKIN, MUS, BLD		CTCF
	ADRL, MUS, SPLN		
24 tissues	HRT	52 tissues	35 bound proteins
	5 tissues		
BRN, MUS, GI	8 tissues	HRT,MUS	
	BRN, GI, VAS		
	ESC		
23 tissues	6 tissues	35 tissues	6 bound proteins
CRVX	13 tissues	CRVX	
	GI		
	BLD, BRN		
	7 tissues	SKIN	
	9 tissues		
GI	4 tissues	4 tissues	CTCF
	HRT		
6 tissues	11 tissues	6 tissues	
14 tissues		23 tissues	POL2,KAP1
	GI, BLD	BLD	
LIV	5 tissues		
			GATA1
	11 tissues	GI,KID,LIV	HNF4A,RXRA
	LIV		
		SKIN	
	4 tissues		
	IPSC, MUS, BLD	BLD	FOSL1,GATA2,NRSF
BLD	12 tissues	GI,GI,BLD	
24 tissues		53 tissues	51 bound proteins
MUS			
	ESDR, PANC		
	5 tissues		
	BLD		

	SKIN		
7 tissues	14 tissues		
	5 tissues		
HRT	13 tissues	BRN,BRN,PLCNT	
	ADRL		POL2
		OVRY	
	IPSC		
	BLD		
LIV	LNG	LNG,LIV	HNF4A
	LIV		
	BLD		
	BLD		
	BRST, ADRL	BLD	
	LIV		
	ADRL		
24 tissues		52 tissues	38 bound proteins
	GI	GI	
	5 tissues		MAFF,MAFK
	FAT		
	6 tissues		
	11 tissues	OVRY	
	GI, LNG		
24 tissues		45 tissues	POL2,POL2B
	5 tissues		
	9 tissues	SKIN	
LIV, GI		GI,LIV	4 bound proteins
	LIV, GI		
LIV	7 tissues		
	BLD, PANC	BLD	PU1
	ESDR, BRN	BRN,BRN	
BLD	ESDR, BLD, BRN	BRN,BRN	
LIV	4 tissues		
24 tissues		39 tissues	6 bound proteins
	4 tissues	7 tissues	
		THYM	

GI	GI		
	4 tissues		
	4 tissues	PLCNT	
	6 tissues		
BLD	12 tissues		GATA1
BLD	6 tissues		
LIV, BLD	18 tissues	21 tissues	8 bound proteins
	BLD		
	6 tissues		
	14 tissues		
	BRN		
ESDR	4 tissues		
	8 tissues		
	7 tissues	4 tissues	
	7 tissues	SKIN,BLD	
	4 tissues		POL2
	MUS	LNG	
	6 tissues		CTCF
LIV	4 tissues	LIV	
	6 tissues		
	ESC, IPSC		
	ESDR		
	IPSC, BLD		
	BRN		
4 tissues	ESDR	6 tissues	CEBPB
ESC, ESDR, IPSC	8 tissues	GI	FOXA1,FOXA2,RXRA
	10 tissues		
BLD	BLD, GI, PLCNT		
	BLD, THYM	THYM	
	6 tissues		
	9 tissues	BLD	STAT3
	ADRL, GI, BLD		
	ESDR, BLD, KID		GATA2
	BLD		
		BLD,BLD,BLD	18 bound proteins
	BLD	LIV	

			GR
			GR
BLD	BLD, THYM		
23 tissues	BRST, BRN, GI	34 tissues	KAP1
BRN	11 tissues		NRSF,POL24H8,ZNF263
	4 tissues		
	BLD		
LIV, LNG	BLD, LIV		
			GATA2,JUND
	GI		
	7 tissues		
	ESC		
24 tissues		52 tissues	33 bound proteins
17 tissues	18 tissues	34 tissues	15 bound proteins
		4 tissues	7 bound proteins
	BLD		
23 tissues		25 tissues	POL2,POL24H8
	6 tissues		
	4 tissues		
	LIV		
	4 tissues	SKIN,PLCNT,CRVX	CEBPB,P300
18 tissues	15 tissues	11 tissues	POL2
	BLD, BRN, THYM		
	6 tissues	BLD,MUS	
	7 tissues	4 tissues	
22 tissues	BRN	37 tissues	5 bound proteins
	IPSC		
	6 tissues		
19 tissues	9 tissues	8 tissues	KAP1
BLD, GI, THYM	BLD, SKIN	7 tissues	ELF1,ZEB1
BRST, BLD	8 tissues	BLD	POL24H8,POL2
	BLD		
16 tissues	20 tissues	7 tissues	
	BLD, FAT, THYM		
	GI		
SKIN, GI, LIV	13 tissues		
	BLD		

	ESDR, GI, LIV	SKIN	
4 tissues	4 tissues	4 tissues	
4 tissues	4 tissues		
	4 tissues	BLD	GATA2,POL24H8
SKIN, CRVX	19 tissues	9 tissues	BAF155
	5 tissues	BLD,SKIN	4 bound proteins
BLD	BLD, THYM		
	SKIN	SKIN,PANC	FOXA1
		BLD	
BLD	13 tissues	16 tissues	CEBPB
	BLD, FAT, PLCNT		
	LIV		
MUS, LNG	5 tissues	LNG,MUS,MUS	
	STRM, BLD, LIV		
GI	GI, LIV	GI	FOXA1
		BLD	
17 tissues	7 tissues	ESDR,BRN,LNG	
LIV	BRST, SKIN	SKIN,BRST,SKIN	
GI	10 tissues	SKIN	
	BLD, MUS		
9 tissues	7 tissues	23 tissues	USF2,USF1
	BLD, GI	4 tissues	POL2
		BLD,KID	
24 tissues		49 tissues	18 bound proteins
	FAT		
5 tissues	12 tissues	7 tissues	RFX5
	ADRL		
	BLD		KAP1,SETDB1
	BLD, LIV		
			POL2
GI	8 tissues		
23 tissues	BLD, SPLN	4 tissues	
		BLD	
9 tissues	13 tissues	9 tissues	TAF1

	6 tissues		
		BRN,MUS,MUS	
	FAT	BLD	
STRM	15 tissues	HRT,MUS	
BRN	9 tissues	13 tissues	
	ESDR, IPSC, GI		
LIV	MUS		
	4 tissues	ESDR,BLD	GATA2,MAFK,TAL1
BLD, VAS	ESDR, BLD, FAT	ESDR,VAS	GATA2,POL2
		BLD,BRST	
GI	IPSC, GI	IPSC,GI	
	HRT		
		8 tissues	
			SETDB1
9 tissues	12 tissues	7 tissues	
	9 tissues	BLD,SKIN	
BLD	4 tissues		
	4 tissues	7 tissues	
	ESDR, FAT, BLD	BLD,BLD	
		IPSC	
	4 tissues	4 tissues	
	BLD	BLD,VAS	
	LIV		
	7 tissues	ESDR	
BRN	BRST, STRM, BRN	ESDR,BRST	
		BLD,BRN	
	9 tissues		
LIV	6 tissues		
		LNG,KID	
5 tissues	18 tissues	32 tissues	9 bound proteins
	BLD		
4 tissues	14 tissues	KID,BRN	
FAT	7 tissues		
	ADRL	ADRL,BLD	

	4 tissues		
GI	GI, MUS		
GI	BLD, GI	BLD	
	GI		
24 tissues		5 tissues	HMGN3,CTCF
BLD, BRN, PANC	18 tissues	8 tissues	
	BLD	MUS	
	LIV		
	BRST, GI		
	GI		
ESC, ESDR, IPSC	FAT, BLD, SKIN	13 tissues	
LNG	14 tissues	4 tissues	CEBPB
	4 tissues	BLD	
LIV	9 tissues	13 tissues	18 bound proteins
	LIV		
	BLD		
16 tissues	8 tissues	30 tissues	
9 tissues	16 tissues	CRVX	
BLD	9 tissues	24 tissues	CTCF,CMYC,MAX
24 tissues			
	BLD, LIV		
	LIV	ESC,IPSC	POL2
ESDR	12 tissues	ESDR,IPSC	
	12 tissues		
	MUS		POL2
	ESDR, PLCNT, CRVX	BLD,LNG	
	4 tissues	PLCNT,MUS	
24 tissues		42 tissues	27 bound proteins
13 tissues	16 tissues	12 tissues	BAF155
		5 tissues	AP2GAMMA
	ESDR, BLD, MUS	CRVX	
		KID	
14 tissues	6 tissues	4 tissues	
6 tissues	19 tissues	11 tissues	5 bound proteins

BLD	5 tissues	ESC,BLD	
LIV	5 tissues	IPSC,SKIN,THYM	
		6 tissues	NFYA,NFYB,SP1
		LNG	
	BLD		
		ESC,HRT,OVRY	
	BRN, BLD		
	7 tissues	IPSC,GI,CRVX	
		OVRY	
	4 tissues	MUS	
	BLD, PLCNT, CRVX		
	20 tissues	11 tissues	
	4 tissues		
ESC		BLD	

		BRN	
		SKIN	
	8 tissues	LIV	
	5 tissues	CRVX	CTCF
	BLD		
SKIN	BLD		
	6 tissues		
	5 tissues	BLD	
	4 tissues	IPSC	
SPLN	5 tissues	THYM,BLD	
GI	10 tissues	BLD,SKIN,BLD	
	8 tissues	13 tissues	
	BLD, SKIN, CRVX		
	8 tissues		
	BLD, FAT	BLD,BLD,BLD	
		4 tissues	
	LIV, GI	IPSC	
		THYM	
		SKIN	
5 tissues	18 tissues	5 tissues	
	4 tissues		
LIV, GI	PANC		
		4 tissues	HEY1,POL2
FAT, LIV, GI	13 tissues	BLD,OVRY	POL2
	SKIN, GI, PLCNT	SKIN,SKIN	
	BLD	BLD	

	11 tissues	ESDR	POL2
	GI, BLD	ESDR	
	5 tissues		
	6 tissues	ESDR,BLD,SKIN	
	4 tissues		
BLD, SKIN, CRVX	17 tissues	18 tissues	9 bound proteins
BLD	15 tissues	SKIN,OVRY,BLD	
	8 tissues		
		CRVX	CEBPB
	BRN		
MUS	MUS	BLD	
		LNG	
	LIV		
11 tissues	13 tissues	12 tissues	POL2
ESC	ESC, IPSC, FAT	ESC,ESC	
	8 tissues	PLCNT	
	SKIN		
	ESDR, LIV, KID		
	13 tissues		
		4 tissues	
	BLD		USF1
	9 tissues	GI,GI	
		BLD	POL24H8
BLD	BLD, PLCNT		
LIV	6 tissues	6 tissues	NFKB
5 tissues	ESDR, ESC	GI,LIV	
	GI	5 tissues	TCF12
BLD	8 tissues		
BLD	6 tissues	12 tissues	CEBPB,FOXA1,STAT3
FAT, BLD, SKIN	4 tissues	SKIN,BRST	
	BRST, BLD	BLD	
		MUS	
	BLD, THYM, SPLN	BLD,THYM	
	8 tissues	ESDR,MUS	
	12 tissues	14 tissues	

		IPSC,OVRY,LIV	FOXA1,HDAC2,RXRA
6 tissues	12 tissues	25 tissues	12 bound proteins
	BLD, LIV		
	8 tissues	8 tissues	
	BLD		
BRN, GI	18 tissues	PANC,LNG	
SKIN, BRN, KID	16 tissues	OVRY	
23 tissues	BRN, LNG	17 tissues	POL2,HAE2F1
SPLN	10 tissues	6 tissues	
	8 tissues		
		BLD	
	5 tissues	IPSC,LNG	
HRT	FAT, SKIN, BRN	MUS	
	BLD, LIV		
22 tissues	GI	9 tissues	BAF155
	BRN, BLD, LIV	BLD	
	THYM, MUS, BLD		
	5 tissues		
	BLD		
			POL24H8
	BLD	BLD,OVRY	
	21 tissues	10 tissues	P300
	4 tissues		
	GI		
	5 tissues	ESDR	
			FOXA1
LIV	16 tissues	22 tissues	JUND,FOSL2
LNG, BLD	13 tissues		
	8 tissues	CRVX	
			PAX5N19,PAX5C20

		MUS	
20 tissues	9 tissues	12 tissues	
	FAT, BRN, GI		
IPSC, LIV, HRT	5 tissues	7 tissues	
	ADRL	4 tissues	
		4 tissues	
4 tissues	10 tissues	ESDR,ESC,GI	
4 tissues	13 tissues	7 tissues	
	4 tissues	PANC	
	11 tissues	11 tissues	
	LIV	BLD	
BLD	6 tissues		
	18 tissues	ESC,SKIN	CTCF,SMC3
	LIV	CRVX	
MUS, BLD	19 tissues	19 tissues	4 bound proteins
BLD	12 tissues	20 tissues	9 bound proteins
	9 tissues		MAX
BLD	11 tissues	BLD	
BRN	14 tissues	8 tissues	
24 tissues		53 tissues	29 bound proteins
		BLD	
	LIV, GI		
	11 tissues	SKIN	
11 tissues	19 tissues	22 tissues	9 bound proteins
	ADRL, LIV		
	ESC, IPSC	LIV	
	ESDR, BLD		
	7 tissues		
5 tissues	9 tissues	GI,GI,MUS	ELF1
LNG	5 tissues	53 tissues	26 bound proteins
	4 tissues		
13 tissues	14 tissues	29 tissues	NRF1,SUZ12,CTCF
IPSC	5 tissues		
23 tissues	5 tissues	39 tissues	7 bound proteins
	9 tissues	4 tissues	CTCF
17 tissues	20 tissues	9 tissues	
GI	16 tissues	47 tissues	5 bound proteins
	7 tissues	GI,OVRY,MUS	
LIV	15 tissues	6 tissues	POL2
	4 tissues	OVRY	
	4 tissues	4 tissues	POL2
	SKIN, SPLN, BLD	BLD	
	5 tissues	LIV	
	CRVX		

12 tissues	16 tissues	14 tissues	USF1
	SKIN, PLCNT, LIV		
8 tissues	15 tissues	10 tissues	
	BRST, SKIN, GI	BLD	
	4 tissues	BLD	NRSF
	BLD		
23 tissues	BRST, SPLN	51 tissues	10 bound proteins
BLD, GI, THYM	15 tissues	15 tissues	EBF1,POL2,TCF12
	BLD, THYM		
SKIN	7 tissues		
		ESDR,BLD	
21 tissues	10 tissues	18 tissues	CEBPB
SKIN	11 tissues	8 tissues	
BLD	BLD, LIV, THYM		
	LIV		
6 tissues	15 tissues	7 tissues	
7 tissues	18 tissues		
	6 tissues	THYM,LIV	
	LIV		
PANC	IPSC		POL24H8
24 tissues		49 tissues	15 bound proteins
LIV	17 tissues	6 tissues	13 bound proteins
BRN	12 tissues	9 tissues	
	LNG	IPSC,LIV	
	MUS, BLD		
	BLD		
22 tissues	4 tissues	11 tissues	
	THYM, MUS		
14 tissues	12 tissues	21 tissues	AP2GAMMA
	THYM, LIV		
21 tissues	5 tissues	36 tissues	CTCF,POL2,TAF1
	BLD		
CRVX	6 tissues	CRVX,LIV	AP2ALPHA,AP2GAMMA,TCF4
BLD	7 tissues	9 tissues	4 bound proteins
		BRN	
BLD	BLD, GI	BLD,BLD	
	BLD, BRN, THYM		
	FAT, LNG, HRT	MUS,SKIN	
LIV	BRST		
BLD, LIV	FAT, BLD		
LIV			

	FAT		
BLD, GI, SKIN	14 tissues	12 tissues	
5 tissues	15 tissues	24 tissues	
	IPSC, BLD		
	7 tissues	BLD	
	ESC, ESDR	ESDR	
	IPSC, SKIN		
6 tissues	12 tissues	4 tissues	
BRN	15 tissues	27 tissues	13 bound proteins
HRT, MUS	12 tissues	6 tissues	
14 tissues	11 tissues	10 tissues	
SKIN, MUS	18 tissues	5 tissues	
		6 tissues	
GI, LIV	10 tissues	LIV	
	BLD		
4 tissues	18 tissues	13 tissues	CTCF,EBF1,RAD21
	5 tissues		
	4 tissues	GI,GI,GI	
	5 tissues	OVRY,MUS	
MUS	15 tissues	12 tissues	ZNF263
4 tissues	16 tissues	16 tissues	GR,AP2GAMMA,POL2
	BLD, SKIN, MUS	MUS	
		LNG	
FAT, HRT, MUS	5 tissues		
	BRST, GI		
BLD, BRN	8 tissues	6 tissues	CTCF
SKIN	5 tissues	ESC,IPSC,IPSC	
	4 tissues		
	PLCNT, VAS		
	15 tissues	4 tissues	MAFK
	BLD		
LIV	GI, LNG		
	BRN		
5 tissues	13 tissues	ESDR,MUS,VAS	
4 tissues			
		BRN	

	ESDR		
GI, BLD	7 tissues	10 tissues	
BLD			
6 tissues	18 tissues	26 tissues	4 bound proteins
	9 tissues	SKIN,HRT	
7 tissues	22 tissues	4 tissues	GATA2
ESC, ESDR, IPSC	10 tissues	8 tissues	MAX
		IPSC	
16 tissues	BLD, GI, SPLN	6 tissues	
	4 tissues		
	5 tissues	5 tissues	
GI, CRVX	8 tissues	7 tissues	
	BLD	MUS	
	ESC, BLD		
	10 tissues	VAS	
23 tissues	4 tissues	39 tissues	NANOG,TAF1,MAX
PANC, LNG, BLD	7 tissues	13 tissues	18 bound proteins
		5 tissues	TFIIIC110
	19 tissues	44 tissues	10 bound proteins
	ESDR, IPSC, BRN	IPSC	
	11 tissues		
BLD, BRN	9 tissues	5 tissues	CMYC
	BLD		
SKIN	LIV	IPSC	
	BLD, GI		
	7 tissues	6 tissues	
7 tissues	13 tissues		
	12 tissues	GI	
	4 tissues		
	SKIN, BRN		
10 tissues	10 tissues	BLD,PANC	
BLD	BLD, SKIN		
	SKIN	4 tissues	
	BLD, PANC, LIV	BLD,PANC,BLD	CMYC,GATA2,GATA1
	SKIN, MUS	BLD,LIV	POL2
SKIN, GI	15 tissues		
		LIV	
	IPSC, BLD, ADRL	IPSC	
11 tissues	10 tissues		ZNF263

STRM, BONE	12 tissues	12 tissues	
LIV	8 tissues	IPSC,LIV	4 bound proteins
LIV	SKIN, FAT, LIV		
LIV	ESDR, GI, PLCNT		
4 tissues	13 tissues	6 tissues	
BLD			
23 tissues			PU1
ESDR, IPSC			
	4 tissues		
	LIV		
	ESDR, MUS, PLCNT		
SKIN, LIV	16 tissues	49 tissues	21 bound proteins
	IPSC, SKIN	OVRY,MUS	
18 tissues	17 tissues		
		SKIN	
	SKIN		
12 tissues	16 tissues	25 tissues	EBF1,FOXA1
	BLD, SKIN	BLD	
		BRST	
	LIV		
			SETDB1
	ADRL		
	BLD, LNG, LIV	LNG	
5 tissues	17 tissues	11 tissues	NFKB
	6 tissues		
	MUS	6 tissues	
	6 tissues	LNG	
LIV, BRN	IPSC, ESC, ADRL	LIV	
	LIV, ADRL, PLCNT		
BLD, SKIN, LIV	14 tissues	22 tissues	25 bound proteins
SKIN, LIV	SKIN, LIV	IPSC	
	4 tissues		
23 tissues	7 tissues	20 tissues	POL2,POL24H8
6 tissues	9 tissues	IPSC,BLD,MUS	
6 tissues	18 tissues	6 tissues	
MUS	19 tissues	GI	

BRST, BLD, BRN	19 tissues	6 tissues	CTCF
	8 tissues	MUS	
	MUS, SKIN		
4 tissues	21 tissues	18 tissues	AP2ALPHA,AP2GAMMA,POL24H8
		PLCNT	
	MUS		
	GI	IPSC	
24 tissues	ESC, BRN, GI	26 tissues	POL2
	6 tissues	4 tissues	
4 tissues	10 tissues	38 tissues	9 bound proteins
9 tissues	6 tissues		
BLD	BLD, PLCNT	6 tissues	
		IPSC	
	BLD		
	ESDR, BLD, BRN		
	ESC		
BLD	BLD	ESDR	
ESC	6 tissues	IPSC,BLD	
LIV	11 tissues	SKIN,BLD	TCF4
	4 tissues		
	LIV	ESDR	
BLD	4 tissues		
		IPSC	
	6 tissues		
	IPSC		
	11 tissues	SKIN,THYM	
	LIV, GI	HRT,GI,GI	POL24H8,MAFK,POL2
BLD	16 tissues		
	4 tissues	ADRL,PLCNT	
	SKIN		
4 tissues	17 tissues	SKIN,MUS,LNG	
IPSC	BLD, MUS	OVRY	CTCF
	LIV	5 tissues	
	4 tissues		POL2
SKIN	17 tissues	25 tissues	CJUN
	4 tissues		
		45 tissues	POL2
	IPSC		
	BLD		

	ESDR, IPSC, BLD		
	BRN, HRT		
	FAT, BRST, BRN		
	6 tissues	6 tissues	USF1
BRN	13 tissues	BLD	PU1
	7 tissues	4 tissues	ZNF263
BLD	BLD, STRM, GI	BLD	
SKIN, MUS, BLD	20 tissues	40 tissues	19 bound proteins
22 tissues	11 tissues	9 tissues	HNF4A

Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes
Pax-4			143 hits	TMEM50A
LXR		6 hits	130 hits	RHCE
Maf,p300			124 hits	TMEM57
PTF1-beta		3 hits	1 hit	RPS6KA1
4 altered motifs			20 hits	16kb 3' of RP5-968P14.2
Gm397			21 hits	RP5-968P14.2
5 altered motifs			6 hits	610bp 5' of ARID1A
6 altered motifs			17 hits	PIGV
COMP1,MZF1::1-4			17 hits	1.2kb 5' of Metazoa_SRP
			22 hits	5.3kb 5' of RP1-50O24.6
Pitx2			21 hits	GPN2
7 altered motifs			21 hits	GPATCH3
			21 hits	NR0B2
7 altered motifs			17 hits	NUDC
6 altered motifs			20 hits	5.6kb 5' of C1orf172
Cphx			46 hits	KIAA0754
Fox			46 hits	MACF1
10 altered motifs			44 hits	BMP8A
Mef2,Osr			49 hits	RP11-69E11.4
Pou2f2			51 hits	PABPC4
			49 hits	18kb 5' of PABPC4
Zfx			41 hits	14kb 3' of HEYL
GR,Irf				TMEM61
4 altered motifs			6 hits	11kb 3' of BSND
	2 hits			PCSK9
Irf				USP24
Zfp691				USP24
Mef2,Rhox11				RP11-101C11.1
5 altered motifs			3 hits	3kb 5' of USP1
4 altered motifs		5 hits	29 hits	USP1
Cdx2,Foxp1,Ncx		5 hits	27 hits	DOCK7
AIRE,HMG-IY		7 hits	29 hits	DOCK7
			4 hits	26kb 3' of RP11-230B22.1
Zfp187			62 hits	5.1kb 5' of MTF2
STAT		2 hits	68 hits	TMED5
12 altered motifs			64 hits	CCDC18
6 altered motifs			65 hits	RP4-717I23.3
4 altered motifs		3 hits	62 hits	DR1

5 altered motifs			4 hits	24kb 3' of Y_RNA
7 altered motifs			13 hits	KIAA1324
Pou2f2				SARS
5 altered motifs	3 hits	11 hits	10 hits	CELSR2
10 altered motifs		1 hit	10 hits	34bp 3' of PSRC1
Foxd3			5 hits	3.8kb 3' of MYBPHL
30 altered motifs			7 hits	SORT1
Pax-4,RREB-1		4 hits	9 hits	PSMA5
HNF4			6 hits	SYPL2
			5 hits	ATXN7L2
4 altered motifs			2 hits	39bp 5' of CYB561D1
7 altered motifs			6 hits	AMIGO1
CEBPB				15kb 5' of GPR61
FXR,Nkx3		7 hits	10 hits	4.1kb 5' of GPR61
E2F,Znf143				GNAI3
4 altered motifs				GNAT2
4 altered motifs				AMPD2
		6 hits	9 hits	GSTM4
Cdx,Pax-4		4 hits	42 hits	GSTM3
4 altered motifs			1 hit	149bp 5' of RN5S69
Pitx2				GS1-122H1.2
INSM1				GS1-122H1.2
9 altered motifs			1 hit	MARC1
6 altered motifs			21 hits	HLA-AS1
			8 hits	HLX
FXR,Sin3Ak-20,Sox	1 hit	2 hits		GALNT2
8 altered motifs				IRF2BP2
6 altered motifs			1 hit	4.2kb 5' of RP4-781K5.7
Sox			4 hits	RP4-781K5.7
4 altered motifs			2 hits	9kb 3' of RP4-781K5.8
4 altered motifs			15 hits	SMC6
HNF4,NF-kappaB				3.7kb 5' of Metazoa_SRP
8 altered motifs				C2orf43
TBX5	1 hit	10 hits		62kb 3' of AC012361.1
5 altered motifs			1 hit	22kb 5' of APOB
Tel2			2 hits	38kb 5' of AC010872.2
			2 hits	27kb 5' of AC067959.1
4 altered motifs				AC067959.1
13 altered motifs				KCNK3
GATA,GR,NRSF			6 hits	DPYSL5
			1 hit	MAPRE3
BCL,HMGN3,TAL1				AGBL5
Mxi1,NRSF	1 hit		14 hits	898bp 5' of CGREF1
GR,RXRA				ABHD1
STAT,ZBRK1			9 hits	PREB
Pbx3,SEF-1		1 hit	28 hits	22kb 3' of TCF23
5 altered motifs			29 hits	5.8kb 3' of SLC5A6

RXRA			27 hits	C2orf28
4 altered motifs		1 hit	33 hits	CAD
Irf			29 hits	SLC30A3
5 altered motifs			31 hits	DNAJC5G
5 altered motifs			32 hits	TRIM54
Evi-1,GATA,HDAC2			2 hits	351bp 5' of UCN
HNF4,SP1,ZBRK1			51 hits	MPV17
Hic1,YY1			50 hits	GTF3C2
7 altered motifs			42 hits	AC074117.10
10 altered motifs		2 hits	55 hits	AC074117.10
Ik-1,ZBRK1	2 hits	36 hits	26 hits	SNX17
LUN-1,Pitx2			56 hits	PPM1G
PPAR,Pou3f2,XBP-1	1 hit	6 hits	8 hits	2.9kb 5' of PPM1G
			57 hits	1.9kb 5' of NRBP1
NF-Y,SIX5,Znf143		8 hits	59 hits	NRBP1
			54 hits	IFT172
SETDB1			54 hits	FNDC4
NRSF	40 hits	477 hits	28 hits	GCKR
Lhx4,Mef2,Nobox		10 hits	2 hits	AC109829.1
Arid5b,CDP		9 hits	5 hits	ZNF512
10 altered motifs	1 hit	11 hits	4 hits	ZNF512
GATA,RXRA,Smad4		14 hits	3 hits	ZNF512
29 altered motifs			4 hits	SUPT7L
E2F,Egr-1			3 hits	SLC4A1AP
			4 hits	AC074091.13
Smad			3 hits	12kb 5' of AC074091.13
CIZ		3 hits	2 hits	MRPL33
PU.1			1 hit	MRPL33
SRF,TAL1		1 hit	1 hit	MRPL33
				12kb 3' of FOSL2
4 altered motifs				13kb 3' of AC104695.4
	1 hit	1 hit		ABCG8
	5 hits	1 hit	1 hit	ABCG8
VDR			9 hits	ASB3
CEBPB,Cdx,Foxo				AC092155.4
FXR		2 hits	1 hit	EHBP1
7 altered motifs			1 hit	WDPCP
TCF4		1 hit	3 hits	DDX18
5 altered motifs			2 hits	12kb 3' of AC009404.2
SREBP			2 hits	35kb 3' of CCDC93
			2 hits	34kb 5' of INSIG2
Egr-1,Ets,Irf			1 hit	3.2kb 5' of INSIG2
Osf2			1 hit	INSIG2
18 altered motifs	3 hits	1 hit	24 hits	RAB3GAP1
PU.1,Pax-5			1 hit	5.3kb 3' of COBLL1
COMP1,Nanog,Pou2f2			1 hit	COBLL1
CEBPG,Mef2,Pou3f1				ABCB11

Rad21,SREBP,VDR	2 hits			CPS1
10 altered motifs		1 hit	1 hit	66kb 5' of AC068138.1
Dobox4,Ik-2,Nanog				62kb 5' of PPARG
5 altered motifs			5 hits	19kb 5' of TSEN2
BDP1,GR,LUN-1			12 hits	TSEN2
GR			13 hits	MKRN2-AS1
4 altered motifs			7 hits	MKRN2
Mef2,Zfp105			11 hits	RAF1
BDP1,CACD,STAT			2 hits	26kb 3' of TMEM40
6 altered motifs		3 hits	90 hits	965bp 5' of MON1A
CAC-binding-protein,NRSF			84 hits	RBM6
	1 hit	4 hits	84 hits	RBM5
22 altered motifs			78 hits	RP11-493K19.3
Pax-5,SREBP			14 hits	PPP2R3A
Dbx1,Foxj2,Sox	1 hit	1 hit	13 hits	9.1kb 5' of MSL2
Mef2,NRSF,Sin3Ak-20			11 hits	PCCB
Pbx3,SIX5,Znf143			13 hits	PCCB
6 altered motifs	1 hit		3 hits	1.8kb 3' of RP11-6F2.4
7 altered motifs				ETV5
Mxi1,Myc,Sin3Ak-20	1 hit		17 hits	TMEM175
NRSF			4 hits	MSANTD1
NRSF		1 hit		RGS12
NRSF			1 hit	HGFAC
Nkx2,RREB-1				1.1kb 3' of HGFAC
DMRT1		1 hit		96kb 3' of C4orf52
AP-1				MAPK10
Pax-2			1 hit	AFF1
4 altered motifs			13 hits	9.4kb 3' of RP11-529H2.1
7 altered motifs			9 hits	9.1kb 3' of MIR5705
Cart1,Evi-1,Otx2		3 hits	19 hits	HSD17B13
4 altered motifs				SLC39A8
GATA,HDAC2,NRSF				RP11-499E18.1
Hoxa7,NF-Y				13kb 5' of RP11-93L9.1
11 altered motifs				TRIM2
GCM				AC022431.2
ATF3			1 hit	CTD-2503O16.4
			10 hits	4.2kb 5' of GCNT4
Rad21,SRF,Zfx			4 hits	7.2kb 3' of ANKRD31
SETDB1			6 hits	37kb 5' of ANKRD31
10 altered motifs	5 hits	1 hit	8 hits	HMGCR
PPAR			8 hits	COL4A3BP
Hoxa13,Hoxa9,Hoxb9			8 hits	POLK
			6 hits	ANKDD1B
VDR			15 hits	POC5
5 altered motifs	3 hits		18 hits	1.9kb 5' of POC5
5 altered motifs			6 hits	130kb 5' of POC5
6 altered motifs			3 hits	48bp 3' of HSPA4

Maf,SRF,TFIIA				SGCD
4 altered motifs				22kb 5' of U6
Maf,PPAR,ZNF263				9.3kb 3' of U6
Zfx				7.4kb 5' of TIMD4
Ik-1,LUN-1				HAVCR1
LXR				ITK
				38kb 3' of RP11-32D16.1
Mtf1				MYLIP
Nanog				MYLIP
Mef2				16kb 5' of U6
DMRT2,SIX5		1 hit	33 hits	SLC17A1
HNF4,LBP-1		8 hits	37 hits	SLC17A3
YY1			36 hits	SLC17A2
			18 hits	TRIM38
BDP1,GCNF,Nr2f2			18 hits	14kb 3' of TRIM38
HDAC2,HNF4,Rad21		1 hit	36 hits	1.8kb 3' of HIST1H1A
Irf			33 hits	34bp 5' of HIST1H4A
DMRT1,Foxo,RFX5			17 hits	960bp 3' of HIST1H4B
		5 hits	20 hits	1.3kb 3' of HIST1H3B
STAT			33 hits	3.8kb 5' of HIST1H2AB
HP1-site-factor,Pou2f2,Znf143			31 hits	774bp 5' of HIST1H3C
Pax-5,YY1			15 hits	2.5kb 3' of HIST1H3C
CEBPA,CEBPB,CEBPD			32 hits	11kb 5' of HIST1H1C
17 altered motifs			36 hits	4kb 5' of HFE
6 altered motifs			19 hits	1.6kb 3' of HFE
BCL,STAT			20 hits	1.8kb 5' of HIST1H1T
GATA			19 hits	HIST1H2BC
GATA			36 hits	HIST1H2AC
6 altered motifs			46 hits	4.8kb 3' of HIST1H3G
			2 hits	BTN3A2
9 altered motifs			53 hits	1.3kb 3' of BTN3A3
Evi-1,Mrg,STAT			19 hits	5kb 5' of HLA-B
7 altered motifs			108 hits	522bp 5' of MICB
21 altered motifs			105 hits	MICB
BCL,MZF1::1-4,NF-kappaB			1 hit	4.5kb 5' of MCCD1
			5 hits	ATP6V1G2-DDX39B
4 altered motifs			107 hits	ATP6V1G2
AhR,Roaz		1 hit	11 hits	LTA
6 altered motifs			127 hits	736bp 3' of TNF
4 altered motifs			6 hits	2.8kb 5' of NCR3
11 altered motifs			4 hits	6.5kb 5' of AIF1
5 altered motifs			9 hits	ABHD16A
Sox,TATA,p300			5 hits	MSH5
COMP1,NRSF			5 hits	SAPCD1-AS1
4 altered motifs			5 hits	VWA7
Nrf-2,RXRA,TCF11::MafG			5 hits	VARS
5 altered motifs			5 hits	LSM2

Ik-1,Rad21,Znf143			5 hits	6.7kb 3' of NEU1
22 altered motifs			114 hits	SLC44A4
		6 hits	108 hits	188bp 5' of SLC44A4
BDP1,Maf			96 hits	339bp 3' of EHMT2
8 altered motifs		20 hits	185 hits	STK19
	1 hit	1 hit	93 hits	TNXB
36 altered motifs			18 hits	C6orf106
Mrg,Pax-2			20 hits	16kb 5' of SNRPC
Nanog,Sox,TCF4			14 hits	UHRF1BP1
4 altered motifs				CCND3
6 altered motifs			93 hits	6.3kb 5' of GNMT
HDAC2,Irf,PRDM1		51 hits	129 hits	PEX6
STAT	3 hits			3.7kb 3' of VEGFA
MZF1::1-4,p300				6.1kb 3' of VEGFA
5 altered motifs			8 hits	GSTA2
Hsf,Pou2f2				78kb 3' of RP11-14I4.3
19 altered motifs			26 hits	7.7kb 5' of FRK
6 altered motifs				RP11-73O6.4
Irf,Pax-4				41kb 5' of RP11-12A2.3
6 altered motifs			1 hit	IGF2R
5 altered motifs	5 hits	6 hits		SLC22A1
DMRT7,HDAC2				SLC22A2
			1 hit	SLC22A2
GR,Lmo2-complex,Myc		1 hit	1 hit	SLC22A3
				34kb 3' of SLC22A3
SRF				12kb 5' of LPA
EBF,NF-E2,Sin3Ak-20				11kb 5' of RP1-81D8.3
Irf			36 hits	RAC1
Ik-2,NF-AT1			36 hits	DAGLB
7 altered motifs			2 hits	SNX13
10 altered motifs				2.9kb 3' of AC080080.1
RXRA			3 hits	DNAH11
8 altered motifs	3 hits			2.2kb 5' of MIR148A
CTCF,Pbx3,Rad21		1 hit	8 hits	3.6kb 5' of NPC1L1
Myc		1 hit	10 hits	DDX56
			2 hits	5.5kb 5' of TMED4
Hand1,RP58			6 hits	OGDH
CACD,NRSF			1 hit	8.5kb 3' of Y_RNA
8 altered motifs		7 hits	5 hits	FZD9
		1 hit	9 hits	BAZ1B
Hand1		8 hits	11 hits	4.9kb 5' of BCL7B
TCF12		8 hits	8 hits	6kb 5' of TBL2
DMRT3,Pou1f1		2 hits	9 hits	MLXIPL
LXR,ZEB1			10 hits	21kb 5' of MLXIPL
HNF4,Myb		3 hits	1 hit	DNAJC30
5 altered motifs				WBSCR22
Nr2f2,RXRA,Znf143				WBSCR22

HNF4,NF-kappaB,PRDM1			4 hits	STX1A
GR				GNAT3
BATF				CD36
NF-kappaB,RBP-Jkappa			2 hits	14kb 3' of CD36
Irf				27kb 3' of SEMA3C
Nkx2				5.8kb 5' of KLF14
4 altered motifs				CREB3L2
5 altered motifs			2 hits	AGPAT5
10 altered motifs			17 hits	CTA-398F10.1
CTCF,SP1	5 hits	1 hit		RP11-115J16.1
ATF3,HNF4,SREBP				RP11-115J16.3
CCNT2,TAL1,Zfx				RP11-115J16.1
7 altered motifs				RP11-115J16.1
5 altered motifs			1 hit	PINX1
6 altered motifs			1 hit	PINX1
				18kb 5' of GATA4
Mxi1,Pitx2,TCF12			42 hits	GATA4
5 altered motifs		2 hits	23 hits	830bp 3' of C8orf49
Mrg,Tgif1			42 hits	NEIL2
		1 hit	40 hits	FDFT1
			6 hits	CTSB
6 altered motifs	1 hit	21 hits		15kb 3' of NAT2
				1kb 5' of CSGALNACT1
Pax-5		1 hit		23kb 5' of INTS10
11 altered motifs				18kb 3' of INTS10
Pax-4,Pax-6				7.8kb 5' of LPL
AIRE,Cdx2,Hoxb8				LPL
4 altered motifs	4 hits	20 hits	1 hit	6.2kb 3' of LPL
7 altered motifs		20 hits		53kb 5' of AC100802.3
Lmo2-complex		1 hit	1 hit	AC100802.3
8 altered motifs				45kb 5' of RP11-53M11.3
5 altered motifs			2 hits	UBXN2B
Irf,STAT			5 hits	17kb 3' of CYP7A1
5 altered motifs				TRPS1
GR				TRPS1
Pax-4				47kb 5' of SNTB1
4 altered motifs	3 hits			RP11-136O12.2
4 altered motifs	1 hit			RP11-136O12.2
Myc,Pou5f1,RFX5			9 hits	15kb 5' of GPIHBP1
CTCF,Rad21,Znf143			9 hits	1.7kb 3' of GPIHBP1
			4 hits	TTC39B
Foxj1,Gm397,p300			1 hit	PCSK5
Ets				21kb 5' of NIPSNAP3A
GR,Hand1,Osf2	1 hit	2 hits		ABCA1
13 altered motifs			8 hits	30kb 3' of RP11-217B7.2
ERalpha-a,TLX1::NFIC,YY1			1 hit	9.8kb 3' of RP11-217B7.3
5 altered motifs			26 hits	ZER1

4 altered motifs				3kb 5' of GBGT1
7 altered motifs				20kb 5' of GBGT1
4 altered motifs				6.2kb 5' of OBP2B
4 altered motifs			1 hit	1kb 3' of ABO
7 altered motifs	7 hits	6 hits	5 hits	4.2kb 5' of ABO
15 altered motifs			13 hits	6.8kb 3' of Y_RNA
4 altered motifs			16 hits	MED22
16 altered motifs			30 hits	SURF4
Smad3			28 hits	C9orf96
			7 hits	MARCH8
GR				A1CF
10 altered motifs			10 hits	1.4kb 3' of RP11-144G16.1
5 altered motifs			14 hits	NRBF2
SETDB1,Zfx			14 hits	JMJD1C
11 altered motifs			14 hits	REEP3
5 altered motifs			15 hits	REEP3
Pou4f3,Pou6f1		1 hit	12 hits	10kb 3' of REEP3
Hic1,Zfx			3 hits	EXOC6
6 altered motifs		3 hits	1 hit	CYP26C1
8 altered motifs				2.1kb 3' of CYP26A1
				GPAM
5 altered motifs		1 hit	3 hits	12kb 5' of GPAM
GCNF		3 hits	4 hits	TECTB
4 altered motifs			1 hit	CUZD1
CEBPB,Hdx,Pax-4			6 hits	8.1kb 5' of FAM24A
8 altered motifs			8 hits	7.8kb 3' of FAM24A
4 altered motifs			12 hits	C10orf88
6 altered motifs			1 hit	ARNTL
			23 hits	SPTY2D1
Hbp1,Nanog,Pou5f1				AMBRA1
GR,TATA			7 hits	ATG13
4 altered motifs			17 hits	ARHGAP1
TEF			17 hits	ZNF408
8 altered motifs			17 hits	F2
5 altered motifs			9 hits	CKAP5
HDAC2		1 hit	12 hits	LRP4
Myc			22 hits	C11orf49
5 altered motifs			21 hits	C11orf49
CIZ			19 hits	5.1kb 5' of PACSIN3
7 altered motifs		5 hits	45 hits	DDB2
10 altered motifs			41 hits	ACP2
			41 hits	NR1H3
Irf,Pbx-1,SIX5		1 hit	41 hits	MADD
GR,TCF12			41 hits	MADD
9 altered motifs			28 hits	MYBPC3
5 altered motifs			41 hits	SPI1
GATA			14 hits	RP11-750H9.5

HDAC2			11 hits	RP11-750H9.5
HNF4			24 hits	4.3kb 5' of PSMC3
4 altered motifs			48 hits	4.5kb 5' of RAPSN
CTCF,Rad21			49 hits	CELF1
5 altered motifs			46 hits	PTPMT1
14 altered motifs			9 hits	NDUFS3
Zfp105			50 hits	NDUFS3
			42 hits	368bp 3' of NDUFS3
7 altered motifs			50 hits	5.9kb 5' of C1QTNF4
HDAC2		9 hits	56 hits	8.5kb 5' of C1QTNF4
GCM,TEF-1		1 hit	53 hits	AGBL2
4 altered motifs		2 hits	49 hits	FNBP4
Gfi1			46 hits	20kb 5' of NUP160
5 altered motifs			30 hits	55kb 5' of PTPRJ
			2 hits	PTPRJ
Dmbx1			14 hits	15kb 5' of OR4B1
NF-kappaB,PU.1			15 hits	9.8kb 5' of OR4X2
Myf,Pax-5,TATA			4 hits	OR4X1
CIZ,Mef2			3 hits	2.9kb 5' of OR4S1
4 altered motifs			3 hits	8.7kb 5' of OR4C3
CTCF,Egr-1,Myf			2 hits	49kb 5' of OR4C5
			2 hits	41kb 3' of OR4A47
5 altered motifs			1 hit	6.6kb 3' of TRIM49B
GATA			1 hit	16kb 5' of TRIM64C
AP-1,Hltf,TFE			1 hit	25kb 5' of FOLH1
12 altered motifs			2 hits	264kb 5' of FOLH1
Dobox4,Obox3				34kb 3' of OR4A5
5 altered motifs				26kb 5' of OR4A16
7 altered motifs				5.9kb 5' of OR4A16
GR,TATA,YY1				91kb 3' of OR4A15
4 altered motifs				87kb 5' of OR4C15
Bbx,STAT				316bp 5' of OR4C16
Irf,PRDM1				8.3kb 3' of OR4C11
CDP				13kb 5' of OR4P4
14 altered motifs				2.8kb 5' of OR4S2
				303bp 3' of RP11-674C21.9
CTCF,Rad21,SP1				25kb 5' of OR5D13
Nanog,Sox				1.6kb 3' of OR5D14
GATA,GR				6kb 5' of OR5L1
Crx,Sin3Ak-20				2.4kb 3' of OR5L2
6 altered motifs				4.2kb 5' of OR5D16
				17kb 5' of TRIM51
Nrf-2,Smad3				OR5W2
14 altered motifs				5.3kb 3' of OR5I1
Zfp105		1 hit		4.2kb 5' of OR10AG1
29 altered motifs				11kb 3' of OR5F1
Pou2f2				15kb 5' of OR5F1

Mef2		1 hit		17kb 5' of OR5AS1
				16kb 5' of OR8I2
				OR8H3
4 altered motifs				OR8J3
Mxi1,SREBP				5.3kb 5' of OR8K5
Hmbox1,PLZF,RORalpha1				24kb 3' of OR5J2
DMRT2				4.8kb 5' of OR5T2
4 altered motifs				585bp 3' of OR5T3
Nkx3		1 hit		2.8kb 3' of OR5T1
10 altered motifs				13kb 5' of OR8H1
Pax-6		1 hit		5kb 5' of OR8K3
Maf,Pax-4				11kb 5' of OR8K1
Rhox11				723bp 5' of OR8J1
Mef2,TATA,YY1				7.1kb 3' of OR8U1
Pax-3				4kb 3' of OR5R1
4 altered motifs				2.2kb 3' of OR5R1
Ets				1.2kb 3' of OR5M11
Pax-2				4kb 3' of OR5M10
7 altered motifs				11kb 5' of AP002517.1
HEN1,ZBTB7A	2 hits	114 hits	44 hits	C11orf9
EWSR1-FLI1		16 hits	41 hits	C11orf10
Nanog	7 hits	102 hits	44 hits	FEN1
8 altered motifs			41 hits	FADS1
		16 hits	40 hits	FADS1
	1 hit	72 hits	18 hits	611bp 3' of FADS3
5 altered motifs		2 hits	11 hits	RAB3IL1
Sin3Ak-20,Znf143			5 hits	FLRT1
EBF,RREB-1			3 hits	MACROD1
RXRA			3 hits	VEGFB
HNF4,LRH1			3 hits	PLCB3
			5 hits	3.4kb 5' of AP003774.1
AP-1			2 hits	5.5kb 3' of Metazoa_SRP
4 altered motifs			2 hits	CTD-2530H12.1
			2 hits	RP11-535A19.2
9 altered motifs			2 hits	UVRAG
4 altered motifs				11kb 5' of AP000770.1
Evi-1		23 hits	9 hits	4.2kb 3' of AP000770.1
4 altered motifs		27 hits	8 hits	12kb 3' of BUD13
HEN1,Pax-4		30 hits	9 hits	ZNF259
		36 hits	8 hits	APOA5
DMRT5,Foxp3			33 hits	2.4kb 3' of AP006216.5
AP-1,ERalpha-a			20 hits	APOC3
AP-1		11 hits	21 hits	898bp 3' of APOA1
29 altered motifs		9 hits	23 hits	APOA1
6 altered motifs		3 hits	26 hits	SIK3
			28 hits	PAFAH1B2
Foxo,GATA		4 hits	39 hits	SIDT2

14 altered motifs		1 hit	37 hits	TAGLN
Isl2,Nkx6-1			38 hits	PCSK7
SREBP,Zbtb3				RNF214
4 altered motifs			2 hits	BACE1
Hoxa3,PLAG1		4 hits	40 hits	11kb 3' of RPUSD4
		8 hits	47 hits	RPUSD4
Pdx1,Smad3			2 hits	DCPS
11 altered motifs			16 hits	4.2kb 5' of ST3GAL4
CTCF			16 hits	ST3GAL4
4 altered motifs			1 hit	72kb 3' of RP11-284H19.1
				TUBA1C
Foxp1,HMG-IY,Mef2				3.9kb 3' of DNAJC22
8 altered motifs		1 hit	3 hits	RP11-123K3.4
			2 hits	R3HDM2
6 altered motifs			1 hit	RP11-756H6.1
		3 hits	5 hits	INHBE
SIX5			25 hits	MYO1H
Foxj2,Mef2		6 hits	30 hits	KCTD10
BDP1,STAT		3 hits	30 hits	UBE3B
GCNF,LRH1,Pax-6	2 hits	8 hits	28 hits	MMAB
SREBP		2 hits	29 hits	MVK
ERalpha-a			1 hit	SH2B3
CHX10,ELF1,Hoxa5			10 hits	SH2B3
SP1			1 hit	ATXN2
HEY1,Spz1,Zic			32 hits	BRAP
GR,Zbtb3			33 hits	ACAD10
BDP1,PU.1,STAT			38 hits	712bp 5' of RP3-462E2.3
BATF,GATA,ZBRK1			40 hits	MAPKAPK5
SP2		5 hits	46 hits	4.2kb 3' of MAPKAPK5
			40 hits	17kb 3' of TMEM116
6 altered motifs			43 hits	NAA25
4 altered motifs			6 hits	32kb 3' of HNF1A-AS1
Irf			3 hits	7.8kb 3' of HNF1A-AS1
8 altered motifs	1 hit		5 hits	HNF1A-AS1
18 altered motifs			1 hit	C12orf43
Evi-1,TAL1	1 hit		5 hits	OASL
PPAR			1 hit	RP11-324E6.6
Hic1			1 hit	RP11-324E6.6
8 altered motifs			1 hit	RP11-324E6.6
4 altered motifs			1 hit	HCAR1
Crx,Pitx2			5 hits	3.2kb 3' of RN5S375
10 altered motifs			4 hits	SBNO1
12 altered motifs			5 hits	7.8kb 5' of SETD8
En-1,PRDM1		2 hits	19 hits	DNAH10OS
GATA			20 hits	CCDC92
HEN1,HNF4,Nr2f2			18 hits	ZNF664
4 altered motifs			5 hits	RP11-522N14.1

				SCARB1
GATA,Lmo2-complex,ZID				RP11-592O2.1
AP-2,SRF				SCARB1
5 altered motifs				5.7kb 5' of SCARB1
12 altered motifs			2 hits	BRCA2
OTX,Obox3			5 hits	N4BP2L1
4 altered motifs			1 hit	GAS6
37 altered motifs		1 hit	7 hits	NYNRIN
4 altered motifs				279bp 5' of AKT1
Sox			1 hit	1.6kb 3' of ZBTB42
Pbx3			1 hit	RP11-164J13.1
CIZ			1 hit	ZFP106
6 altered motifs			2 hits	CDAN1
Pax-6,Pou3f2,Pou3f4			3 hits	TTBK2
Bbx			3 hits	UBR1
5 altered motifs				EPB42
MZF1::1-4,Maf,PU.1			14 hits	TGM7
10 altered motifs			122 hits	7kb 3' of LCMT2
			9 hits	ADAL
CDP,GATA,SREBP		8 hits	126 hits	ZSCAN29
9 altered motifs			11 hits	TUBGCP4
Hlx1,Sox			11 hits	TP53BP1
			20 hits	MAP1A
AP-1,Hand1,Myc			111 hits	PPIP5K1
Cdc5,DMRT4			102 hits	CKMT1B
		2 hits	106 hits	AC011330.12
CEBPB,SP2			8 hits	CATSPER2
Evi-1,Sin3Ak-20		1 hit	105 hits	CKMT1A
12 altered motifs			10 hits	1.6kb 5' of U6
7 altered motifs			53 hits	PDIA3
GATA,Pax-5		2 hits	126 hits	ELL3
			121 hits	RP11-296A16.1
4 altered motifs		2 hits	107 hits	RP11-296A16.1
		1 hit	103 hits	MFAP1
		3 hits	85 hits	WDR76
4 altered motifs			2 hits	FRMD5
13 altered motifs			2 hits	16kb 3' of RP11-616K22.3
Hoxa9,TATA				CTDSPL2
	15 hits	39 hits		ALDH1A2
4 altered motifs	1 hit	44 hits		ALDH1A2
13 altered motifs		1 hit	18 hits	8.2kb 3' of TPM1
21 altered motifs			19 hits	RP11-69G7.1
4 altered motifs				FTO
ATF3				GNAO1
Mef2				AMFR
BCL,GATA,PPAR			4 hits	16kb 5' of MT4
PU.1,Pax-5				2.6kb 3' of MT3

6 altered motifs				8.3kb 3' of MT3
6 altered motifs				5.9kb 5' of RP11-249C24.10
E2A,Maf,Myf				641bp 5' of MT1E
DEC,Nkx2			7 hits	881bp 5' of MT1A
Hic1			6 hits	2.4kb 3' of MT1A
ATF3			3 hits	675bp 3' of MT1G
4 altered motifs			4 hits	842bp 5' of MT1H
				MT1H
DEC,Rad21,ZEB1				5kb 5' of MT1X
TCF12			3 hits	RP11-343H19.2
10 altered motifs				6.2kb 3' of RP11-343H19.1
Arnt,BHLHE40,Myc				RP11-343H19.1
8 altered motifs				NUP93
				5.1kb 3' of NUP93
			1 hit	SLC12A3
5 altered motifs				SLC12A3
5 altered motifs			2 hits	5.6kb 5' of AC012181.1
AIRE,Foxj2,Foxp1		19 hits		CETP
7 altered motifs				NLRC5
HES1,Smad3				CPNE2
Pax-5,STAT		1 hit	4 hits	FAM192A
7 altered motifs			3 hits	RSPRY1
6 altered motifs		3 hits	4 hits	ARL2BP
4 altered motifs			2 hits	PLLP
Gfi1				TK2
7 altered motifs				CMTM4
PLZF,Pax-5				CCDC79
				1.2kb 5' of PDP2
E2F				CDH16
				CES3
4 altered motifs		2 hits	10 hits	1.4kb 5' of Metazoa_SRP
9 altered motifs			5 hits	CBFB
		5 hits	10 hits	C16orf70
ATF4,Pax-5,Pax-6				FBXL8
15 altered motifs			2 hits	HSF4
		3 hits	9 hits	NOL3
Ets			9 hits	KIAA0895L
BDP1,ZBTB33			15 hits	EXOC3L1
ZBTB33			7 hits	E2F4
8 altered motifs			6 hits	ELMO3
Myc		5 hits	12 hits	LRRC29
Osr			12 hits	LRRC29
BDP1,THAP1			12 hits	FHOD1
6 altered motifs			11 hits	SLC9A5
8 altered motifs		4 hits	25 hits	PLEKHG4
SIX5			25 hits	KCTD19
HP1-site-factor			4 hits	LRRC36

CCNT2,PRDM1			4 hits	225bp 3' of ZDHHC1
7 altered motifs			27 hits	ZDHHC1
			25 hits	HSD11B2
6 altered motifs			24 hits	ATP6V0D1
6 altered motifs			3 hits	1.5kb 5' of AGRP
Pax-6		8 hits	24 hits	2.4kb 5' of AGRP
4 altered motifs			4 hits	CTD-2012K14.1
E2A,Nkx2,SMC3			43 hits	1.2kb 3' of FAM65A
			33 hits	3.9kb 3' of CTD-2012K14.7
HNF4			21 hits	CTCF
14 altered motifs			25 hits	RLTPR
Foxp3,NRSF			29 hits	ACD
6 altered motifs		2 hits	47 hits	C16orf48
GR			26 hits	GFOD2
46 altered motifs			32 hits	RANBP10
Rad21		7 hits	36 hits	TSNAXIP1
LUN-1			27 hits	CENPT
		8 hits	36 hits	NUTF2
4 altered motifs			31 hits	EDC4
Irf			31 hits	CTC-479C5.10
4 altered motifs			31 hits	PSKH1
E2A,HIF1,RP58		1 hit	48 hits	CTRL
			56 hits	PSMB10
AP-2,SRF		4 hits	54 hits	LCAT
SP1,TATA			51 hits	SLC12A4
7 altered motifs			38 hits	1.5kb 5' of DPEP3
Eomes,INSM1,SREBP	1 hit	15 hits	44 hits	DPEP2
RFX5			45 hits	DUS2L
NRSF			38 hits	DUS2L
Foxp1			46 hits	DUS2L
31 altered motifs			49 hits	NFATC3
Hbp1,Mef2,Pou1f1			50 hits	ESRP2
GCNF			52 hits	1.3kb 5' of PLA2G15
4 altered motifs			46 hits	504bp 5' of SLC7A6
5 altered motifs			49 hits	SLC7A6OS
12 altered motifs			48 hits	PRMT7
4 altered motifs			49 hits	SMPD3
Gm397				17kb 5' of AP1G1
Brachyury,Eomes,TBX5			2 hits	1.6kb 5' of ATXN1L
Brachyury,LUN-1,STAT			4 hits	RP11-498D10.4
4 altered motifs			4 hits	IST1
AP-1				PKD1L3
Sp4		1 hit	19 hits	DHODH
Zfp105		1 hit	21 hits	2.6kb 3' of TXNL4B
			5 hits	TXNL4B
Mef2		1 hit	48 hits	TXNL4B
		1 hit	20 hits	DHX38

			8 hits	PMFBP1
4 altered motifs			1 hit	22kb 3' of RP11-328J14.1
	4 hits			CMIP
6 altered motifs			10 hits	8.9kb 3' of RP11-690G19.3
Foxp3		5 hits	18 hits	FBXL20
4 altered motifs			12 hits	MED1
4 altered motifs			8 hits	CDK12
HES1			11 hits	16kb 3' of CDK12
6 altered motifs			15 hits	13kb 3' of NEUROD2
Ets,GLI			24 hits	4.5kb 5' of NEUROD2
8 altered motifs			22 hits	PPP1R1B
Hmx,Nkx2,Roaz			31 hits	STARD3
8 altered motifs		9 hits	32 hits	TCAP
12 altered motifs		2 hits	21 hits	PNMT
STAT			33 hits	PGAP3
HEN1			35 hits	ERBB2
5 altered motifs			23 hits	695bp 5' of GRB7
Zfp691			35 hits	IKZF3
HNF4,NRSF			50 hits	8.6kb 3' of ZPBP2
4 altered motifs			47 hits	GSDMB
E2A		3 hits	37 hits	ORMDL3
YY1,p300			39 hits	RP11-387H17.4
7 altered motifs			44 hits	GSDMA
STAT,Smad			46 hits	869bp 3' of GSDMA
6 altered motifs			27 hits	100bp 3' of CSF3
4 altered motifs		4 hits	20 hits	MED24
Rad21,TEF-1			1 hit	38kb 5' of MEOX1
12 altered motifs				2.6kb 3' of DUSP3
5 altered motifs				CD300LG
Nanog,Pou5f1,Sox			2 hits	8.1kb 5' of RP11-527L4.2
28 altered motifs			1 hit	RP11-527L4.2
6 altered motifs			3 hits	PPY
SP1		19 hits	58 hits	RP11-290H9.4
4 altered motifs			55 hits	RP11-290H9.4
NF-AT,RXR::LXR,SP1		6 hits	62 hits	CTD-2026D20.2
CDP,E2A,NF-E2			65 hits	20kb 3' of C17orf57
11 altered motifs			64 hits	NPEPPS
32 altered motifs		7 hits	64 hits	KPNB1
E2F			52 hits	3.9kb 3' of KPNB1
		1 hit	33 hits	10kb 5' of TBX21
TATA				7.2kb 5' of CEP112
CACD,Klf4				APOH
GATA,Rhox11				37kb 3' of ABCA8
4 altered motifs				ABCA8
9 altered motifs				ABCA9
7 altered motifs				ABCA6
Ets,TATA,TR4				ABCA10

6 altered motifs				ABCA5
4 altered motifs				16kb 5' of SNORA40
				MAP2K6
E2F,Zbtb3				22kb 3' of MAP2K6
Irf			1 hit	3.7kb 5' of Metazoa_SRP
BDP1,Znf143				PGS1
				SMAD7
6 altered motifs				8.9kb 5' of SMAD7
Maf,SREBP,Zbtb3				6.8kb 5' of DYM
		3 hits	1 hit	793bp 3' of C18orf32
6 altered motifs		10 hits	1 hit	RP11-110H1.2
		2 hits	5 hits	26kb 3' of RP11-110H1.8
6 altered motifs				LIPG
DMRT5,p300	3 hits	1 hit	1 hit	62kb 3' of LIPG
Pdx1		1 hit		66kb 3' of ACAA2
Pitx2,STAT				3.6kb 3' of ACAA2
Foxp1			2 hits	2.5kb 3' of SCARNA18
Evi-1				MYO5B
5 altered motifs	2 hits			1.7kb 5' of U4
4 altered motifs				18kb 3' of U4
			1 hit	INSR
LUN-1				512bp 3' of AC010323.1
				ANGPTL4
6 altered motifs			3 hits	970bp 3' of MIR4999
Klf7,Pax-4			4 hits	258bp 5' of MIR4999
Rad21,SP1			7 hits	RAB11B
5 altered motifs		3 hits	10 hits	MARCH2
Zbtb3			7 hits	HNRNPM
LBP-1,Pitx2			2 hits	PRAM1
				MYO1F
8 altered motifs			1 hit	12kb 5' of S1PR5
9 altered motifs				ATG4D
4 altered motifs			1 hit	KRI1
BDP1,LUN-1			1 hit	965bp 5' of CDKN2D
			1 hit	AP1M2
9 altered motifs			1 hit	SLC44A2
				ILF3
Foxa,YY1,p300		1 hit	42 hits	QTRT1
20 altered motifs			5 hits	DNM2
Nr2f2,Pax-4		1 hit	1 hit	TMED1
CIZ,ERalpha-a,GR			6 hits	3.1kb 5' of TMED1
7 altered motifs			1 hit	YIPF2
HNF4,Nkx2			23 hits	137bp 3' of C19orf52
4 altered motifs			7 hits	14kb 3' of C19orf52
4 altered motifs			3 hits	11kb 3' of SMARCA4
DEC,Nkx2				8.4kb 5' of LDLR
				SPC24

			1 hit	KANK2
			1 hit	DOCK6
RXRA				DOCK6
GCNF,Nr2f2			3 hits	SUGP2
GATA,TCF12			2 hits	ARMC6
Smad4,ZID,Znf143			3 hits	SLC25A42
			15 hits	MEF2BNB-MEF2B
11 altered motifs			15 hits	MEF2BNB
Zbtb3				305bp 5' of NR2C2AP
p53		2 hits	7 hits	NCAN
Mef2,STAT			2 hits	HAPLN4
BCL,Ets,Sin3Ak-20			3 hits	TM6SF2
Ets,LF-A1			2 hits	SUGP1
7 altered motifs			1 hit	8.3kb 3' of MAU2
MZF1::1-4,RFX5			5 hits	GATAD2A
4 altered motifs		1 hit	6 hits	NDUFA13
5 altered motifs			2 hits	NDUFA13
			5 hits	6.6kb 3' of CILP2
EWSR1-FLI1,HDAC2,Pax-4			3 hits	PBX4
		3 hits	5 hits	GMIP
PPAR,STAT,Znf143			1 hit	ZNF101
5 altered motifs				1.4kb 3' of ZNF14
ZEB1				10kb 5' of ZNF14
AIRE,Pax-4,p300			1 hit	PEPD
Pax-4				ZNF285
Nkx2,Nkx3,Pou2f2			2 hits	ZNF229
			1 hit	ZNF180
Osr,Pax-6				CEACAM20
Znf143				7.5kb 5' of CEACAM20
			1 hit	IGSF23
			1 hit	CEACAM19
		25 hits		2.8kb 5' of snoZ6
		1 hit		8.8kb 5' of BCL3
5 altered motifs				CBLC
GATA				BCAM
6 altered motifs				PVRL2
Ets,Znf143,p300				TOMM40
10 altered motifs	7 hits	1 hit	1 hit	APOE
Sin3Ak-20		21 hits	1 hit	APOC1
LUN-1,Mxi1			1 hit	4.5kb 3' of APOC1
4 altered motifs				APOC4
Zfx		3 hits	8 hits	APOC4
GATA				CLPTM1
RFX5,SREBP			3 hits	345bp 5' of RELB
NRSF				329bp 3' of RELB
5 altered motifs		1 hit	16 hits	GEMIN7
TATA			4 hits	PPP1R37

4 altered motifs			4 hits	814bp 3' of NKPD1
9 altered motifs				NKPD1
Egr-1,Pax-4,SREBP				TRAPPC6A
NRSF,Zfx				2.9kb 3' of BLOC1S3
6 altered motifs				2.2kb 3' of PPP1R13L
GR,LBP-1				VASP
SZF1-1,Spz1,ZBTB33			3 hits	GIPR
9 altered motifs		5 hits	15 hits	FAM83E
BCL,RFX5			12 hits	6.1kb 3' of NTN5
5 altered motifs			19 hits	NTN5
		1 hit	31 hits	FUT2
Pou2f2,RREB-1			30 hits	MAMSTR
4 altered motifs			26 hits	RASIP1
Foxo,GR	2 hits	1 hit	25 hits	IZUMO1
E2A,Pitx2,Spz1			21 hits	FUT1
BAF155,Spz1			2 hits	FPR3
7 altered motifs			9 hits	14kb 3' of FPR3
AhR,RFX5			9 hits	ZNF577
Nanog,STAT				339bp 3' of RPS9
Mef2,Mrg,TATA			6 hits	1.4kb 3' of U6
			22 hits	6.8kb 3' of LILRA3
4 altered motifs			18 hits	LILRA3
			7 hits	AC008984.2
9 altered motifs			6 hits	AC008984.2
7 altered motifs				14kb 3' of AL035045.1
LUN-1,NRSF,Sin3Ak-20	1 hit			22kb 3' of RP5-905G11.3
		5 hits	62 hits	EDEM2
Foxp1			45 hits	EDEM2
				44kb 3' of SNORD112
CTCF,Foxa,PU.1				114kb 3' of SNORD112
DMRT5				134kb 3' of SNORD112
Rad21,Zbtb3			1 hit	1.5kb 3' of U2
Foxp1			4 hits	TOP1
Hand1,Maf,SEF-1			4 hits	RP1-1J6.2
4 altered motifs			3 hits	PLCG1
ERalpha-a,RORalpha1		3 hits	2 hits	PLCG1
7 altered motifs				ZHX3
Pax-5,Pax-6,SP1			2 hits	11kb 5' of LPIN3
BAF155,Cdx				1.3kb 5' of EMILIN3
Maf			1 hit	16kb 3' of CHD6
				6.9kb 5' of R3HDML
ERalpha-a,Nkx2,RAR	7 hits			HNF4A
		8 hits	9 hits	1kb 3' of UBE2C
CTCF,DMRT1,Sox		17 hits	8 hits	11kb 5' of PLTP
18 altered motifs		16 hits	3 hits	259bp 5' of PCIF1
5 altered motifs		13 hits	3 hits	PCIF1
NF-E2,Zbtb3		16 hits	3 hits	ZNF335

Osr,Pax-6		15 hits	2 hits	6.7kb 5' of MMP9
		15 hits	3 hits	SLC12A5
				EYA2
4 altered motifs		1 hit	6 hits	PTTG1IP
			22 hits	UBE2L3
Foxp3,NF-I,TLX1::NFIC			22 hits	1.7kb 3' of YDJC
11 altered motifs		1 hit	20 hits	740bp 5' of YDJC
Irf			5 hits	704bp 3' of SDF2L1
8 altered motifs			13 hits	PLA2G6
4 altered motifs			7 hits	MAFF

RefSeq genes	dbSNP func annot
TMEM50A	intronic
3.7kb 5' of TMEM57	
TMEM57	intronic
RPS6KA1	intronic
20kb 5' of ARID1A	
2.4kb 5' of ARID1A	
607bp 5' of ARID1A	
PIGV	intronic
13kb 5' of ZDHHC18	
6.4kb 3' of SFN	
GPN2	intronic
GPATCH3	intronic
NR0B2	missense
NUDC	intronic
5.6kb 5' of C1orf172	
KIAA0754	3'-UTR
MACF1	intronic
BMP8A	intronic
PPIEL	intronic
PABPC4	intronic
18kb 5' of PABPC4	
13kb 3' of HEYL	
TMEM61	intronic
13kb 3' of BSND	
PCSK9	missense
USP24	intronic
USP24	intronic
292bp 3' of MIR4422	
3kb 5' of USP1	
USP1	intronic
DOCK7	intronic
DOCK7	intronic
48kb 5' of ATG4C	
5.1kb 5' of MTF2	
TMED5	intronic
CCDC18	intronic
LOC100131564	intronic
DR1	intronic

38kb 5' of FNBP1L	
KIAA1324	intronic
SARS	intronic
CELSR2	3'-UTR
31bp 3' of PSRC1	
3.8kb 3' of MYBPHL	
SORT1	intronic
PSMA5	intronic
SYPL2	missense
ATXN7L2	intronic
22bp 5' of CYB561D1	
AMIGO1	3'-UTR
15kb 5' of GPR61	
4.1kb 5' of GPR61	
GNAI3	intronic
GNAT2	intronic
267bp 5' of AMPD2	
GSTM4	intronic
GSTM3	intronic
12kb 3' of C1orf220	
114kb 5' of ZNF648	intronic
146kb 5' of ZNF648	intronic
MOSC1	missense
31kb 3' of MOSC1	
HLX	synonymous
GALNT2	intronic
IRF2BP2	intronic
19kb 5' of LOC100506810	
11kb 5' of LOC100506810	
9kb 3' of LOC100506810	
SMC6	intronic
29kb 3' of SDC1	
C2orf43	intronic
101kb 5' of C2orf43	
22kb 5' of APOB	
42kb 5' of APOB	
150kb 5' of APOB	
257kb 5' of APOB	
KCNK3	intronic
DPYSL5	intronic
MAPRE3	intronic
848bp 5' of AGBL5	
898bp 5' of CGREF1	
PREB	3'-UTR
PREB	intronic
22kb 3' of TCF23	
5.8kb 3' of SLC5A6	

C2orf28	intronic
CAD	intronic
SLC30A3	intronic
DNAJC5G	intronic
TRIM54	intronic
534bp 5' of UCN	
681bp 3' of GTF3C2	
GTF3C2	intronic
3.3kb 5' of GTF3C2	
2.6kb 3' of EIF2B4	
SNX17	intronic
PPM1G	intronic
3kb 5' of PPM1G	
2.7kb 5' of NRBP1	
NRBP1	intronic
IFT172	intronic
FNDC4	3'-UTR
GCKR	missense
21kb 5' of C2orf16	
ZNF512	intronic
GPN1	missense
GPN1	intronic
SUPT7L	intronic
SLC4A1AP	intronic
16kb 3' of SLC4A1AP	intronic
33kb 3' of SLC4A1AP	
565bp 3' of MRPL33	
RBKS	intronic
LOC100302650	intronic
15kb 3' of FOSL2	
20kb 3' of FOSL2	
ABCG8	missense
ABCG8	intronic
GPR75-ASB3	intronic
59kb 5' of EHBP1	
EHBP1	intronic
WDPCP	intronic
DDX18	intronic
22kb 3' of DDX18	
35kb 3' of CCDC93	
34kb 5' of INSIG2	
3.2kb 5' of INSIG2	
INSIG2	intronic
RAB3GAP1	intronic
26kb 5' of GRB14	
13kb 3' of COBLL1	
ABCB11	intronic

CPS1	missense
480kb 3' of IRS1	
33kb 3' of SYN2	
19kb 5' of TSEN2	
TSEN2	intronic
LOC100129480	intronic
MKRN2	intronic
RAF1	intronic
27kb 3' of TMEM40	
1.1kb 5' of MON1A	
4.1kb 3' of RBM6	
RBM5	intronic
5.3kb 3' of RBM5	intronic
PPP2R3A	intronic
11kb 5' of MSL2	
PCCB	intronic
3.2kb 3' of STAG1	
1.8kb 3' of LOC339894	
ETV5	intronic
TMEM175	missense
6.8kb 3' of C4orf44	
RGS12	intronic
HGFAC	intronic
1.1kb 3' of HGFAC	
96kb 3' of C4orf52	
47kb 5' of PTPN13	
AFF1	intronic
32kb 5' of KLHL8	
12kb 3' of HSD17B13	
HSD17B13	3'-UTR
SLC39A8	intronic
77kb 5' of NFKB1	
16kb 5' of LOC285419	
TRIM2	intronic
279kb 5' of ANKRD55	
54kb 3' of GCNT4	
4.2kb 5' of GCNT4	
7.3kb 3' of ANKRD31	
37kb 5' of ANKRD31	
HMGCR	3'-UTR
COL4A3BP	intronic
POLK	intronic
15kb 3' of POLK	intronic
POC5	intronic
1.9kb 5' of POC5	
130kb 5' of POC5	
1.5kb 3' of HSPA4	

SGCD	intronic
24kb 3' of SGCD	
27kb 5' of PPP1R2P3	
7.4kb 5' of TIMD4	
HAVCR1	intronic
ITK	intronic
124kb 3' of EBF1	
MYLIP	intronic
MYLIP	intronic
41kb 3' of MYLIP	
SLC17A1	intronic
SLC17A3	5'-UTR
SLC17A2	intronic
TRIM38	intronic
14kb 3' of TRIM38	
1.8kb 3' of HIST1H1A	
33bp 5' of HIST1H4A	
959bp 3' of HIST1H4B	
1.3kb 3' of HIST1H3B	
3.8kb 5' of HIST1H2AB	
773bp 5' of HIST1H3C	
2.5kb 3' of HIST1H3C	
11kb 5' of HIST1H1C	
4kb 5' of HFE	
4kb 5' of HIST1H4C	
1.8kb 5' of HIST1H1T	
1kb 3' of HIST1H2BC	
8.2kb 3' of HIST1H2AC	
4.8kb 3' of HIST1H3G	
BTN3A2	3'-UTR
1.3kb 3' of BTN3A3	
4.9kb 5' of HLA-B	
3.7kb 5' of MICB	
MICB	intronic
4.7kb 5' of MCCD1	
DDX39B	intronic
ATP6V1G2	intronic
LTA	missense
737bp 3' of TNF	
2.8kb 5' of NCR3	
6.5kb 5' of AIF1	
ABHD16A	intronic
MSH5	intronic
317bp 3' of C6orf26	
C6orf27	intronic
VARS	intronic
LSM2	intronic

8.1kb 3' of NEU1	
SLC44A4	intronic
188bp 5' of SLC44A4	
339bp 3' of EHMT2	
STK19	intronic
TNXB	intronic
C6orf106	intronic
16kb 5' of SNRPC	
UHRF1BP1	intronic
CCND3	intronic
6.3kb 5' of GNMT	
PEX6	intronic
3.7kb 3' of VEGFA	
6.1kb 3' of VEGFA	
GSTA2	intronic
78kb 3' of LOC728012	
7.7kb 5' of FRK	
2.9kb 5' of RSPO3	
40kb 5' of LOC645434	
IGF2R	intronic
SLC22A1	intronic
5.1kb 5' of SLC22A2	
7.4kb 5' of SLC22A2	
SLC22A3	intronic
LPAL2	intronic
12kb 5' of LPA	
15kb 5' of PLG	
RAC1	intronic
DAGLB	intronic
SNX13	intronic
36kb 3' of PRPS1L1	
DNAH11	intronic
2.2kb 5' of MIR148A	
3.6kb 5' of NPC1L1	
DDX56	intronic
5.6kb 5' of TMED4	
OGDH	intronic
37kb 3' of FKBP6	
FZD9	3'-UTR
BAZ1B	intronic
5.2kb 5' of BCL7B	
6.1kb 5' of TBL2	
MLXIPL	intronic
21kb 5' of MLXIPL	
DNAJC30	3'-UTR
WBSCR22	intronic
STX1A	intronic

STX1A	intronic
GNAT3	intronic
43kb 5' of CD36	
14kb 3' of CD36	
27kb 3' of SEMA3C	
5.8kb 5' of KLF14	
CREB3L2	3'-UTR
AGPAT5	intronic
42kb 5' of SGK223	
LOC157273	
18kb 3' of LOC157273	
29kb 3' of LOC157273	
32kb 3' of LOC157273	
PINX1	intronic
PINX1	intronic
45kb 5' of GATA4	
GATA4	intronic
4.8kb 3' of GATA4	
NEIL2	intronic
5.4kb 5' of FDFT1	
CTSB	intronic
15kb 3' of NAT2	
58kb 5' of INTS10	
23kb 5' of INTS10	
18kb 3' of INTS10	
42kb 3' of INTS10	
26kb 5' of LPL	
6.2kb 3' of LPL	
59kb 3' of LPL	
33kb 3' of SLC18A1	
48kb 3' of SOX17	
UBXN2B	intronic
17kb 3' of CYP7A1	
TRPS1	intronic
100kb 5' of TRPS1	
48kb 5' of SNTB1	
31kb 3' of TRIB1	
57kb 3' of TRIB1	
15kb 5' of GPIHBP1	
1.7kb 3' of GPIHBP1	
TTC39B	intronic
PCSK5	intronic
21kb 5' of NIPSNAP3A	
ABCA1	intronic
31kb 5' of ABCA1	
53kb 5' of ABCA1	
ZER1	intronic

3kb 5' of GBGT1	
20kb 5' of GBGT1	
6.2kb 5' of OBP2B	
549bp 3' of ABO	
4.2kb 5' of ABO	
13kb 3' of SURF6	
MED22	intronic
SURF4	intronic
C9orf96	intronic
70bp 3' of MARCH8	
A1CF	missense
11kb 5' of NRBF2	
NRBF2	3'-UTR
JMJD1C	intronic
REEP3	intronic
REEP3	intronic
10kb 3' of REEP3	
EXOC6	intronic
CYP26C1	intronic
2.1kb 3' of CYP26A1	
6.9kb 5' of GPAM	
44kb 5' of GPAM	
TECTB	intronic
FAM24B-CUZD1	intronic
3.9kb 3' of LOC399815	
7.8kb 3' of FAM24A	
C10orf88	intronic
ARNTL	intronic
SPTY2D1	intronic
AMBRA1	intronic
ATG13	intronic
ARHGAP1	intronic
ZNF408	intronic
F2	intronic
CKAP5	intronic
LRP4	intronic
C11orf49	intronic
C11orf49	intronic
5.1kb 5' of PACSIN3	
DDB2	intronic
ACP2	missense
NR1H3	intronic
MADD	intronic
MADD	synonymous
MYBPC3	intronic
SPI1	intronic
7.3kb 5' of SLC39A13	

5.1kb 5' of SLC39A13	
4.3kb 5' of PSMC3	
4.5kb 5' of RAPSN	
3.9kb 5' of PTPMT1	
PTPMT1	intronic
KBTBD4	intronic
NDUFS3	intronic
367bp 3' of NDUFS3	
6.2kb 5' of C1QTNF4	
8.8kb 5' of C1QTNF4	
AGBL2	intronic
FNBP4	intronic
20kb 5' of NUP160	
55kb 5' of PTPRJ	
PTPRJ	intronic
15kb 5' of OR4B1	
9.9kb 5' of OR4X2	
OR4X1	missense
2.9kb 5' of OR4S1	
8.7kb 5' of OR4C3	
63kb 5' of OR4C45	
41kb 3' of OR4A47	
6.6kb 3' of LOC283116	
16kb 5' of TRIM64C	
25kb 5' of FOLH1	
86kb 5' of LOC440040	
34kb 3' of OR4A5	
20kb 5' of LOC440041	
5.9kb 5' of OR4A16	
91kb 3' of OR4A15	
87kb 5' of OR4C15	
315bp 5' of OR4C16	
8.3kb 3' of OR4C11	
13kb 5' of OR4P4	
2.8kb 5' of OR4S2	
18kb 3' of OR4C6	
25kb 5' of OR5D13	
1.6kb 3' of OR5D14	
6kb 5' of OR5L1	
2.4kb 3' of OR5L2	
4.2kb 5' of OR5D16	
17kb 5' of SPRYD5	
OR5W2	missense
5.3kb 3' of OR5I1	
4.3kb 5' of OR10AG1	
OR7E5P	intronic
15kb 5' of OR5F1	

17kb 5' of OR5AS1	
16kb 5' of OR8I2	
OR8H3	missense
OR8J3	missense
5.3kb 5' of OR8K5	
24kb 3' of OR5J2	
4.9kb 5' of OR5T2	
585bp 3' of OR5T3	
2.8kb 3' of OR5T1	
13kb 5' of OR8H1	
5kb 5' of OR8K3	
11kb 5' of OR8K1	
722bp 5' of OR8J1	
OR8U8	
OR8U8	
OR8U8	
OR8U8	
OR8U8	
OR8U8	
C11orf9	intronic
C11orf10	intronic
FEN1	3'-UTR
FADS1	intronic
3.3kb 5' of FADS2	
617bp 3' of FADS3	
RAB3IL1	intronic
FLRT1	intronic
MACROD1	intronic
VEGFB	intronic
PLCB3	missense
7.3kb 5' of CCDC88B	
17kb 3' of MOGAT2	
6.1kb 5' of DGAT2	intronic
5kb 5' of UVRAG	
UVRAG	intronic
119kb 3' of BUD13	
86kb 3' of BUD13	
12kb 3' of BUD13	
ZNF259	intronic
APOA5	intronic
9.9kb 3' of APOA4	
APOC3	intronic
899bp 3' of APOA1	
APOA1	intronic
SIK3	intronic
PAFAH1B2	intronic
SIDT2	intronic

TAGLN	intronic
PCSK7	intronic
RNF214	intronic
BACE1	intronic
11kb 3' of RPUSD4	
RPUSD4	intronic
DCPS	intronic
FLJ39051	intronic
ST3GAL4	intronic
79kb 5' of PDE3A	
28kb 5' of TUBA1A	
5.5kb 5' of SPATS2	
819bp 5' of STAC3	
21kb 5' of INHBC	
1.6kb 5' of INHBC	
INHBE	intronic
MYO1H	intronic
KCTD10	intronic
UBE3B	intronic
MMAB	intronic
MVK	intronic
SH2B3	intronic
SH2B3	intronic
ATXN2	intronic
BRAP	intronic
ACAD10	intronic
2.1kb 3' of ALDH2	
MAPKAPK5	intronic
ADAM1	
12kb 3' of ADAM1	
NAA25	intronic
33kb 5' of SPPL3	
9kb 3' of HNF1A-AS1	
HNF1A	intronic
C12orf43	intronic
OASL	synonymous
2.8kb 3' of HCAR2	
171bp 5' of HCAR2	
380bp 3' of HCAR3	
3kb 3' of HCAR1	
7.6kb 5' of CDK2AP1	
SBNO1	intronic
8.2kb 5' of SETD8	
DNAH10	intronic
CCDC92	intronic
ZNF664	intronic
ZNF664-FAM101A	intronic

SCARB1	intronic
5.3kb 5' of SCARB1	
15kb 5' of SCARB1	
23kb 3' of UBC	
BRCA2	intronic
N4BP2L1	3'-UTR
GAS6	intronic
NYNRIN	intronic
287bp 5' of AKT1	
1.6kb 3' of ZBTB42	
CAPN3	intronic
ZFP106	intronic
CDAN1	intronic
TTBK2	intronic
UBR1	intronic
12kb 5' of TMEM62	
TGM7	intronic
7kb 3' of LCMT2	
ADAL	intronic
ZSCAN29	intronic
TUBGCP4	intronic
TP53BP1	intronic
MAP1A	missense
PPIP5K1	intronic
CKMT1B	intronic
STRC	intronic
9.7kb 5' of CATSPER2	
CKMT1A	intronic
97bp 3' of CATSPER2P1	
PDIA3	intronic
ELL3	3'-UTR
SERF2	intronic
SERF2-C15ORF63	intronic
MFAP1	intronic
WDR76	intronic
FRMD5	intronic
16kb 5' of CASC4	
CTDSPL2	intronic
41kb 5' of LIPC	
694bp 5' of LIPC	
8.2kb 3' of TPM1	
23kb 5' of LACTB	
FTO	intronic
GNAO1	intronic
AMFR	intronic
16kb 5' of MT4	
2.6kb 3' of MT3	

8.3kb 3' of MT3	
211bp 5' of MT1L	
838bp 5' of MT1E	
697bp 3' of MT1JP	
1.2kb 5' of MT1DP	
684bp 3' of MT1G	
841bp 5' of MT1H	
MT1H	intronic
MT1IP	
3.2kb 3' of MT1X	
18kb 3' of MT1X	
5.4kb 5' of NUP93	
NUP93	intronic
6.5kb 5' of MIR138-2	
SLC12A3	intronic
SLC12A3	intronic
7.8kb 3' of HERPUD1	
CETP	intronic
NLRC5	intronic
CPNE2	intronic
39bp 5' of FAM192A	
RSPRY1	intronic
ARL2BP	intronic
PLLP	intronic
853bp 5' of CKLF	
CMTM4	intronic
CCDC79	5'-UTR
3.1kb 5' of PDP2	
CDH16	missense
CES3	intronic
8.4kb 3' of CES4A	
CBFB	intronic
C16orf70	intronic
FBXL8	synonymous
HSF4	intronic
NOL3	5'-UTR
KIAA0895L	intronic
EXOC3L1	missense
E2F4	3'-UTR
ELMO3	intronic
LRRC29	3'-UTR
LRRC29	intronic
FHOD1	synonymous
SLC9A5	intronic
PLEKHG4	missense
KCTD19	intronic
LRRC36	intronic

224bp 3' of ZDHHC1	
ZDHHC1	intronic
HSD11B2	intronic
ATP6V0D1	intronic
1.5kb 5' of AGRP	
2.4kb 5' of AGRP	
7.4kb 5' of FAM65A	intronic
1.2kb 3' of FAM65A	
4.9kb 5' of CTCF	
CTCF	intronic
RLTPR	intronic
ACD	intronic
C16orf48	intronic
GFOD2	intronic
RANBP10	intronic
TSNAXIP1	intronic
CENPT	intronic
NUTF2	intronic
EDC4	intronic
NRN1L	missense
PSKH1	intronic
CTRL	missense
PSMB10	missense
SLC12A4	3'-UTR
SLC12A4	intronic
1.7kb 5' of DPEP3	
DPEP2	intronic
9.1kb 3' of DDX28	
DUS2L	intronic
DUS2L	intronic
NFATC3	intronic
ESRP2	intronic
1.4kb 5' of PLA2G15	
493bp 5' of SLC7A6	
SLC7A6OS	intronic
PRMT7	intronic
SMPD3	intronic
17kb 5' of AP1G1	
1.6kb 5' of ATXN1L	
ZNF821	intronic
KIAA0174	intronic
PKD1L3	intronic
DHODH	intronic
13kb 5' of HP	
HP	intronic
HPR	intronic
DHX38	intronic

PMFBP1	intronic
31kb 5' of PMFBP1	
CMIP	intronic
8.9kb 3' of FBXL20	
FBXL20	intronic
MED1	intronic
CDK12	intronic
23kb 3' of NEUROD2	
14kb 3' of NEUROD2	
6.3kb 5' of NEUROD2	
PPP1R1B	intronic
STARD3	intronic
162bp 5' of TCAP	
166bp 5' of PNMT	
PGAP3	intronic
ERBB2	intronic
676bp 5' of GRB7	
IKZF3	intronic
8.6kb 3' of ZPBP2	
GSDMB	intronic
ORMDL3	intronic
5.8kb 5' of ORMDL3	
GSDMA	intronic
869bp 3' of GSDMA	
100bp 3' of CSF3	
MED24	intronic
38kb 5' of MEOX1	
2.6kb 3' of DUSP3	
CD300LG	missense
11kb 3' of PPY	
2.4kb 3' of PPY	
PPY	intronic
ITGB3	intronic
873bp 3' of ITGB3	
C17orf57	intronic
MRPL45P2	intronic
NPEPPS	intronic
KPNB1	intronic
5.8kb 3' of KPNB1	
10kb 5' of TBX21	
7.2kb 5' of CEP112	
APOH	intronic
37kb 3' of ABCA8	
ABCA8	intronic
ABCA9	intronic
ABCA6	intronic
ABCA10	intronic

ABCA5	intronic
44kb 5' of ABCA5	
MAP2K6	intronic
22kb 3' of MAP2K6	
3.8kb 5' of PGS1	
PGS1	intronic
SMAD7	intronic
8.9kb 5' of SMAD7	
7.5kb 5' of DYM	
312bp 3' of C18orf32	
RPL17	intronic
34kb 5' of LIPG	
LIPG	3'-UTR
62kb 3' of LIPG	
66kb 3' of ACAA2	
3.6kb 3' of ACAA2	
2.5kb 3' of SCARNA17	
MYO5B	intronic
209kb 3' of MC4R	
189kb 3' of MC4R	
INSR	intronic
2.2kb 5' of KANK3	
ANGPTL4	missense
LOC100507567	intronic
LOC100507567	intronic
RAB11B	intronic
MARCH2	intronic
HNRNPM	intronic
PRAM1	intronic
MYO1F	intronic
12kb 5' of S1PR5	
ATG4D	intronic
KRI1	intronic
965bp 5' of CDKN2D	
AP1M2	synonymous
SLC44A2	intronic
ILF3	3'-UTR
QTRT1	intronic
DNM2	intronic
TMED1	intronic
3.1kb 5' of TMED1	
YIPF2	
135bp 3' of C19orf52	
14kb 3' of C19orf52	
11kb 3' of SMARCA4	
8.4kb 5' of LDLR	
SPC24	intronic

KANK2	3'-UTR
DOCK6	intronic
DOCK6	intronic
SUGP2	intronic
ARMC6	intronic
SLC25A42	intronic
MEF2BNB-MEF2B	intronic
MEF2BNB	intronic
287bp 5' of NR2C2AP	
NCAN	missense
HAPLN4	3'-UTR
TM6SF2	missense
SUGP1	intronic
8.3kb 3' of MAU2	
GATAD2A	intronic
NDUFA13	intronic
YJEFN3	intronic
6.6kb 3' of CILP2	
PBX4	intronic
GMIP	intronic
ZNF101	intronic
1.4kb 3' of ZNF14	
10kb 5' of ZNF14	
PEPD	intronic
ZFP112	intronic
ZNF229	intronic
ZNF180	intronic
CEACAM20	intronic
CEACAM22P	
IGSF23	intronic
CEACAM19	synonymous
18kb 3' of CEACAM16	
9.8kb 5' of BCL3	
CBLC	intronic
BCAM	intronic
PVRL2	intronic
TOMM40	intronic
APOE	missense
APOC1	intronic
2.9kb 5' of APOC1P1	
APOC4	intronic
APOC4	missense
CLPTM1	intronic
356bp 5' of RELB	
325bp 3' of RELB	
GEMIN7	3'-UTR
LRRC68	intronic

813bp 3' of NKPD1	
NKPD1	missense
TRAPPC6A	intronic
2.9kb 3' of BLOC1S3	
2.2kb 3' of PPP1R13L	
VASP	intronic
GIPR	intronic
FAM83E	intronic
SEC1	intronic
NTN5	intronic
FUT2	synonymous
MAMSTR	intronic
RASIP1	intronic
IZUMO1	intronic
FUT1	intronic
FPR3	intronic
14kb 3' of FPR3	
ZNF577	intronic
1.1kb 3' of LILRB5	
5.3kb 5' of LILRB5	
6.8kb 3' of LILRA3	
LILRA3	intronic
3kb 5' of LILRA5	
7.5kb 3' of LILRA4	
85kb 3' of SNX5	
76kb 3' of SNX5	
EDEM2	intronic
16kb 3' of PROCR	
225kb 3' of MAFB	
155kb 3' of MAFB	
135kb 3' of MAFB	
2.9kb 5' of TOP1	
TOP1	intronic
1.6kb 3' of TOP1	intronic
PLCG1	intronic
PLCG1	missense
ZHX3	intronic
11kb 5' of LPIN3	
1.3kb 5' of EMILIN3	
16kb 3' of CHD6	
6.9kb 5' of R3HDML	
HNF4A	missense
1kb 3' of UBE2C	
11kb 5' of PLTP	
308bp 5' of PCIF1	
PCIF1	intronic
ZNF335	intronic

6.7kb 5' of MMP9	
SLC12A5	intronic
EYA2	intronic
PTTG1IP	3'-UTR
UBE2L3	3'-UTR
1.7kb 3' of YDJC	
753bp 5' of YDJC	
703bp 3' of SDF2L1	
PLA2G6	intronic
MAFF	intronic

Web Table 11: eQTL information from GTEx and RegulomeDB scores for variants si
DF Joint *P* -value). Any significant variant with eQTL effects within +/- 1 Mbp of the

rsID	CHR	BP (hg19)	BP (hg38)	HUGO Gene	Role
rs9645452	1	25668326	25341835	*TMEM50A*	intron-variant
rs926438	1	25753638	25427147	*RHCE*	intron-variant
rs9438905	1	25764177	25437686	*TMEM57*	intron-variant
rs12759594	1	27002991	26676500	*LOC105376888*	
rs35738294	1	27020133	26693642	*LOC101928728*	nc-transcript-variant
rs114165349	1	27021913	26695422	*ARID1A*	upstream-variant-2KB
rs35615194	1	27118171	26791680	*PIGV*	intron-variant
rs35583548	1	27140149	26813658	*ZDHHC18*	
rs12753968	1	27197363	26870872	*SFN*	
rs34353981	1	27213362	26886871	*GPN2*	intron-variant
rs34339345	1	27226089	26899598	*GPATCH3*	intron-variant
rs6659176	1	27239920	26913429	*NR0B2*	missense
rs12728150	1	27268737	26942246	*NUDC*	intron-variant
rs6656815	1	27292462	26965971	*KDF1*	
rs17343193	1	39881468	39415796	*KIAA0754*	utr-variant-3-prime
rs61779313	1	39944249	39478577	*MACF1*	intron-variant
rs60069508	1	39964912	39499240	*BMP8A*	intron-variant
rs61779359	1	40010235	39544563	*PPIEL*	intron-variant
rs2068663	1	40038571	39572899	*LOC101929516*	intron-variant
rs4660303	1	40060473	39594801	*PABPC4*	
rs61781390	1	40075894	39610222	*HEYL*	
rs12117661	1	55487346	55021673	*BSND*	
rs60500353	1	62898984	62433313	*LOC105378768*	downstream-variant-500B
rs10493322	1	62905893	62440222	*USP1*	intron-variant
rs10789117	1	63072265	62606594	*ANGPTL3*	downstream-variant-500B
rs4495740	1	63124465	62658794	*DOCK7*	intron-variant
rs7532549	1	93539656	93074099	*MTF2*	
rs10874762	1	93639101	93173544	*TMED5*	intron-variant
rs35940311	1	93663604	93198047	*CCDC18*	intron-variant
rs10874772	1	93787770	93322213	*CCDC18-AS1*	intron-variant
rs4847240	1	93817946	93352389	*DR1*	intron-variant
rs12740374	1	109817590	109274968	*CELSR2*	utr-variant-3-prime
rs1277930	1	109822143	109279521	*PSRC1*	downstream-variant-500B
rs650985	1	110201580	109658958	*GSTM4*	intron-variant
rs1537234	1	110279821	109737199	*GSTM3*	intron-variant
rs1335920	1	221018288	220844946	*HLX-AS1*	intron-variant
rs487738	1	234840803	234705056	*LOC105373208*	
rs486142	1	234848609	234712862	*LINC01132*	
rs11580878	1	234876434	234740687	*LOC105373210*	
rs581411	2	21289432	21066560	*APOB*	
rs10221768	2	21417431	21194559	*LOC105374317*	

rs72804857	2	27161476	26938608	*DPYSL5*	intron-variant
rs2580754	2	27398196	27175328	*TCF23*	
rs1275504	2	27416702	27193834	*SLC5A6*	
rs1275535	2	27437496	27214628	*ATRAID*	intron-variant
rs3769143	2	27450724	27227856	*CAD*	intron-variant
rs11693052	2	27484620	27261752	*SLC30A3*	intron-variant
rs4665961	2	27500381	27277513	*DNAJC5G*	intron-variant
rs4665963	2	27528692	27305824	*TRIM54*	intron-variant
rs6731600	2	27531665	27308797	*UCN*	upstream-variant-2KB
rs4665378	2	27548038	27325171	*MPV17*	
rs10205592	2	27568871	27346004	*GTF3C2*	intron-variant
rs6729709	2	27583156	27360289	*LOC105374363*	
rs7586601	2	27584666	27361799	*EIF2B4*	
rs4665972	2	27598097	27375230	*SNX17*	intron-variant
rs1271144	2	27615294	27392427	*FTH1P3*	downstream-variant-500B
rs1728918	2	27635463	27412596	*PPM1G*	
rs4665978	2	27648726	27425859	*NRBP1*	upstream-variant-2KB
rs1260342	2	27663416	27440549	*KRTCAP3*	upstream-variant-2KB
rs780108	2	27684957	27462090	*IFT172*	intron-variant
rs8395	2	27715207	27492340	*FNDC4*	utr-variant-3-prime
rs1260326	2	27730940	27508073	*GCKR*	downstream-variant-500B
rs12995461	2	27778167	27555300	*C2rf16*	
rs12467476	2	27825715	27602848	*ZNF512*	intron-variant
rs3749147	2	27851918	27629051	*CCDC121*	upstream-variant-2KB
rs34502053	2	27854524	27631657	*GPN1*	intron-variant
rs4299376	2	44072576	43845437	*ABCG8*	intron-variant
rs17508045	2	118576719	117819143	*DDX18*	intron-variant
rs72834335	2	118611529	117853953	*LOC107985939*	
rs72834351	2	118638336	117880760	*CCDC93*	
rs56145894	2	118812449	118054873	*LOC102723413*	downstream-variant-500B
rs55809639	2	118842801	118085225	*LOC107985940*	intron-variant
rs72839616	2	118846970	118089394	*INSIG2*	intron-variant
rs2972143	2	227116365	226251649	*LOC646736*	
rs17819602	3	12507119	12465620	*PPARG*	intron-variant
rs111973309	3	12561138	12519639	*TSEN2*	intron-variant
rs113760078	3	12585073	12543574	*MKRN2OS*	intron-variant
rs113671109	3	12620885	12579386	*MKRN2*	intron-variant
rs11711419	3	12667784	12626285	*RAF1*	intron-variant
rs113026294	3	12748879	12707380	*TMEM40*	
rs6771546	3	49968572	49931139	*MON1A*	upstream-variant-2KB
rs34831713	3	50118748	50081315	*RBM6*	
rs2013208	3	50129399	50091966	*RBM5*	intron-variant
rs2856236	3	50161717	50124284	*SEMA3F-AS1*	intron-variant
rs17451107	3	156797609	157079820	*LINC02029*	
rs34311866	4	951947	958159	*TMEM175*	missense
rs3129320	4	3265130	3263403	*MSANTD1*	
rs7656630	4	88173692	87252540	*KLHL8*	

rs13141053	4	88212545	87291393	*MIR5705*	
rs11735092	4	88226231	87305079	*HSD17B13*	utr-variant-3-prime
rs6897082	5	74330957	75035132	*GCNT4*	
rs7700965	5	74356857	75061032	*LINC01336*	
rs4704200	5	74569856	75274031	*ANKRD31*	
rs12916	5	74656539	75360714	*HMGCR*	utr-variant-3-prime
rs4704220	5	74757556	75461731	*COL4A3BP*	intron-variant
rs5744672	5	74877803	75581978	*POLK*	intron-variant
rs984976	5	74910870	75615045	*ANKDD1B*	intron-variant
rs34361	5	74971846	75676021	*POC5*	intron-variant
rs2112347	5	75015242	75719417	*LOC441087*	intron-variant
rs56076449	5	132442190	133106498	*HSPA4*	
rs13201341	6	25822661	25822433	*SLC17A1*	intron-variant
rs13198474	6	25874423	25874195	*SLC17A3*	utr-variant-5-prime
rs17526722	6	25918855	25918627	*SLC17A2*	intron-variant
rs36012762	6	25980523	25980295	*TRIM38*	intron-variant
rs116201501	6	25999149	25998921	*LOC107986581*	nc-transcript-variant
rs13191445	6	26015489	26015261	*HIST1H1A*	
rs41266779	6	26021872	26021644	*HIST1H4A*	upstream-variant-2KB
rs35249036	6	26026163	26025935	*HIST1H4B*	
rs10484433	6	26030492	26030264	*HIST1H3B*	
rs13210041	6	26037601	26037373	*HIST1H2AB*	
rs35506517	6	26044864	26044636	*HIST1H2BB*	upstream-variant-2KB
rs35050608	6	26067360	26067132	*HIST1H1C*	
rs34197618	6	26083519	26083291	*HFE*	
rs13200888	6	26100198	26099970	*HIST1H4C*	
rs13206501	6	26110148	26109920	*HIST1H1T*	upstream-variant-2KB
rs13197334	6	26122648	26122420	*HIST1H2AC*	upstream-variant-2KB
rs36109883	6	26133070	26132842	*HIST1H2BC*	
rs55706012	6	26266311	26266083	*LOC105374986*	
rs66757203	6	26454956	26454728	*BTN3A3*	
rs2523569	6	31329921	31362144	*HLA-B*	
rs3130923	6	31462135	31494358	*LOC102725068*	nc-transcript-variant
rs3130616	6	31473746	31505969	*MICB*	intron-variant
rs9267488	6	31514247	31546470	*ATP6V1G2*	intron-variant
rs2229094	6	31540556	31572779	*LOC100287329*	upstream-variant-2KB
rs1800628	6	31546850	31579073	*TNF*	
rs114276434	6	31669585	31701808	*ABHD16A*	intron-variant
rs28745895	6	31709969	31742192	*MSH5*	intron-variant
rs187911831	6	31732942	31765165	*MSH5-SAPCD1*	intron-variant
rs114936741	6	31744148	31776371	*VWA7*	intron-variant
rs142006308	6	31757791	31790014	*VARS*	intron-variant
rs146752130	6	31768538	31800761	*LSM2*	intron-variant
rs115302857	6	31818719	31850942	*NEU1*	
rs2763981	6	31840021	31872244	*SLC44A4*	intron-variant
rs605203	6	31847012	31879235	*LOC107986588*	upstream-variant-2KB
rs570263	6	31847196	31879419	*EHMT2*	downstream-variant-500B

rs389883	6	31947460	31979683	*STK19*	intron-variant
rs1150754	6	32050758	32082981	*TNXB*	intron-variant
rs6907508	6	34592090	34624313	*C6rf106*	intron-variant
rs2764203	6	34708901	34741124	*LOC107986591*	
rs112563428	6	34800435	34832658	*UHRF1BP1*	intron-variant
rs6458314	6	42922215	42954477	*CNPY3-GNMT*	intron-variant
rs2395943	6	42940673	42972935	*PEX6*	intron-variant
rs2749008	6	52626120	52761322	*GSTA2*	intron-variant
rs13210143	6	116389636	116068473	*FRK*	intron-variant
rs146203232	6	160521885	160100853	*IGF2R*	intron-variant
rs3729790	7	6426954	6387323	*RAC1*	intron-variant
rs836546	7	6479668	6440037	*DAGLB*	intron-variant
rs66476925	7	21611399	21571781	*DNAH11*	intron-variant
rs10260606	7	44584551	44544952	*NPC1L1*	
rs217381	7	44606217	44566618	*DDX56*	intron-variant
rs42132	7	72809618	73395288	*FKBP6*	
rs1178947	7	72850178	73435848	*FZD9*	utr-variant-3-prime
rs79862839	7	72921609	73507279	*BAZ1B*	intron-variant
rs34594435	7	72977249	73562919	*BCL7B*	
rs9638182	7	72999105	73584775	*TBL2*	
rs79624003	7	73012785	73598455	*MLXIPL*	intron-variant
rs8891	7	73096993	73682663	*DNAJC30*	utr-variant-3-prime
rs139906208	7	80322438	80693122	*CD36*	
rs2911971	8	6607634	6750113	*AGPAT5*	intron-variant
rs2921097	8	8281142	8423632	*LOC105379222*	
rs804281	8	11611865	11754356	*GATA4*	intron-variant
rs1004712	8	11622293	11764784	*C8rf49*	
rs1090107	8	11632528	11775019	*NEIL2*	intron-variant
rs2686187	8	11654796	11797287	*FDFT1*	intron-variant
rs6601616	8	11703652	11846143	*CTSB*	intron-variant
rs9650459	8	144280215	143198753	*LOC107986906*	
rs56960668	8	144300760	143218568	*GPIHBP1*	
rs1215112	9	15303583	15303585	*TTC39B*	intron-variant
rs1125873	9	107721423	104959142	*LOC105376196*	
rs13284665	9	131513370	128751091	*ZER1*	intron-variant
rs11794634	9	136090813	133215426	*OBP2B*	intron-variant
rs8176757	9	136130012	133254625	*LOC107987136*	upstream-variant-2KB
rs495828	9	136154867	133279294	*ABO*	
rs9650778	9	136184798	133317963	*SURF6*	
rs28658542	9	136214276	133347421	*MED22*	intron-variant
rs56343119	9	136237672	133370796	*SURF4*	intron-variant
rs17474001	9	136267149	133402020	*STKLD1*	intron-variant
rs10761716	10	64882300	63122540	*LOC105378328*	
rs13095	10	64914372	63154612	*NRBF2*	utr-variant-3-prime
rs10822164	10	65127258	63367498	*JMJD1C*	intron-variant
rs7085018	10	65286667	63526907	*REEP3*	intron-variant
rs7895549	10	65357438	63597678	*LOC105378329*	intron-variant

rs10740138	10	65395133	63635373	*LOC101929846*	intron-variant
rs4573621	10	113987548	112227790	*LOC101927600*	nc-transcript-variant
rs7910726	10	124662143	122902627	*LOC399815*	
rs7082181	10	124680468	122920952	*FAM24A*	
rs7904973	10	124693587	122934071	*C10rf88*	intron-variant
rs10832961	11	18653957	18632410	*SPTY2D1*	intron-variant
rs4576779	11	47121547	47099996	*C11rf49*	intron-variant
rs4752968	11	47185457	47163906	*ARFGAP2*	downstream-variant-500B
rs11039122	11	47213117	47191566	*PACSIN3*	
rs901746	11	47260319	47238768	*DDB2*	intron-variant
rs2167079	11	47270255	47248704	*ACP2*	missense
rs3758673	11	47278917	47257366	*NR1H3*	intron-variant
rs10501321	11	47294626	47273075	*LOC101928943*	upstream-variant-2KB
rs326214	11	47298360	47276809	*MADD*	reference
rs10769254	11	47362465	47340914	*MYBPC3*	intron-variant
rs12146565	11	47398963	47377412	*SPI1*	intron-variant
rs74206205	11	47422772	47401221	*MIR4487*	downstream-variant-500B
rs11820650	11	47424963	47403412	*SLC39A13*	
rs7130693	11	47452321	47430770	*PSMC3*	
rs35184771	11	47475189	47453637	*RAPSN*	
rs12798346	11	47583121	47561569	*CELF1*	intron-variant
rs7945473	11	47589707	47568155	*PTPMT1*	intron-variant
rs59837204	11	47596783	47575231	*KBTBD4*	intron-variant
rs2030166	11	47602729	47581177	*NDUFS3*	intron-variant
rs11605348	11	47606483	47584931	*FAM180B*	upstream-variant-2KB
rs12799623	11	47622139	47600587	*C1QTNF4*	
rs12419692	11	47624714	47603162	*MTCH2*	
rs10838747	11	47716324	47694772	*AGBL2*	intron-variant
rs7927771	11	47781306	47759754	*FNBP4*	intron-variant
rs12798109	11	47889850	47868298	*NUP160*	
rs2930191	11	47946836	47925284	*PTPRJ*	
rs11530224	11	48552070	48530518	*OR4A47*	
rs10769562	11	49066148	49044596	*TRIM49B*	
rs11040242	11	49096981	49075429	*TRIM64C*	
rs658118	11	49255042	49233490	*FOLH1*	
rs11040387	11	49493736	49472184	*LOC440040*	
rs174536	11	61551927	61784455	*MYRF*	intron-variant
rs102274	11	61557826	61790354	*TMEM258*	intron-variant
rs4246215	11	61564299	61796827	*FEN1*	utr-variant-3-prime
rs174551	11	61573684	61806212	*FADS1*	intron-variant
rs174566	11	61592362	61824890	*FADS2*	intron-variant
rs174449	11	61640379	61872907	*FADS3*	
rs174469	11	61667443	61899971	*RAB3IL1*	intron-variant
rs11231698	11	63877163	64109691	*FLRT1*	intron-variant
rs190528931	11	63911273	64143801	*MACROD1*	intron-variant
rs56271783	11	64004723	64237251	*VEGFB*	intron-variant
rs35169799	11	64031241	64263769	*PLCB3*	missense

rs73502335	11	64100401	64332929	*LOC102723878*	intron-variant
rs11236519	11	75459015	75747970	*LOC105369393*	
rs1806895	11	75473715	75762670	*LOC283214*	intron-variant
rs509728	11	116533167	116662450	*LOC101929011*	
rs10750096	11	116656788	116786072	*ZPR1*	intron-variant
rs6589572	11	116681563	116810847	*APOA4*	
rs5141	11	116702123	116831407	*APOC3*	intron-variant
rs10750098	11	116705568	116834852	*APOA1-AS*	upstream-variant-2KB
rs2070665	11	116707684	116836968	*APOA1*	intron-variant
rs6589574	11	116730638	116859922	*SIK3*	intron-variant
rs7925256	11	117045335	117174619	*PAFAH1B2*	intron-variant
rs1242229	11	117062370	117191654	*SIDT2*	intron-variant
rs641620	11	117074229	117203513	*LOC100652768*	upstream-variant-2KB
rs659955	11	117080379	117209663	*PCSK7*	intron-variant
rs670712	11	126060666	126190771	*RPUSD4*	
rs580145	11	126079939	126210044	*FAM118B*	upstream-variant-2KB
rs78471630	11	126221298	126351403	*ST3GAL4-AS1*	intron-variant
rs76970536	11	126250680	126380785	*ST3GAL4*	intron-variant
rs6606717	12	109873227	109435422	*MYO1H*	intron-variant
rs2058804	12	109909011	109471206	*KCTD10*	intron-variant
rs10744826	12	109965512	109527707	*UBE3B*	intron-variant
rs7134594	12	110000193	109562388	*MMAB*	intron-variant
rs7954144	12	110015893	109578088	*MVK*	intron-variant
rs7310615	12	111865049	111427245	*SH2B3*	intron-variant
rs10849948	12	111875410	111437606	*LOC105369985*	intron-variant
rs7137828	12	111932800	111494996	*ATXN2*	intron-variant
rs12579287	12	112090814	111653010	*BRAP*	intron-variant
rs594570	12	112164622	111726818	*ACAD10*	intron-variant
rs6489793	12	112249884	111812080	*ALDH2*	
rs2269803	12	112326145	111888341	*MAPKAPK5*	intron-variant
rs3742000	12	112338539	111900735	*ADAM1A*	nc-transcript-variant
rs61670030	12	112351854	111914050	*TMEM116*	intron-variant
rs7972112	12	112505182	112067378	*NAA25*	intron-variant
rs2004910	12	121374727	120936924	*XLOC009911*	
rs7954331	12	121398657	120960854	*HNF1A-AS1*	
rs1169314	12	121443116	121005313	*C12rf43*	intron-variant
rs7956284	12	123183017	122698470	*LOC107984443*	intron-variant
rs545234	12	123188076	122703529	*HCAR2*	upstream-variant-2KB
rs2262194	12	123198921	122714374	*HCAR3*	downstream-variant-500B
rs2454702	12	123209159	122724612	*HCAR1*	
rs10444449	12	123764271	123279724	*CDK2AP1*	
rs7298909	12	123830939	123346392	*SBNO1*	intron-variant
rs28786830	12	123860472	123375925	*KMT5A*	
rs12298484	12	124418674	123934127	*DNAH10*	intron-variant
rs4765219	12	124440110	123955563	*CCDC92*	intron-variant
rs11057413	12	124489162	124004615	*ZNF664*	intron-variant
rs825452	12	124509177	124024630	*ZNF664-FAM101A*	intron-variant

rs6573778	14	24872209	24403003	*NYNRIN*	intron-variant
rs117578063	15	43580645	43288447	*TGM7*	intron-variant
rs528517	15	43612925	43320727	*LCMT2*	
rs2278860	15	43659046	43366848	*ZSCAN29*	intron-variant
rs55707100	15	43820717	43528519	*MAP1A*	missense
rs2470130	15	43829615	43537417	*PPIP5K1*	intron-variant
rs56397895	15	43891235	43599037	*CKMT1B*	intron-variant
rs2260160	15	43895643	43603445	*STRC*	intron-variant
rs2467426	15	43989518	43697320	*CKMT1A*	intron-variant
rs117519814	15	44052248	43760050	*PDIA3*	intron-variant
rs2788	15	44064886	43772688	*ELL3*	utr-variant-3-prime
rs28546844	15	44082088	43789890	*SERF2*	intron-variant
rs3759791	15	44090798	43798600	*HYPK*	upstream-variant-2KB
rs28509275	15	44098105	43805907	*MFAP1*	intron-variant
rs13329084	15	44151063	43858865	*WDR76*	intron-variant
rs7174174	15	63372327	63080128	*TPM1*	
rs76127683	15	63391362	63099163	*LOC107984798*	
rs72824235	16	56676399	56642487	*MT1DP*	upstream-variant-2KB
rs13336686	16	57256949	57223037	*RSPRY1*	intron-variant
rs7185839	16	67052047	67018144	*CES4A*	
rs66907233	16	67079680	67045777	*CBFB*	intron-variant
rs7184692	16	67180171	67146268	*C16rf70*	intron-variant
rs2233455	16	67207933	67174030	*NOL3*	intron-variant
rs13339140	16	67213923	67180020	*KIAA0895L*	intron-variant
rs9939768	16	67219107	67185204	*EXOC3L1*	missense
rs9932087	16	67232360	67198457	*E2F4*	utr-variant-3-prime
rs73586989	16	67234741	67200838	*ELMO3*	intron-variant
rs12051247	16	67241282	67207379	*LRRC29*	utr-variant-3-prime
rs13338688	16	67248831	67214928	*LOC105369155*	intron-variant
rs6499118	16	67265360	67231457	*FHOD1*	nc-transcript-variant
rs9940665	16	67289841	67255938	*SLC9A5*	intron-variant
rs8044843	16	67318242	67284339	*PLEKHG4*	missense
rs16957291	16	67326102	67292199	*KCTD19*	intron-variant
rs8052687	16	67446037	67412134	*ZDHHC1*	intron-variant
rs12935253	16	67466430	67432527	*HSD11B2*	intron-variant
rs55877766	16	67473389	67439486	*ATP6V0D1*	intron-variant
rs13338499	16	67520123	67486220	*LOC101927837*	intron-variant
rs13334205	16	67581883	67547980	*FAM65A*	
rs8046907	16	67591389	67557486	*LOC107984813*	
rs111893345	16	67607848	67573945	*CTCF*	intron-variant
rs60990105	16	67680956	67647053	*CARMIL2*	intron-variant
rs67114979	16	67691645	67657742	*ACD*	downstream-variant-500B
rs7187476	16	67699948	67666045	*C16rf86*	upstream-variant-2KB
rs56047901	16	67742326	67708423	*GFOD2*	intron-variant
rs55661503	16	67836552	67802649	*RANBP10*	intron-variant
rs2292316	16	67861134	67827231	*TSNAXIP1*	intron-variant
rs8060967	16	67871501	67837598	*CENPT*	intron-variant

rs1124324	16	67897487	67863584	*NUTF2*	intron-variant
rs56374641	16	67908713	67874810	*EDC4*	intron-variant
rs73594554	16	67920049	67886146	*NRN1L*	missense
rs55781197	16	67940350	67906447	*PSKH1*	intron-variant
rs1134760	16	67964203	67930300	*CTRL*	missense
rs20549	16	67969930	67936027	*PSMB10*	missense
rs1109166	16	67977382	67943479	*LCAT*	intron-variant
rs2292318	16	67985706	67951803	*SLC12A4*	intron-variant
rs255056	16	68016185	67982282	*DPEP3*	upstream-variant-2KB
rs255052	16	68024995	67991092	*DPEP2*	intron-variant
rs112358753	16	68046052	68012149	*LOC100131303*	
rs55682260	16	68057880	68023977	*DDX28*	upstream-variant-2KB
rs79323429	16	68084594	68050691	*DUS2*	intron-variant
rs55857142	16	68236741	68202838	*NFATC3*	intron-variant
rs8057119	16	68268836	68234933	*ESRP2*	intron-variant
rs7189155	16	68277882	68243979	*PLA2G15*	upstream-variant-2KB
rs12447119	16	68297928	68264025	*SLC7A6*	nc-transcript-variant
rs8060690	16	68340085	68306182	*SLC7A6OS*	intron-variant
rs73613962	16	68361974	68328071	*PRMT7*	intron-variant
rs57434514	16	68402649	68368746	*SMPD3*	intron-variant
rs4788561	16	71878255	71844352	*ATXN1L*	upstream-variant-2KB
rs2288030	16	71914107	71880204	*ZNF821*	intron-variant
rs4788450	16	71955400	71921497	*IST1*	intron-variant
rs11648003	16	72052348	72018449	*DHODH*	intron-variant
rs12924886	16	72075593	72041694	*TXNL4B*	
rs4788458	16	72088675	72054776	*HP*	intron-variant
rs3794695	16	72097827	72063928	*HPR*	intron-variant
rs2287997	16	72140553	72106654	*DHX38*	intron-variant
rs8076462	17	37400025	39243772	*LOC101929578*	intron-variant
rs8076494	17	37516722	39360469	*FBXL20*	intron-variant
rs12948560	17	37570986	39414733	*MED1*	intron-variant
rs34957982	17	37647716	39491463	*CDK12*	intron-variant
rs412430	17	37737094	39580841	*LOC105371770*	
rs11078917	17	37746359	39590106	*LOC105371771*	
rs9915323	17	37770481	39614228	*NEUROD2*	
rs1495099	17	37784464	39628211	*PPP1R1B*	intron-variant
rs881844	17	37810218	39653965	*STARD3*	intron-variant
rs931992	17	37821435	39665182	*TCAP*	upstream-variant-2KB
rs3764351	17	37824339	39668086	*PNMT*	intron-variant
rs732083	17	37834367	39678114	*PGAP3*	intron-variant
rs11653998	17	37877447	39721194	*ERBB2*	intron-variant
rs4795393	17	37893484	39737231	*GRB7*	upstream-variant-2KB
rs11658993	17	37940808	39784555	*IKZF3*	intron-variant
rs9908132	17	38042777	39886524	*ZPBP2*	
rs62067034	17	38063738	39907485	*GSDMB*	downstream-variant-500B
rs8076131	17	38080912	39924659	*ORMDL3*	intron-variant
rs7221814	17	38089717	39933464	*LRRC3C*	intron-variant

rs4580194	17	38126477	39970224	*GSDMA*	intron-variant
rs3907022	17	38134889	39978636	*PSMD3*	
rs2227333	17	38174167	40017914	*CSF3*	downstream-variant-500B
rs2302776	17	38178149	40021896	*MED24*	intron-variant
rs35946235	17	42007616	43930248	*LOC102724183*	intron-variant
rs3809863	17	45385012	47307646	*ITGB3*	intron-variant
rs12600603	17	45390951	47313585	*THCAT158*	intron-variant
rs9911944	17	45498937	47421571	*EFCAB13*	intron-variant
rs9895274	17	45539117	47461751	*MRPL45P2*	intron-variant
rs8077106	17	45653291	47575925	*NPEPPS*	intron-variant
rs11870935	17	45732605	47655239	*KPNB1*	intron-variant
rs56325564	17	45766771	47689405	*TBKBP1*	
rs9893629	17	45800177	47722811	*TBX21*	
rs62079153	17	76370896	78374815	*LOC101928674*	
rs2156499	18	47007234	49480864	*C18rf32*	downstream-variant-500B
rs1943676	18	47017820	49491450	*RPL17*	intron-variant
rs104223	18	47343351	49816981	*SNHG22*	intron-variant
rs74377788	19	8453203	8388319	*RAB11B-AS1*	intron-variant
rs10421495	19	8454523	8389639	*MIR4999*	upstream-variant-2KB
rs12976739	19	8461663	8396779	*RAB11B*	intron-variant
rs3815783	19	8503025	8438141	*MARCH2*	intron-variant
rs1812467	19	8546920	8482036	*HNRNPM*	intron-variant
rs1465700	19	10680621	10569945	*CDKN2D*	upstream-variant-2KB
rs1811376	19	10751080	10640404	*SLC44A2*	intron-variant
rs4425006	19	10813364	10702688	*QTRT1*	intron-variant
rs12978180	19	11041052	10930376	*TIMM29*	intron-variant
rs12611283	19	11055299	10944623	*YIPF2*	
rs73015007	19	11183837	11073161	*SMARCA4*	
rs4804573	19	11277232	11166556	*KANK2*	utr-variant-3-prime
rs72999033	19	19366632	19255823	*HAPLN4*	utr-variant-3-prime
rs58542926	19	19379549	19268740	*TM6SF2*	missense
rs56255430	19	19477877	19367068	*MAU2*	
rs7252888	19	19628037	19517228	*NDUFA13*	intron-variant
rs56397647	19	19642795	19531986	*YJEFN3*	intron-variant
rs17216588	19	19664077	19553268	*CILP2*	
rs17217098	19	19702384	19591575	*PBX4*	intron-variant
rs5167	19	45448465	44945208	*APOC2*	upstream-variant-2KB
rs35577563	19	45504349	45001091	*RELB*	upstream-variant-2KB
rs3178166	19	45594170	45090912	*GEMIN7*	utr-variant-3-prime
rs7255018	19	45603962	45100704	*PPP1R37*	intron-variant
rs12981729	19	45652193	45148935	*NKPD1*	
rs28469095	19	45655333	45152075	*LOC105372420*	upstream-variant-2KB
rs10402523	19	45687930	45184672	*BLOC1S3*	intron-variant
rs454715	19	49114236	48610979	*FAM83E*	intron-variant
rs112593985	19	49158532	48655275	*SEC1P*	intron-variant
rs12462111	19	49171306	48668049	*NTN5*	intron-variant
rs681343	19	49206462	48703205	*FUT2*	reference

rs35866622	19	49218060	48714803	*MAMSTR*	intron-variant
rs8112983	19	49229525	48726268	*RASIP1*	intron-variant
rs838145	19	49248730	48745473	*IZUMO1*	intron-variant
rs8103840	19	49254955	48751698	*FUT1*	intron-variant
rs3848561	19	52379623	51876370	*ZNF577*	intron-variant
rs377681	19	54766423	54262573	*LILRB5*	
rs398217	19	54793038	54289184	*LILRB2*	
rs367070	19	54800500	54296648	*LILRA3*	intron-variant
rs1645783	19	54827401	54316130	*LILRA5*	
rs12979085	19	54837165	54325893	*LILRA4*	
rs3746427	20	33730464	35142661	*EDEM2*	intron-variant
rs4911477	20	33780985	35193182	*PROCR*	intron-variant
rs6072263	20	39705546	41076906	*TOP1*	intron-variant
rs6029549	20	39754695	41126055	*PLCG1-AS1*	intron-variant
rs3795128	20	39774163	41145523	*PLCG1*	intron-variant
rs6016545	20	39958950	41330310	*LPIN3*	
rs4810315	20	40014674	41386034	*CHD6*	
rs79833227	20	44446643	45818004	*UBE2C*	
rs6073958	20	44551855	45923216	*PLTP*	
rs235314	21	46271452	44851537	*PTTG1IP*	missense
rs7445	22	21977047	21622758	*UBE2L3*	nc-transcript-variant
rs5754426	22	21980638	21626349	*YDJC*	
rs5754467	22	21985094	21630805	*CCDC116*	upstream-variant-2KB
rs5749600	22	21999292	21645003	*SDF2L1*	
rs4384	22	38572440	38176433	*PLA2G6*	intron-variant
rs4820323	22	38599767	38203760	*MAFF*	intron-variant

gnificant in the combined Stage 1 + 2 analyses (2
index variant is shown here.

GENCODE Gene	dbSNP func annot	RegulomeDB Score	eQTLs_Pval
TMEM50A	intronic	No Data	9E-8--1.2E-51
RHCE		6	7.5E-8--2E-49
TMEM57	intronic	No Data	7.2E-8--5.7E-50
16kb 3' of RP5-968P14.2		No Data	2.4E-8--1E-14
RP5-968P14.2		3a	7.1E-8--1.1E-14
610bp 5' of ARID1A		2a	5.8E-9--2.6E-9
PIGV	intronic	2b	9.3E-9--2.9E-15
1.2kb 5' of Metazoa_SRP		5	7.3E-9--2.8E-15
5.3kb 5' of RP1-50O24.6		No Data	6.6E-8--1.5E-14
GPN2	intronic	6	4.5E-8--4.1E-15
GPATCH3	intronic	4	8.2E-9--3E-14
NR0B2	missense	5	2.7E-8--9.9E-14
NUDC	intronic	6	7E-8--3.2E-12
5.6kb 5' of C1orf172		6	6.5E-8--8.5E-13
KIAA0754	3'-UTR	5	8.1E-8--2.4E-11
MACF1	intronic	5	5.1E-8--2.3E-15
BMP8A	intronic	5	9.5E-8--2E-14
RP11-69E11.4	intronic	4	4.4E-8--1.2E-14
PABPC4	intronic	5	7E-8--1.6E-14
18kb 5' of PABPC4		No Data	7.2E-8--2.1E-15
14kb 3' of HEYL		4	9.8E-8--1E-13
11kb 3' of BSND		5	1.9E-12--1.4E-22
3kb 5' of USP1		6	2.30E-08
USP1	intronic	4	1E-11--1.6E-16
DOCK7	intronic	No Data	8.4E-8--6.9E-21
DOCK7	intronic	6	1.1E-11--3.8E-19
5.1kb 5' of MTF2		No Data	2.6E-8--5.9E-33
TMED5	intronic	5	9.1E-8--5.9E-33
CCDC18	intronic	No Data	6.3E-8--2.7E-33
RP4-717I23.3	intronic	6	2.2E-8--5.9E-33
DR1	intronic	5	4.7E-8--5.9E-29
CELSR2	3'-UTR	2b	2E-12--6E-35
34bp 3' of PSRC1		6	7.8E-11--1.8E-28
GSTM4	intronic	1f	1.5E-10--4.1E-11
GSTM3	intronic	No Data	2.9E-8--2.1E-26
HLA-AS1		6	5.6E-8--7.9E-10
4.2kb 5' of RP4-781K5.7		5	1.70E-09
RP4-781K5.7		5	2.6E-10--1.5E-26
9kb 3' of RP4-781K5.8		6	1.1E-8--3.7E-16
22kb 5' of APOB		No Data	5.90E-08
27kb 5' of AC067959.1		No Data	5.90E-09

DPYSL5	intronic	4	2.20E-08
22kb 3' of TCF23		6	9.1E-8--4E-12
5.8kb 3' of SLC5A6		5	1.2E-8--6.4E-13
C2orf28	intronic	6	5E-9--6.3E-13
CAD	intronic	1f	9.6E-8--3.8E-13
SLC30A3	intronic	3a	3.7E-8--4.8E-13
DNAJC5G	intronic	6	7.9E-8--1.1E-12
TRIM54	intronic	5	4.6E-8--6.9E-13
351bp 5' of UCN		2b	1.80E-09
MPV17		5	9.3E-8--6.5E-32
GTF3C2	intronic	6	7.8E-8--7.9E-29
AC074117.10		6	7.8E-8--5.7E-26
AC074117.10		6	8.2E-8--2.7E-30
SNX17	intronic	No Data	3.9E-8--5E-15
PPM1G	intronic	6	9.9E-8--3.9E-41
2.9kb 5' of PPM1G		4	6.4E-8--2E-9
1.9kb 5' of NRBP1		6	8.6E-8--8.3E-32
NRBP1	intronic	5	8E-8--4.9E-40
IFT172	intronic	No Data	9.1E-8--3.8E-29
FNDC4	3'-UTR	5	8.2E-8--3.1E-37
GCKR	missense	5	3.7E-8--8.1E-16
AC109829.1		No Data	5.30E-08
ZNF512	intronic	No Data	3.20E-08
ZNF512	missense	2b	1.90E-08
ZNF512	intronic	No Data	4.60E-08
ABCG8	intronic	No Data	9.60E-08
DDX18	intronic	4	2.60E-10
12kb 3' of AC009404.2		5	1.90E-08
35kb 3' of CCDC93		No Data	5.90E-11
34kb 5' of INSIG2		5	4.00E-11
3.2kb 5' of INSIG2		5	6.80E-09
INSIG2	intronic	4	7.30E-09
66kb 5' of AC068138.1		5	8.00E-08
19kb 5' of TSEN2		5	1.7E-8--3.2E-17
TSEN2	intronic	6	2.5E-8--3.8E-28
MKRN2-AS1	intronic	5	3.2E-8--1.5E-34
MKRN2	intronic	6	8E-8--2.4E-13
RAF1	intronic	3a	8.7E-8--2E-15
26kb 3' of TMEM40		5	2.2E-9--2E-18
965bp 5' of MON1A		4	9.3E-8--3.1E-44
RBM6		5	9.1E-8--5E-40
RBM5	intronic	No Data	8.1E-8--8.1E-42
RP11-493K19.3	intronic	2b	6.4E-8--2.3E-38
1.8kb 3' of RP11-6F2.4		5	2.00E-09
TMEM175	missense	4	9.5E-8--2.4E-11
MSANTD1		5	2.50E-16
9.4kb 3' of RP11-529H2.1		No Data	1.2E-8--1.3E-13

9.1kb 3' of MIR5705		No Data	3.60E-12
HSD17B13	3'-UTR	4	3.10E-12
4.2kb 5' of GCNT4		5	7.90E-08
7.2kb 3' of ANKRD31		No Data	2.1E-8--2.5E-24
37kb 5' of ANKRD31		5	2.20E-11
HMGCR	3'-UTR	6	7.20E-08
COL4A3BP	intronic	4	3.5E-9--2.3E-12
POLK	intronic	No Data	5.8E-9--2.3E-12
ANKDD1B	intronic	No Data	5.3E-9--2.3E-12
POC5	intronic	4	1.20E-12
1.9kb 5' of POC5		6	1.80E-10
48bp 3' of HSPA4		5	6.10E-10
SLC17A1	intronic	No Data	5.7E-8--2E-21
SLC17A3	5'-UTR	6	5.6E-8--2E-21
SLC17A2	intronic	5	4.8E-8--1.5E-20
TRIM38	intronic	No Data	6.30E-08
14kb 3' of TRIM38		No Data	5.90E-08
1.8kb 3' of HIST1H1A		6	3.5E-8--1.6E-16
34bp 5' of HIST1H4A		4	4.8E-8--4.6E-21
960bp 3' of HIST1H4B		3a	5.90E-08
1.3kb 3' of HIST1H3B		1f	5.90E-08
3.8kb 5' of HIST1H2AB		No Data	5.2E-8--5.9E-21
774bp 5' of HIST1H3C		4	3.7E-8--4.3E-16
11kb 5' of HIST1H1C		6	4.4E-8--1.1E-16
4kb 5' of HFE		6	8.9E-8--1.5E-21
1.6kb 3' of HFE		6	7.6E-8--1.1E-8
1.8kb 5' of HIST1H1T		4	8.4E-8--4E-8
HIST1H2BC		4	8.9E-8--9.4E-9
HIST1H2AC		5	3.8E-8--1.8E-21
4.8kb 3' of HIST1H3G		No Data	6.7E-8--2.2E-28
1.3kb 3' of BTN3A3		5	7.3E-8--6E-55
5kb 5' of HLA-B		No Data	6E-8--6.1E-9
522bp 5' of MICB		2b	9.2E-8--1.5E-14
MICB	intronic	6	9.7E-8--1.4E-14
ATP6V1G2	intronic	4	9.5E-8--2.7E-15
LTA	missense	4	4E-8--3.9E-8
736bp 3' of TNF		4	7.8E-8--3.8E-18
ABHD16A	intronic	2b	2.40E-08
MSH5	intronic	6	3.90E-09
SAPCD1-AS1		No Data	8.30E-08
VWA7	intronic	2b	1.60E-08
VARS	intronic	5	3.30E-08
LSM2	intronic	No Data	4.20E-08
6.7kb 3' of NEU1		5	6.90E-08
SLC44A4	intronic	6	9.8E-8--6.4E-17
188bp 5' of SLC44A4		1f	4.1E-8--4.2E-14
339bp 3' of EHMT2		5	3.7E-8--4.2E-14

STK19	intronic	1f	8.7E-8--8.7E-17
TNXB	intronic	1f	7.4E-8--3.9E-15
C6orf106	intronic	6	9.1E-8--8.8E-9
16kb 5' of SNRPC		3a	7.9E-8--1.1E-10
UHRF1BP1	intronic	6	9.6E-8--5.3E-9
6.3kb 5' of GNMT		2b	9.7E-8--1.2E-90
PEX6	intronic	6	2.3E-8--2.1E-92
GSTA2	intronic	6	1E-8--4.5E-13
7.7kb 5' of FRK		6	1.1E-8--3.7E-20
IGF2R	intronic	5	6.60E-09
RAC1	intronic	5	5.3E-8--5E-42
DAGLB	intronic	No Data	7.5E-8--2.7E-42
DNAH11	intronic	No Data	9.3E-9--2.7E-12
3.6kb 5' of NPC1L1		1f	1.60E-08
DDX56	intronic	1d	4.10E-08
8.5kb 3' of Y_RNA		No Data	3.40E-08
FZD9	3'-UTR	4	7.8E-8--5.3E-12
BAZ1B	intronic	5	4.7E-9--9E-19
4.9kb 5' of BCL7B		4	1.7E-10--3.3E-20
6kb 5' of TBL2		No Data	6.3E-10--2.6E-17
MLXIPL	intronic	5	1.4E-8--7.8E-22
DNAJC30	3'-UTR	5	9.80E-08
14kb 3' of CD36		No Data	2.4E-11--2.3E-15
AGPAT5	intronic	2b	5.40E-08
CTA-398F10.1		5	6.5E-8--1E-21
GATA4	intronic	5	8E-8--2.1E-12
830bp 3' of C8orf49		1f	6E-8--3E-19
NEIL2	intronic	5	7.9E-8--1.9E-15
FDFT1		5	7.2E-8--6.8E-17
CTSB	intronic	4	5.8E-8--6.6E-9
15kb 5' of GPIHBP1		5	3E-8--1.2E-11
1.7kb 3' of GPIHBP1		4	8.3E-8--4.9E-12
TTC39B	intronic	No Data	7.1E-8--6.1E-17
30kb 3' of RP11-217B7.2		5	7.00E-08
ZER1	intronic	5	2.9E-8--2.2E-24
6.2kb 5' of OBP2B		5	3.20E-11
1kb 3' of ABO		5	8.9E-8--1.5E-19
4.2kb 5' of ABO		5	2.6E-8--9.1E-19
6.8kb 3' of Y_RNA		5	4.3E-9--1.9E-10
MED22	intronic	4	8.8E-8--2.2E-11
SURF4	intronic	2b	8.3E-8--2.6E-13
C9orf96	intronic	4	7E-8--1.1E-12
1.4kb 3' of RP11-144G16.1		6	6E-8--1.2E-9
NRBF2	3'-UTR	No Data	5.8E-8--2.3E-11
JMJD1C	intronic	6	7.6E-9--2.4E-11
REEP3	intronic	6	6E-8--3.3E-11
REEP3	intronic	6	2.2E-8--3.2E-9

10kb 3' of REEP3		5	6E-8--2.3E-11
12kb 5' of GPAM		2a	9.60E-09
8.1kb 5' of FAM24A		6	1.8E-9--2.3E-12
7.8kb 3' of FAM24A		6	1.3E-9--2.3E-11
C10orf88	intronic	No Data	6.3E-11--4.9E-14
SPTY2D1	intronic	6	1.6E-8--1.7E-22
C11orf49	intronic	4	5.9E-9--1.2E-9
C11orf49	intronic	5	4.2E-8--8E-10
5.1kb 5' of PACSIN3		1f	8.2E-8--1.5E-26
DDB2	intronic	6	4.4E-8--1.4E-17
ACP2	missense	4	6.1E-8--9.7E-18
NR1H3	intronic	4	5.7E-8--1.4E-16
MADD	intronic	1f	8.1E-9--3.4E-17
MADD	synonymous	4	9.1E-8--2.7E-18
MYBPC3	intronic	1f	1.3E-9--7E-13
SPI1	intronic	2b	8E-8--3.6E-26
RP11-750H9.5		4	6.60E-10
RP11-750H9.5		5	2.40E-10
4.3kb 5' of PSMC3		4	8.3E-8--2.1E-8
4.5kb 5' of RAPSN		2b	5.4E-8--1E-31
CELF1		5	6.2E-8--4.6E-32
PTPMT1	intronic	6	8E-8--9.8E-32
NDUFS3	intronic	No Data	3.50E-08
NDUFS3	intronic	6	8.3E-8--1.8E-32
368bp 3' of NDUFS3		No Data	6.4E-8--6.9E-32
5.9kb 5' of C1QTNF4		6	6.2E-8--4.4E-32
8.5kb 5' of C1QTNF4		1f	5.8E-8--4.1E-32
AGBL2	intronic	6	8.7E-8--3.6E-31
FNBP4	intronic	6	5.9E-8--1.3E-28
20kb 5' of NUP160		No Data	9.5E-8--4.2E-28
55kb 5' of PTPRJ		No Data	9.5E-8--1.7E-16
41kb 3' of OR4A47		6	3.00E-08
6.6kb 3' of TRIM49B		6	4.00E-09
16kb 5' of TRIM64C		No Data	5.60E-09
25kb 5' of FOLH1		5	6.10E-08
264kb 5' of FOLH1		6	4.50E-08
C11orf9	intronic	5	2.9E-8--3.5E-29
C11orf10	intronic	No Data	9.3E-8--4.5E-29
FEN1	3'-UTR	1f	3.2E-8--1.6E-25
FADS1	intronic	No Data	8.9E-8--2E-29
FADS1		6	6.8E-9--2.1E-27
611bp 3' of FADS3		1f	7.4E-8--4.5E-13
RAB3IL1	intronic	5	2.1E-8--1.4E-10
FLRT1	intronic	5	4.50E-11
MACROD1	intronic	5	7.3E-10--2.4E-18
VEGFB	intronic	5	4.3E-10--4.9E-20
PLCB3	missense	4	4.4E-8--1.6E-17

3.4kb 5' of AP003774.1		No Data	1.30E-08
5.5kb 3' of Metazoa_SRP		No Data	3.90E-09
CTD-2530H12.1	intronic	6	3.30E-08
4.2kb 3' of AP000770.1		6	8.3E-9--1.3E-9
ZNF259	intronic	5	3.40E-08
2.4kb 3' of AP006216.5		No Data	5.1E-8--3.5E-16
APOC3	intronic	No Data	2.4E-8--1.5E-13
898bp 3' of APOA1		1f	2.5E-8--3.5E-13
APOA1	intronic	3a	2.4E-8--2E-15
SIK3	intronic	6	3.3E-8--8.7E-15
PAFAH1B2	intronic	3a	6E-8--1.8E-15
SIDT2	intronic	6	9.3E-8--5.5E-20
TAGLN	intronic	5	3.4E-8--7E-21
PCSK7	intronic	4	9.6E-8--2.7E-21
11kb 3' of RPUSD4		1f	7.8E-9--1.6E-29
RPUSD4	intronic	6	2.3E-8--1.3E-22
4.2kb 5' of ST3GAL4	intronic	2b	6E-9--3.2E-10
ST3GAL4	intronic	No Data	5.1E-10--2.3E-11
MYO1H	intronic	5	4.1E-8--1.7E-22
KCTD10	intronic	6	2.3E-8--7.3E-22
UBE3B	intronic	1f	1.8E-8--6.8E-22
MMAB	intronic	5	2.6E-8--5.9E-22
MVK	intronic	No Data	3.8E-8--5.9E-22
SH2B3	intronic	No Data	5.80E-08
SH2B3	intronic	5	1.2E-8--1.4E-9
ATXN2	intronic	5	1.80E-08
BRAP	intronic	3a	9.4E-9--1.5E-14
ACAD10	intronic	5	8.3E-8--7.3E-15
712bp 5' of RP3-462E2.3		No Data	6.2E-8--7.2E-13
MAPKAPK5	intronic	5	7.4E-8--1.8E-13
4.2kb 3' of MAPKAPK5		1f	7.4E-8--1.8E-13
17kb 3' of TMEM116		No Data	7.3E-8--1.8E-13
NAA25	intronic	6	4E-8--1.8E-13
32kb 3' of HNF1A-AS1		6	6.4E-8--4.4E-15
7.8kb 3' of HNF1A-AS1		3a	5.40E-08
C12orf43	intronic	2b	6.30E-08
RP11-324E6.6		6	1.2E-9--2.6E-17
RP11-324E6.6		4	2.7E-9--5.7E-17
RP11-324E6.6		5	2.6E-8--5.7E-23
HCAR1		6	6.6E-8--1.7E-22
3.2kb 3' of RN5S375		6	8.2E-10--2.2E-23
SBNO1	intronic	No Data	1.30E-19
7.8kb 5' of SETD8		6	8.8E-10--2.2E-23
DNAH10OS	intronic	4	9E-8--1.5E-18
CCDC92	intronic	5	7.5E-8--2.5E-18
ZNF664	intronic	5	5.2E-8--4.1E-17
RP11-522N14.1	intronic	4	8.20E-08

NYNRIN	intronic	6	4.60E-10
TGM7	intronic	5	4.9E-8--2.8E-8
7kb 3' of LCMT2		No Data	8.6E-8--8.9E-41
ZSCAN29	intronic	6	7.4E-8--3.4E-46
MAP1A	missense	5	9.8E-8--2.3E-11
PPIP5K1	intronic	No Data	9.6E-8--2.4E-27
CKMT1B	intronic	No Data	6.9E-8--1.6E-25
AC011330.12	intronic	6	3.2E-8--6.7E-24
CKMT1A	intronic	No Data	5.4E-8--2.5E-17
PDIA3	intronic	5	9.4E-8--5.6E-15
ELL3	3'-UTR	1f	8.6E-8--2.2E-19
RP11-296A16.1	intronic	No Data	8.8E-8--2E-19
RP11-296A16.1	intronic	1d	8.9E-8--2E-17
MFAP1	intronic	5	6.2E-8--3E-21
WDR76	intronic	1f	7.8E-8--1.4E-20
8.2kb 3' of TPM1		1b	7.1E-9--4.1E-9
RP11-69G7.1		6	6.5E-8--3.9E-9
2.4kb 3' of MT1A		5	1.80E-09
RSPRY1	intronic	6	7.90E-08
1.4kb 5' of Metazoa_SRP		2b	4.3E-8--1.6E-9
CBFB	intronic	6	4.9E-8--1.8E-9
C16orf70	intronic	5	1.9E-8--9.4E-12
NOL3	5'-UTR	4	3.1E-8--1E-12
KIAA0895L	intronic	4	5.7E-9--1.7E-10
EXOC3L1	missense	4	5.5E-8--2.6E-12
E2F4	3'-UTR	4	5.3E-9--6.1E-12
ELMO3	intronic	4	5.1E-9--6.7E-12
LRRC29	3'-UTR	1d	6.2E-9--2.1E-12
LRRC29	intronic	3a	5.7E-9--5.4E-11
FHOD1	synonymous	4	4.1E-8--1.3E-12
SLC9A5	intronic	6	3.90E-09
PLEKHG4	missense	5	2.3E-8--1.7E-10
KCTD19	intronic	6	9.8E-8--1.5E-10
ZDHHC1	intronic	6	1.1E-8--1E-11
HSD11B2	intronic	4	1.2E-8--1.3E-12
ATP6V0D1	intronic	4	7.3E-8--3.6E-12
2.4kb 5' of AGRP		6	3.5E-8--2.8E-12
1.2kb 3' of FAM65A		4	6.3E-8--1.4E-8
3.9kb 3' of CTD-2012K14.7		No Data	7.3E-8--2.2E-8
CTCF	intronic	No Data	1.9E-9--5.7E-11
RLTPR	intronic	5	3.2E-8--3E-11
ACD	intronic	5	5.9E-9--7E-11
C16orf48	intronic	4	1.9E-8--5E-11
GFOD2	intronic	4	8.5E-10--1.1E-11
RANBP10	intronic	6	5.1E-8--1.9E-10
TSNAXIP1	intronic	1f	5.2E-8--1.9E-10
CENPT	intronic	6	9.5E-8--7.1E-11

NUTF2	intronic	1f	8.9E-8--2.5E-10
EDC4	intronic	5	9.2E-8--2.6E-10
CTC-479C5.10	missense	5	8.8E-8--3E-10
PSKH1	intronic	6	9.3E-8--1.7E-11
CTRL	missense	2b	9.4E-8--1.4E-10
PSMB10	missense	4	5.2E-8--4.8E-11
LCAT	3'-UTR	4	6.8E-8--1.7E-10
SLC12A4	intronic	1f	9E-8--1.6E-12
1.5kb 5' of DPEP3		5	9.1E-8--1.4E-10
DPEP2	intronic	1f	2.1E-8--4.7E-11
DUS2L		No Data	7.3E-8--1E-11
DUS2L	intronic	5	9.5E-8--5.4E-11
DUS2L	intronic	6	6.7E-8--1.1E-12
NFATC3	intronic	6	9.4E-9--1E-13
ESRP2	intronic	4	5.7E-8--1.2E-12
1.3kb 5' of PLA2G15		6	8.4E-8--1.1E-14
504bp 5' of SLC7A6		4	3.8E-8--3.4E-16
SLC7A6OS	intronic	6	4.2E-8--2E-21
PRMT7	intronic	3a	4.7E-8--1.6E-20
SMPD3	intronic	1f	3.9E-8--8.3E-21
1.6kb 5' of ATXN1L		5	4.7E-8--5.9E-13
RP11-498D10.4	intronic	6	2.1E-8--8.4E-13
IST1	intronic	6	7.6E-9--2E-10
DHODH	intronic	5	8.7E-8--6.1E-15
2.6kb 3' of TXNL4B		6	4.8E-8--4.2E-21
TXNL4B	intronic	4	2.10E-09
TXNL4B	intronic	6	2.2E-8--3.9E-21
DHX38	intronic	No Data	3.8E-8--6.1E-19
8.9kb 3' of RP11-690G19.3		No Data	2.7E-8--1.8E-8
FBXL20	intronic	6	3.60E-11
MED1	intronic	6	9.3E-8--1.4E-11
CDK12	intronic	6	7.2E-8--6.3E-9
16kb 3' of CDK12		4	2.90E-08
13kb 3' of NEUROD2		6	8.2E-8--3E-10
4.5kb 5' of NEUROD2		No Data	5.5E-8--5.9E-13
PPP1R1B	intronic	2b	6.2E-8--3.1E-12
STARD3	intronic	2b	9.5E-8--9.7E-15
TCAP		2b	9.5E-8--2.4E-15
PNMT		2b	8.9E-8--1.3E-12
PGAP3	intronic	4	7.7E-8--5.7E-15
ERBB2	intronic	5	3.9E-8--1.1E-17
695bp 5' of GRB7		5	5.2E-8--6.4E-12
IKZF3	intronic	No Data	5.6E-8--7.9E-22
8.6kb 3' of ZPBP2		No Data	9.3E-8--2E-26
GSDMB	intronic	6	6.9E-8--5E-25
ORMDL3	intronic	1d	3.5E-8--1.1E-29
RP11-387H17.4		6	7.6E-8--1.5E-23

GSDMA	intronic	5	8.4E-8--1.4E-39
869bp 3' of GSDMA		No Data	3.4E-8--4.3E-51
100bp 3' of CSF3		4	4.3E-8--6.9E-18
MED24	intronic	4	5.4E-8--3.1E-12
8.1kb 5' of RP11-527L4.2		6	6.60E-10
RP11-290H9.4	intronic	1f	7.3E-8--5.8E-20
RP11-290H9.4		6	3.9E-8--6.2E-20
CTD-2026D20.2	intronic	6	6E-8--1.2E-25
20kb 3' of C17orf57	intronic	No Data	9.6E-8--1.5E-24
NPEPPS	intronic	6	8.1E-8--5.1E-23
KPNB1	intronic	2b	4.2E-8--1.6E-23
3.9kb 3' of KPNB1		No Data	7.9E-8--9.3E-20
10kb 5' of TBX21		No Data	4.2E-8--6.9E-17
3.7kb 5' of Metazoa_SRP		2b	2.50E-08
793bp 3' of C18orf32		No Data	1.00E-08
RP11-110H1.2	intronic	4	6.80E-13
2.5kb 3' of SCARNA18		6	4.60E-10
970bp 3' of MIR4999	intronic	2b	4.50E-10
258bp 5' of MIR4999	intronic	5	1.1E-8--6.3E-9
RAB11B	intronic	2b	5.9E-8--4.6E-13
02-Mar	intronic	5	7.9E-8--9.4E-14
HNRNPM	intronic	5	7.7E-9--3.9E-13
965bp 5' of CDKN2D		6	2.90E-09
SLC44A2	intronic	5	1.60E-08
QTRT1	intronic	5	2.20E-09
137bp 3' of C19orf52		No Data	4.90E-10
14kb 3' of C19orf52		6	3.70E-12
11kb 3' of SMARCA4		No Data	1.40E-08
KANK2	3'-UTR	5	2.50E-08
HAPLN4	3'-UTR	5	8.00E-08
TM6SF2	missense	5	4.20E-08
8.3kb 3' of MAU2		4	1.10E-08
NDUFA13	intronic	1f	7.2E-8--1.3E-8
NDUFA13	intronic	5	4.70E-11
6.6kb 3' of CILP2		5	1.30E-08
PBX4	intronic	2b	7.90E-08
APOC4	missense	5	4.6E-8--1.5E-10
345bp 5' of RELB		4	9.9E-10--1.7E-12
GEMIN7	3'-UTR	4	2.8E-8--6.8E-30
PPP1R37	intronic	5	4.5E-11--7.7E-17
814bp 3' of NKPD1		6	6.7E-8--4E-19
NKPD1	missense	3a	7.40E-08
2.9kb 3' of BLOC1S3		No Data	1.30E-08
FAM83E	intronic	2b	1.8E-10--4.9E-17
6.1kb 3' of NTN5	intronic	6	9.1E-8--1.4E-17
NTN5	intronic	5	5.1E-8--1.1E-25
FUT2	synonymous	5	4.4E-8--3.4E-74

MAMSTR	intronic	4	7.6E-8--5.9E-51
RASIP1	intronic	No Data	7.4E-8--3.8E-39
IZUMO1	intronic	3a	9.7E-8--1.5E-38
FUT1	intronic	No Data	3.2E-8--6E-26
ZNF577	intronic	5	9.7E-8--4.2E-12
1.4kb 3' of U6		3a	2.5E-9--2.1E-17
6.8kb 3' of LILRA3		5	9.1E-8--1.6E-30
LILRA3	intronic	6	4.2E-8--7.9E-45
AC008984.2		5	2E-9--4.4E-12
AC008984.2		2b	4.9E-8--1.7E-11
EDEM2	intronic	6	3.9E-8--3.4E-14
EDEM2		5	2.6E-8--2E-17
TOP1	intronic	5	2.10E-09
RP1-1J6.2	intronic	5	2.80E-09
PLCG1	intronic	5	3.10E-09
11kb 5' of LPIN3		4	1.00E-09
16kb 3' of CHD6		6	2.30E-08
1kb 3' of UBE2C		4	4.9E-9--1.5E-9
11kb 5' of PLTP		6	8.10E-09
PTTG1IP	3'-UTR	4	2.00E-12
UBE2L3	3'-UTR	2b	7.8E-8--9.4E-22
1.7kb 3' of YDJC		2b	7.1E-8--4.7E-19
740bp 5' of YDJC		5	7.7E-8--2.3E-16
704bp 3' of SDF2L1		No Data	2.50E-13
PLA2G6	intronic	2b	6.1E-8--3.5E-10
MAFF	intronic	4	5.1E-8--3.5E-10

eQTLs
RHCE;RHD;RP3-465N24.5;SDHDP6;TMEM50A;TMEM57
RHCE;RHD;RP3-465N24.5;SDHDP6;TMEM50A;TMEM57
RHCE;RHD;RP3-465N24.5;SDHDP6;TMEM50A;TMEM57
PIGV;RP5-968P14.2;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
PIGV
PIGV;RP5-968P14.2;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
PIGV;ZDHHC18
PIGV;RP5-968P14.2;ZDHHC18
OXCT2P1;PABPC4
OXCT2P1;PABPC4;RP11-69E11.4
OXCT2P1;PABPC4;RP11-69E11.4
OXCT2P1;PABPC4;RP11-69E11.4
OXCT2P1;PABPC4;RP11-69E11.4
OXCT2P1;PABPC4;RP11-69E11.4
OXCT2P1;PABPC4;RP11-69E11.4
BSND;PCSK9
DOCK7
DOCK7
DOCK7
DOCK7
CCDC18;DR1;RP4-717I23.3;TMED5
CCDC18;DR1;RP4-717I23.3;TMED5
CCDC18;DR1;RP4-717I23.3;TMED5
CCDC18;DR1;RP4-717I23.3;TMED5
CCDC18;DR1;RP4-717I23.3;TMED5
CELSR2;PSRC1;SORT1
CELSR2;PSRC1;SORT1
SYPL2
GSTM3;GSTM5
RP11-295M18.2;RP11-295M18.6
RP4-781K5.7
RP4-781K5.7
RP4-781K5.7
APOB
APOB

KHK
ATRAID;CAD
ATRAID
ATRAID
ATRAID;SNX17
ATRAID;SNX17
AC074117.10;ATRAID;NRBP1;SNX17
AC074117.10;ATRAID;NRBP1;SNX17
GTF3C2
AC074117.10;FNDC4;NRBP1;SNX17
AC074117.10;NRBP1;SNX17
AC074117.10;NRBP1;SNX17
AC074117.10;NRBP1;SNX17
AC074117.10;FNDC4;SNX17
AC074117.10;KRTCAP3;NRBP1;SNX17
AC074117.10
AC074117.10;NRBP1;SNX17
AC074117.10;KRTCAP3;NRBP1;SNX17
AC074117.10;NRBP1;SNX17
AC074117.10;KRTCAP3;NRBP1;PPM1G;SNX17
AC074117.10;FNDC4;NRBP1;SNX17
GPN1
GPN1
GPN1
GPN1
ABCG8
HTR5BP
HTR5BP
HTR5BP
HTR5BP
HTR5BP
HTR5BP
IRS1
MKRN2
MKRN2
MKRN2
MKRN2
MKRN2
MKRN2
ACTBP13;FAM212A;MST1R;RBM6;RNF123;UBA7
ACTBP13;FAM212A;MST1R;RBM6;RNF123;UBA7
ACTBP13;FAM212A;MST1R;RBM6;RNF123;UBA7
ACTBP13;FAM212A;MST1R;RBM6;RNF123;UBA7
LINC00886
DGKQ
MSANTD1
HSD17B13

HSD17B13
HSD17B13
GCNT4
GCNT4;RP11-229C3.2
GCNT4
ANKDD1B
ANKDD1B;GCNT4
ANKDD1B;GCNT4
ANKDD1B;GCNT4
ANKDD1B
ANKDD1B
HSPA4
BTN3A2;TRIM38
BTN3A2;TRIM38
BTN3A2
BTN3A2
BTN3A2
BTN3A2
BTN3A2;TRIM38
BTN3A2
BTN3A2
BTN3A2;TRIM38
BTN3A2
BTN3A2
BTN3A2
BTN3A2
BTN3A2
BTN3A2
BTN3A2
BTN3A2
BTN3A2
C4A;C4B;HLA-B
C4A;C4B;CCHCR1;CYP21A1P;CYP21A2;HLA-C;MICB;PSORS1C1;STK19P
C4A;C4B;CCHCR1;CYP21A1P;CYP21A2;HLA-C;MICB;PSORS1C1;STK19P
C4A;C4B;CCHCR1;CYP21A1P;CYP21A2;HLA-C;MICB;PSORS1C1;STK19P
XXbac-BPG181B23.7
C4A;C4B;CCHCR1;CYP21A1P;CYP21A2;HLA-C;LINC00243;LY6G6C;MICB;PSORS1C1;STK19P;WASF5P;XXbac-BPG248L24
VWA7
VWA7
VWA7
VWA7
VWA7
VWA7
VWA7
CYP21A1P;HLA-C;HLA-DQA2;HLA-DRB1;HLA-DRB6;LY6G5B;PRRT1;XXbac-BPG299F13.17
CYP21A1P;CYP21A2;HLA-C;HLA-DRB6;PRRT1;SKIV2L;XXbac-BPG299F13.17
CYP21A1P;CYP21A2;HLA-C;HLA-DRB6;PRRT1;SKIV2L;XXbac-BPG299F13.17

CYP21A1P;CYP21A2;HLA-C;HLA-DQA2;HLA-DQB1;HLA-DRB1;HLA-DRB6;SKIV2L
C4A;C4B;CYP21A1P;HLA-C;HLA-DMA;HLA-DRB6;LY6G6C;MICB;PSORS1C1
C6orf106;UHRF1BP1
C6orf106;UHRF1BP1
C6orf106;UHRF1BP1
CNPY3;GNMT;PEX6;RP3-475N16.1
CNPY3;GNMT;PEX6;RP3-475N16.1
GSTA1;GSTA2
FRK;NT5DC1
IGF2R
DAGLB;RAC1
DAGLB;RAC1
DNAH11
NUDCD3
DDX56
MLXIPL
MLXIPL
MLXIPL
MLXIPL
MLXIPL
MLXIPL
DNAJC30
CD36
AGPAT5
ALG1L13P;CTA-398F10.2;ENPP7P1;ERI1;FAM85B;FAM86B3P;SGK223
AF131215.2;AF131215.9;FDFT1;NEIL2;RP11-148O21.3;RP11-148O21.4;RP11-148O21.6
AF131215.9;NEIL2
AF131215.2;AF131215.9;FDFT1;NEIL2
AF131215.9;FDFT1;NEIL2
AF131215.9;CTSB
GPIHBP1
GPIHBP1
TTC39B
RP11-217B7.2
PKN3
RP11-430N14.4
ABO;RP11-430N14.4
ABO;RP11-430N14.4
SURF1
RP11-430N14.4;SURF1
SURF1
SURF1
NRBF2
MRPL35P2;NRBF2
NRBF2
MRPL35P2;NRBF2
MRPL35P2;NRBF2

MRPL35P2
GPAM
C10orf88
C10orf88
C10orf88
SPTY2D1
LRP4
LRP4
C11orf49;C1QTNF4;CTD-2384B9.1;LRP4;LRP4-AS1
ACP2;LRP4;PACSIN3
ACP2;LRP4;PACSIN3
ACP2;PACSIN3
ACP2;PACSIN3
ACP2;PACSIN3
ACP2
C1QTNF4;MTCH2;MYBPC3
FNBP4
FNBP4
C1QTNF4;PSMC3;RAPSN
C1QTNF4;MTCH2;MYBPC3
C1QTNF4;MTCH2;MYBPC3
C1QTNF4;MTCH2
FNBP4
C1QTNF4;FNBP4;MTCH2;MYBPC3
C1QTNF4;MTCH2;MYBPC3
C1QTNF4;MTCH2;MYBPC3
C1QTNF4;MTCH2;MYBPC3
C1QTNF4;MTCH2;MYBPC3
C1QTNF4;MTCH2
C1QTNF4;MTCH2;MYBPC3
C1QTNF4
FOLH1
FOLH1
FOLH1
FOLH1
FOLH1
FADS1;FADS2
FADS1;FADS2
FADS1;FADS2
FADS1;FADS2
FADS1;FADS2
FADS1;FADS2
FADS2
VEGFB
VEGFB
VEGFB
VEGFB

VEGFB
DGAT2
DGAT2
RP11-109L13.1
RP11-109L13.1
AP006216.5;RP11-109L13.1;SIDT2;TAGLN
RP11-109L13.1
RP11-109L13.1
RP11-109L13.1
RP11-109L13.1
RP11-109L13.1;SIDT2;TAGLN
RP11-109L13.1;SIDT2;TAGLN
RP11-109L13.1;SIDT2;TAGLN
RP11-109L13.1;SIDT2;TAGLN
FAM118B;FOXRED1
FAM118B;FOXRED1
ST3GAL4
ST3GAL4
FOXN4;KCTD10;MYO1H
FOXN4;KCTD10;MVK;MYO1H
FOXN4;KCTD10;MVK;MYO1H
FOXN4;KCTD10;MVK;MYO1H
FOXN4;KCTD10;MVK;MYO1H
ALDH2
ALDH2
ALDH2
ALDH2;TMEM116
ALDH2;TMEM116
AC003029.1;ALDH2;TMEM116
AC003029.1;ALDH2;TMEM116
AC003029.1;ALDH2;TMEM116
AC003029.1;ALDH2;TMEM116
AC003029.1;ALDH2;TMEM116
ACADS;SPPL3
C12orf43
C12orf43
HCAR2;HCAR3
HCAR2;HCAR3
HCAR2;HCAR3
HCAR2;HCAR3
C12orf65;CDK2AP1
CDK2AP1
C12orf65;CDK2AP1
CCDC92;DNAH10OS;RP11-380L11.4;ZNF664
CCDC92;DNAH10OS;RP11-380L11.4;ZNF664
CCDC92;DNAH10OS;RP11-380L11.4;ZNF664
CCDC92

NYNRIN
ADAL
ADAL;CATSPER2;CKMT1A;TP53BP1
AC011330.5;ADAL;CATSPER2;CKMT1A;TP53BP1;TUBGCP4
ADAL
AC011330.5;ADAL;CATSPER2;CKMT1A;TP53BP1;TUBGCP4
AC011330.5;ADAL;CATSPER2;CKMT1A;TP53BP1;TUBGCP4
AC011330.5;ADAL;CATSPER2;CKMT1A;STRCP1;TP53BP1
AC011330.5;ADAL;CATSPER2;CKMT1A;TP53BP1
AC011330.5;ADAL;LCMT2
AC011330.5;ADAL;CATSPER2;CKMT1A;STRCP1
AC011330.5;ADAL;CATSPER2;CKMT1A;STRCP1
AC011330.5;ADAL;CATSPER2;CKMT1A;STRCP1;TP53BP1
AC011330.5;ADAL;CATSPER2;CKMT1A;STRCP1
AC011330.5;ADAL;CATSPER2;CKMT1A;STRCP1
TPM1
LACTB;TPM1
MT1L
PLLP
ATP6V0D1;ELMO3;KIAA0895L
ATP6V0D1;ELMO3;KIAA0895L
ATP6V0D1;ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L
ELMO3;KIAA0895L;LRRC29
ELMO3
AC009061.1;ELMO3;HSD11B2;LRRC36
AC009061.1;ATP6V0D1;ELMO3;HSD11B2;LRRC36
AC009061.1;HSD11B2;LRRC36;RANBP10
AC009061.1;HSD11B2;LRRC36;RANBP10
AC009061.1;ATP6V0D1;HSD11B2;LRRC36
AC009061.1;ATP6V0D1;HSD11B2;LRRC36
ELMO3;PRMT7;RANBP10
ATP6V0D1;PRMT7
ATP6V0D1;ELMO3
GFOD2;PRMT7;TSNAXIP1
GFOD2;PRMT7
DUS2;GFOD2;LCAT;PARD6A;PRMT7
GFOD2;PRMT7
GFOD2;PRMT7;TSNAXIP1
GFOD2;PRMT7;TSNAXIP1
GFOD2;PRMT7

GFOD2;PRMT7;TSNAXIP1
GFOD2;PRMT7
PRMT7
CTRL;LCAT;PRMT7
CTRL;DUS2;LCAT;PARD6A;PRMT7
CTRL;DUS2;GFOD2;LCAT;PRMT7
CTRL;DUS2;GFOD2;LCAT;PARD6A;PRMT7;TSNAXIP1
CTRL;LCAT;PRMT7
PRMT7
PRMT7
CTRL;PRMT7
CTRL;LCAT;PRMT7
CTRL;PRMT7
PRMT7
LCAT;PRMT7
CTRL;PRMT7
PRMT7
PRMT7
PRMT7
PRMT7
MARVELD3;TAT
MARVELD3;TAT
MARVELD3;TAT
HP;HPR
HP;HPR
HP
HP;HPR
HP;HPR
AC087491.2;PGAP3
PGAP3
PGAP3
AC087491.2;PGAP3
AC087491.2
PGAP3
PGAP3
PGAP3;PPP1R1B
PGAP3;PNMT;PPP1R1B
PGAP3;PNMT;PPP1R1B
PGAP3;PNMT;PPP1R1B
PGAP3
PGAP3
PGAP3
GSDMA;GSDMB;ORMDL3;PGAP3;ZPBP2
GSDMA;GSDMB;ORMDL3;PGAP3;RP11-387H17.4
GSDMB;ORMDL3;PGAP3;RP11-387H17.4
GSDMA;GSDMB;ORMDL3;ZPBP2
GSDMA;GSDMB;ORMDL3;ZPBP2

GSDMA;GSDMB;MED24;ORMDL3
GSDMA;GSDMB;MED24;ORMDL3
GSDMA;MED24
GSDMA;MED24
MPP2
EFCAB13;MRPL45P2;RP11-290H9.4;TBKBP1
EFCAB13;MRPL45P2;RP11-290H9.4;TBKBP1
EFCAB13;MRPL45P2;RP11-290H9.4;TBKBP1
EFCAB13;MRPL45P2;RP11-290H9.4;TBKBP1
EFCAB13;MRPL45P2;RP11-290H9.4;TBKBP1
EFCAB13;MRPL45P2;RP11-290H9.4;TBKBP1
EFCAB13;MRPL45P2;TBKBP1
MRPL45P2;TBKBP1
PGS1
C18orf32
C18orf32
ACAA2
02-Mar
2-Mar;ANGPTL4
02-Mar
02-Mar
02-Mar
SLC44A2
SLC44A2
SLC44A2
SMARCA4
SMARCA4
SMARCA4
SPC24
GATAD2A
GATAD2A
GATAD2A
GATAD2A;MAU2
GATAD2A
GATAD2A
GATAD2A
APOC2;APOE
APOC2
GEMIN7
GEMIN7
GEMIN7
NKPD1
GEMIN7
FUT2;RASIP1
FUT2;NTN5;RASIP1
FUT2;MAMSTR;RASIP1;SEC1P
FUT2;IZUMO1;MAMSTR;NTN5;RASIP1

FAM83E;FUT2;MAMSTR;NTN5;RASIP1;SEC1P
FUT2;IZUMO1;MAMSTR;NTN5;RASIP1;SEC1P
FUT2;IZUMO1;MAMSTR;NTN5;RASIP1
FUT2;IZUMO1;MAMSTR;NTN5;RASIP1
ZNF577
LILRA3;LILRB2
LILRA3
LILRA3;LILRB2
LILRA3
LILRA3
MAP1LC3A;NCOA6;PIGU;RP4-614O4.12
MAP1LC3A;PIGU;RP4-614O4.12
LPIN3
LPIN3
LPIN3
LPIN3
EMILIN3
SNX21;WFDC3
PLTP
PTTG1IP
CCDC116;UBE2L3
CCDC116;UBE2L3
CCDC116
CCDC116
BAIAP2L2;PLA2G6;TMEM184B
BAIAP2L2;MAFF;TMEM184B

eQTLs_tissue
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Ovary;Pancreas;Pituitary;Skin
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Ovary;Pancreas;Pituitary;Skin
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;S
Adipose;Colon;Esophagus;Skin;Thyroid;blood
Adipose;Breast;Colon;Esophagus;Skin;Stomach;Thyroid;blood
Esophagus;Skin
Adipose;Colon;Esophagus;Skin;Thyroid;blood
Adipose;Colon;Esophagus;Skin;Thyroid;blood
Adipose;Breast;Colon;Esophagus;Skin;Stomach;Thyroid;blood
Adipose;Breast;Colon;Esophagus;Skin;Stomach;Thyroid;blood
Adipose;Breast;Colon;Esophagus;Stomach;Thyroid;blood
Adipose;Breast;Colon;Esophagus;Stomach;Thyroid;blood
Breast;Esophagus;Thyroid;blood
Adipose;Esophagus;Thyroid;blood
Artery;Skin;fibroblasts
Adipose;Artery;Esophagus;Lung;Nerve;Skin;fibroblasts
Adipose;Artery;Breast;Lung;Nerve;fibroblasts
Adipose;Artery;Colon;Esophagus;Lung;Nerve;Skin;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Lung;Nerve;Skin;fibroblasts
Adipose;Artery;Esophagus;Lung;Nerve;Skin;fibroblasts
Adipose;Artery;Breast;Esophagus;Lung;Nerve;Skin;fibroblasts
Nerve;blood
fibroblasts
Skin;fibroblasts
Artery;Skin;blood;fibroblasts
Skin;fibroblasts
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Prostate;Sk
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Prostate;Sk
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Prostate;Sk
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Prostate;Sk
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Prostate;Sk
Esophagus;Liver;Muscle
Esophagus;Liver;Muscle
Artery;Heart
Adipose;Artery;Brain;Esophagus;Heart;Muscle;Pancreas;Stomach;Thyroid;blood;fibroblasts
Adipose;Heart;Lung;Muscle;Nerve;fibroblasts
Thyroid
Liver;Lung;Thyroid
Lung;Thyroid
Heart
Heart

Skin
Adipose;Artery;Esophagus;Heart;Nerve;Pancreas;Thyroid;fibroblasts
Adipose;Artery;Esophagus;Heart;Stomach;Thyroid;fibroblasts
Adipose;Artery;Esophagus;Heart;Thyroid;fibroblasts
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Stomach;Thyroid;fibroblasts
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Nerve;Thyroid;fibroblasts
Adipose;Artery;Esophagus;Heart;Muscle;Nerve;Thyroid;blood;fibroblasts
Adipose;Artery;Esophagus;Heart;Muscle;Nerve;Thyroid;blood;fibroblasts
Thyroid
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Pituitary;Skin;Spleen;Testis;Thyroid;fibroblasts
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Pituitary;Skin;Testis;Thyroid;blood;fibrobl
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Skin;Testis;Thyroid;blood;fibroblasts
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Pituitary;Skin;Testis;Thyroid;blood;fibr
Artery;Esophagus;Lung;Muscle;Testis;Thyroid;fibroblasts
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Pituitary;Skin;Stomach;Testis;Thyroid;b
Artery;Esophagus;Testis;fibroblasts
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Skin;Testis;Thyroid;blood;fibroblasts
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Pituitary;Skin;Testis;Thyroid;blood;fibr
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Skin;Testis;Thyroid;blood;fibroblasts
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Lung;Muscle;Pancreas;Pituitary;Skin;Testis;Thyroid;blood;fibr
Artery;Esophagus;Lung;Muscle;Testis;Thyroid;blood;fibroblasts
Muscle
Muscle
Muscle
Muscle
Colon
Testis
Testis
Testis
Testis
Testis
Testis
Adipose
Esophagus;Muscle
Adipose;Artery;Brain;Esophagus;Lung;Muscle;Skin;Thyroid;fibroblasts
Adipose;Artery;Brain;Esophagus;Heart;Lung;Muscle;Skin;Thyroid;fibroblasts
Artery;Heart;Muscle;Skin
Artery;Heart;Lung;Muscle;Skin
Artery;Muscle
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;Spleen
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Spleen;Stomac
Adipose;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Spleen;Stomach;Testis;Thyroi
Adipose;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Spleen;Stomach;Testis;Thyroi
Artery
Adipose;Artery;Breast;Lung;Nerve;Thyroid
Thyroid
Lung;Skin

Skin
Skin
Artery
Testis
Testis
Nerve
Nerve;Testis
Nerve;Testis
Nerve;Testis
Nerve
Nerve
Muscle
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Heart
Heart
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Nerve;Skin;blood;fibroblasts
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Heart
Heart
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Nerve;Skin;blood;fibroblasts
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Heart;Lung;Muscle;blood
Heart;blood
Heart;Lung;Muscle;blood
Adipose;Artery;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;blood;fibroblasts
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Testis
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Ovary;Pancreas;Skin;Spl
Adipose;Esophagus;Nerve;Skin
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;
Stomach;blood
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;
Muscle
Muscle
Muscle
Muscle
Muscle
Muscle
Muscle
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Testis
Adipose;Artery;Brain;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;Testis;Thyroid;blood
Adipose;Artery;Brain;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;Testis;Thyroid;blood

Adipose;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Testis;Thyroid;blood;fibro
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Testis;Thyroid;blood
Brain;Nerve;Thyroid;fibroblasts
Adipose;Brain;Muscle;Nerve;fibroblasts
Adipose;Brain;Nerve;fibroblasts
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Ovary;Pancreas;Pituitary
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Ovary;Pancreas;Prostate
Esophagus;Liver;Stomach
Muscle;Nerve;Pancreas;Thyroid;fibroblasts
Muscle
Adipose;Artery;Breast;Colon;Esophagus;Heart;Lung;Nerve;Ovary;Pancreas;Pituitary;Prostate;Skin;SmallIntestine;Sple
Adipose;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Nerve;Ovary;Pancreas;Pituitary;Prostate;Skin;SmallIntestir
Esophagus;Liver;Thyroid
Thyroid
Muscle
Thyroid
Skin;Thyroid;fibroblasts
Pancreas;Skin;Thyroid
Skin;Thyroid;fibroblasts
Skin;Thyroid;fibroblasts
Adipose;Esophagus;Pancreas;Skin;Thyroid;fibroblasts
Testis
Muscle;blood
Testis
Adipose;Colon;Esophagus;Pancreas;Skin;Testis;Thyroid;fibroblasts
Artery;Esophagus;Heart;Nerve;Pancreas;Testis;Thyroid;fibroblasts
Artery;Heart;Nerve;Ovary;Thyroid;blood;fibroblasts
Adipose;Artery;Esophagus;Heart;Muscle;Nerve;Ovary;Stomach;Thyroid;blood;fibroblasts
Adipose;Artery;Heart;Muscle;Nerve;Ovary;Pituitary;Thyroid;blood;fibroblasts
Heart;fibroblasts
Esophagus;Heart;Nerve
Esophagus;Heart;Muscle
Esophagus;Lung;Skin
Muscle
Colon;Liver;SmallIntestine;Stomach;blood
blood
Artery;Colon;Nerve;Pancreas;blood
Adipose;Artery;Breast;Esophagus;Heart;Muscle;Nerve;blood
Adipose;Skin
Adipose;Muscle;Skin
Adipose;Brain;Colon;Heart;Muscle;Skin;Thyroid
Adipose;Brain;Colon;Heart;Muscle;Skin;Thyroid
Brain;Esophagus
Artery;Brain;Esophagus;Nerve
Brain;Esophagus;Nerve
Adipose;Artery;Brain;Esophagus;Nerve;Testis
Adipose;Artery;Brain;Breast;Esophagus;Nerve

Adipose;Artery;Breast;Muscle;Nerve;Thyroid
fibroblasts
Lung;Thyroid
Lung;Thyroid
Lung;Thyroid
Artery;Thyroid;fibroblasts
Nerve;Pancreas
Nerve;Pancreas
Lung;Nerve;Pancreas;Testis
Esophagus;Nerve;Skin;Thyroid;blood
Esophagus;Nerve;Skin;Thyroid;blood
Esophagus;Lung;Skin;Thyroid;blood
Esophagus;Skin;Thyroid;blood
Esophagus;Lung;Skin;Thyroid;blood
Esophagus;Thyroid;blood
Adipose;Artery;Brain;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts;lymphocytes
Muscle
Muscle
Colon;Muscle;Skin
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Muscle
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts;lymphoc
Adipose;Artery;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Skin;Spleen;Testis;blood;fibroblasts
Adipose;Artery;Esophagus;Lung;Muscle;Nerve;Skin;blood
Skin
Skin
Skin
Skin
Skin
Brain;Colon;Esophagus;Heart;Muscle;Nerve;Pancreas;Spleen;Thyroid;blood;fibroblasts
Brain;Colon;Esophagus;Heart;Muscle;Nerve;Pancreas;Spleen;Thyroid;blood;fibroblasts
Brain;Colon;Esophagus;Muscle;Nerve;Pancreas;Spleen;Thyroid;blood;fibroblasts
Brain;Colon;Esophagus;Heart;Nerve;Pancreas;Spleen;Thyroid;blood;fibroblasts
Brain;Colon;Esophagus;Heart;Nerve;Pancreas;Thyroid;blood;fibroblasts
Esophagus;Heart;Pancreas;blood
Thyroid;blood
Heart
Adipose;Heart
Adipose;Heart
Adipose;Heart

Heart
blood
blood
Lung;Skin
Skin
Adipose;Artery;Breast;Colon;Esophagus;Heart;Lung;Nerve;Skin;Testis;Thyroid;blood
Adipose;Artery;Esophagus;Lung;Nerve;Skin;Thyroid
Adipose;Artery;Esophagus;Lung;Nerve;Skin;Thyroid
Adipose;Artery;Breast;Esophagus;Lung;Nerve;Skin;Thyroid
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Thyroid
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Thyroid;blood
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Thyroid;Uterus;blood;fibroblas
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Testis;Thyroid;blood
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Thyroid;Uterus;blood;fibroblas
Adipose;Artery;Esophagus;Lung;Muscle;Nerve;Skin;Thyroid;blood;fibroblasts
Adipose;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Thyroid;blood;
Muscle;Pancreas;lymphocytes
Muscle;Pancreas
Adipose;Colon;Esophagus;Lung;Skin;Testis;fibroblasts
Adipose;Colon;Esophagus;Lung;Skin;Testis;blood;fibroblasts
Adipose;Colon;Esophagus;Lung;Skin;Testis;blood;fibroblasts
Adipose;Colon;Esophagus;Lung;Skin;Testis;blood;fibroblasts
Adipose;Colon;Esophagus;Lung;Skin;Testis;blood;fibroblasts
Skin
Skin
Skin
Esophagus;Heart;Skin;Thyroid
Esophagus;Heart;Nerve;Skin;Thyroid
Artery;Esophagus;Heart;Skin;Thyroid
Esophagus;Heart;Skin;Thyroid;blood
Esophagus;Heart;Skin;Thyroid;blood
Esophagus;Heart;Skin;Thyroid;blood
Esophagus;Heart;Skin;Thyroid
Adipose;Nerve;Thyroid;fibroblasts
Artery
Artery
Esophagus;Skin;Testis
Esophagus;Skin;Testis
Esophagus;Skin;Testis
Esophagus;Skin;Testis
blood
blood
blood
Adipose;Artery;Esophagus;Heart;Muscle;Nerve;Skin;Thyroid
Adipose;Artery;Esophagus;Heart;Muscle;Nerve;Skin;Thyroid
Adipose;Artery;Esophagus;Heart;Nerve;Skin;Thyroid
Adipose

Skin
Adipose;fibroblasts
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;SmallI
Adipose;AdrenalGland;Artery;Brain;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Ovary;Pancreas;Skin;Spl
Artery;Breast;Esophagus;Nerve;Skin;Thyroid;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Spleen;Stomach;Thyroid;blooc
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Spleen;Stomach;Thyr
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Thyroid;blo
Adipose;AdrenalGland;Artery;Colon;Esophagus;Heart;Lung;Nerve;Pancreas;Skin;Thyroid;blood;fibroblasts
Adipose;Artery;Breast;Colon;Lung;Pancreas;Skin;Thyroid;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Stomach;Thyroid;blood;fibroblasts;lymphocytes
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Stomach;Thyroid;blood;fibroblasts;lymphocytes
Adipose;Artery;Breast;Colon;Esophagus;Lung;Nerve;Skin;Stomach;Thyroid;blood;fibroblasts;lymphocytes
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Stomach;Thyroid;blood;fibroblasts
Adipose;Artery;Breast;Colon;Esophagus;Lung;Muscle;Nerve;Skin;Stomach;Thyroid;fibroblasts
Adipose;Artery
Adipose;Artery;Muscle
Pancreas
Adipose
Brain;Muscle;fibroblasts
Brain;Muscle;fibroblasts
Brain;Muscle;fibroblasts
Brain;fibroblasts
Brain;fibroblasts
Brain;fibroblasts
Brain;fibroblasts
Brain;fibroblasts
Brain;fibroblasts
Brain;fibroblasts
Brain;Lung;fibroblasts
fibroblasts
Thyroid;fibroblasts
Thyroid;blood;fibroblasts
Adipose;Thyroid
Adipose;Thyroid
Thyroid;blood
Thyroid;blood
Adipose;Artery;fibroblasts
Artery;Esophagus;Testis
Testis;fibroblasts
Esophagus;Thyroid
Esophagus
Artery;Esophagus;Nerve;Pancreas;Skin;blood
Esophagus
Esophagus;Heart;Thyroid
Esophagus;Heart;Thyroid
Artery;Esophagus;Heart

Esophagus;Heart;Thyroid
Esophagus;Heart
Esophagus;Heart
Adipose;Esophagus;Heart;Skin
Artery;Esophagus;Pancreas;Skin;blood
Artery;Esophagus;Nerve;Skin;blood;fibroblasts
Artery;Esophagus;Nerve;Pancreas;Skin;Thyroid;blood;fibroblasts
Adipose;Artery;Esophagus;Heart;Lung;Skin;Thyroid
Artery;Esophagus;Heart;Lung;Thyroid
Artery;Esophagus;Heart;Lung
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Skin;fibroblasts
Adipose;Artery;Esophagus;Lung;Muscle;Skin;blood;fibroblasts
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Skin;fibroblasts
Adipose;Artery;Esophagus;Heart;Lung;Muscle;Thyroid;fibroblasts
Artery;Esophagus;Heart;Muscle;Thyroid;blood;fibroblasts
Adipose;AdrenalGland;Artery;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Thyroid;fibroblasts
Adipose;AdrenalGland;Artery;Esophagus;Heart;Lung;Muscle;Skin;Thyroid;fibroblasts
Adipose;AdrenalGland;Artery;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Thyroid;fibroblasts
Adipose;AdrenalGland;Artery;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Thyroid;fibroblasts
Adipose;AdrenalGland;Artery;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Thyroid;fibroblasts
Adipose;Testis
Adipose;Testis
Adipose;Testis
Brain;blood
Brain;Heart;blood
Lung
Brain;Heart;blood
Brain;Heart;blood
Skin;Thyroid
Thyroid
Skin;Thyroid
Skin;Thyroid
Skin
Colon;Heart;Nerve;Thyroid
Colon;Heart;Muscle;Skin;Thyroid
Esophagus;Heart;Muscle;Nerve;Skin;Stomach;Thyroid
Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Thyroid
Adipose;Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Thyroid
Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;Thyroid
Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Thyroid
Colon;Esophagus;Heart;Liver;Lung;Muscle;Nerve;Pancreas;Skin;Stomach;Thyroid
Heart;Liver;Muscle;Pancreas;Skin;Thyroid
Adipose;Pancreas;Spleen;Testis;Thyroid;blood;lymphocytes
Adipose;Esophagus;Lung;Spleen;Thyroid;blood;fibroblasts;lymphocytes
Adipose;Colon;Lung;Skin;Spleen;Thyroid;blood;lymphocytes
Adipose;Artery;Lung;SmallIntestine;Spleen;Testis;blood;lymphocytes
Adipose;Artery;Breast;Esophagus;Lung;Nerve;Spleen;Testis;Thyroid;blood;lymphocytes

Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Thyroid;blood;fibroblasts;lymphocy
Adipose;AdrenalGland;Artery;Breast;Colon;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Stomach;Thyroid;blood;fibrobl
Adipose;Artery;Brain;Breast;Esophagus;Lung;Muscle;Thyroid
Adipose;Artery;Esophagus;Muscle
Skin
Adipose;AdrenalGland;Artery;Colon;Esophagus;Liver;Lung;Muscle;Nerve;Ovary;Pancreas;Pituitary;Skin;Stomach;Test
Adipose;AdrenalGland;Artery;Esophagus;Liver;Lung;Muscle;Nerve;Ovary;Pancreas;Pituitary;Skin;Stomach;Testis;Thy
Adipose;AdrenalGland;Artery;Esophagus;Liver;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;Spleen;Stomach;Testis;Thy
Adipose;AdrenalGland;Artery;Colon;Esophagus;Liver;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;Stomach;Testis;Thyr
Adipose;AdrenalGland;Artery;Colon;Esophagus;Liver;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;Stomach;Testis;Thyr
Adipose;AdrenalGland;Artery;Colon;Esophagus;Liver;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;Stomach;Testis;Thyr
Adipose;AdrenalGland;Artery;Esophagus;Lung;Muscle;Nerve;Pancreas;Pituitary;Skin;Testis;Thyroid;blood;fibroblasts
Artery;Lung;Muscle;Nerve;Skin;Testis;Thyroid;blood;fibroblasts
fibroblasts
blood
blood
Thyroid
Thyroid
Skin;Thyroid
Artery;Nerve;Thyroid
Artery;Brain;Nerve;Thyroid
Artery;Nerve;Thyroid
Muscle
Muscle
Muscle
Skin
Skin
Skin
Nerve
blood
blood
blood
Muscle;blood
blood
blood
blood
Brain;Lung
Brain;Lung
Adipose;AdrenalGland;Artery;Brain;Esophagus;Heart;Lung;Muscle;Nerve;Skin;Testis;Thyroid;fibroblasts
Muscle;Skin;fibroblasts
Artery;Esophagus;Heart;Muscle;Skin;fibroblasts
Testis
fibroblasts
Esophagus;Stomach;fibroblasts
Esophagus;Pancreas;Skin;Stomach;fibroblasts
Esophagus;Heart;Pancreas;Skin;Stomach;Thyroid;fibroblasts
AdrenalGland;Colon;Esophagus;Heart;Nerve;Pancreas;Skin;Stomach;Testis;Thyroid;fibroblasts

Colon;Esophagus;Heart;Pancreas;Skin;Stomach;Testis;Thyroid;fibroblasts
AdrenalGland;Esophagus;Heart;Pancreas;Skin;Stomach;Testis;Thyroid;fibroblasts
AdrenalGland;Colon;Esophagus;Heart;Pancreas;Skin;Stomach;Testis;Thyroid;fibroblasts
AdrenalGland;Esophagus;Heart;Lung;Pancreas;Skin;Stomach;Testis;fibroblasts
Adipose;Heart;Muscle;Skin
Lung;Skin;blood
Adipose;Artery;Esophagus;Heart;Lung;Spleen;Thyroid;blood
Adipose;Artery;Colon;Esophagus;Heart;Liver;Lung;Nerve;Skin;Spleen;Thyroid;blood
Lung;blood
Lung;blood
Adipose;Artery;Brain;Colon;Lung;Nerve;Skin;Testis;Thyroid;blood
Adipose;Artery;Brain;Lung;Nerve;Skin;Testis;Thyroid
Artery
Artery
Artery
Artery
Esophagus
Esophagus;Skin
Adipose
Liver
Adipose;Artery;Brain;Colon;Esophagus;Lung;Nerve;Skin;Thyroid;blood;fibroblasts
Adipose;Artery;Colon;Esophagus;Lung;Nerve;Thyroid;blood;fibroblasts
Artery;Colon;Esophagus;Lung;Nerve;fibroblasts
Nerve
Skin;Thyroid;fibroblasts
Nerve;Skin;Thyroid;fibroblasts

Web Table 12: DEPICT Gene prioritization results for the genome-wide significant (2 DF Joint P

Locus	Number of genes in locus	Chromosome and position	GWAS P-value
rs4470970;rs17154246;rs7806896	1	chr7:79998891-80308593	6.35E-51
rs10127775	1	chr1:230193536-230417870	1.15E-58
rs113290361	1	chr1:182350839-182361341	1.45E-22
rs2315129;rs4708870;rs78822335;rs93	6	chr6:160592093-161174338	1.71E-27
rs2395943	11	chr6:42896938-43129457	1.94E-13
rs116843064;rs12976739	2	chr19:8429011-8469313	7.38E-36
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs11236519	4	chr11:75469500-75854239	1.97E-25
rs57276302;rs10773112;rs921919;rs83	1	chr12:125261606-125367214	8.08E-49
rs10955992	1	chr8:121547985-121825513	7.38E-16
rs3745683;rs8113156;rs11668537	3	chr19:11274944-11373157	3.93E-65
rs2262194;rs7314976	1	chr12:123104824-123215390	1.11E-20
rs190528931	16	chr11:63766030-64089283	1.85E-16
rs4847240	5	chr1:93544792-93828149	4.03E-31
rs1610216;rs282225;rs147056003;rs78	7	chr16:56126899-56643409	4.93E-25
rs2395943	11	chr6:42896938-43129457	1.94E-13
rs11967262	1	chr6:43737921-43754224	6.95E-26
rs13247874	5	chr7:72848109-73038873	1.36E-30
rs4784733;rs11640954;rs9989419;rs12	10	chr16:56691855-57181878	0.00E+00
rs2575876;rs4149307;rs73664373;rs13	2	chr9:107543283-107691173	5.93E-162
rs509728;rs61905116;rs61905084;rs18	4	chr11:116618886-116663136	0.00E+00
rs4784733;rs11640954;rs9989419;rs12	10	chr16:56691855-57181878	0.00E+00
rs4911477	5	chr20:33516236-33865928	3.25E-09
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs143361185	7	chr7:938415-1204903	1.01E-08
rs174562	4	chr11:61520114-61647626	6.95E-52
rs540730;rs7303542	4	chr12:57637236-57853063	1.11E-20
rs62117205;rs34383825	1	chr19:45250962-45263301	2.06E-18
rs114165349	15	chr1:27022524-27701315	7.22E-156
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs11806638	2	chr1:55505221-55681039	3.25E-11
rs2642438	1	chr1:220960101-220987735	1.36E-21
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs4820323	3	chr22:38480896-38612518	1.49E-11
rs78471630	3	chr11:126173647-126310239	3.24E-13
rs442177	1	chr4:87856154-88062206	4.98E-15
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs2315129;rs4708870;rs78822335;rs93	6	chr6:160592093-161174338	1.71E-27
rs7096937;rs4573621	2	chr10:113909624-114064793	2.47E-32
rs289;rs6999158;rs1569213;rs308;rs32	1	chr8:19759228-19824770	0.00E+00
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs112201728	2	chr6:160390131-160579750	2.66E-12
rs1373068;rs78196338	3	chr17:66863433-67138015	9.10E-20

rs12965067;rs524925;rs9964735;rs178	10	chr18:46570172-47920543	2.20E-121
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs28650790	1	chr5:56111401-56191979	6.64E-17
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs55699415	1	chr12:7623409-7656489	3.97E-09
rs2043082;rs1077835;rs8042174;rs620	1	chr15:58702768-58861151	0.00E+00
rs28873836	1	chr19:52298411-52329334	1.39E-18
rs4911477	5	chr20:33516236-33865928	3.25E-09
rs10744826	5	chr12:109826524-110035067	1.33E-29
rs2315129;rs4708870;rs78822335;rs93	6	chr6:160592093-161174338	1.71E-27
rs7298909	2	chr12:123773656-123893905	2.38E-31
rs235314	4	chr21:46188955-46293752	1.56E-18
rs5167;rs146390218	3	chr19:45445495-45541452	5.91E-45
rs5167;rs146390218	3	chr19:45445495-45541452	5.91E-45
rs114165349	15	chr1:27022524-27701315	7.22E-156
rs12965067;rs524925;rs9964735;rs178	10	chr18:46570172-47920543	2.20E-121
rs1154988	4	chr3:135684515-136471220	8.96E-17
rs4688756	10	chr3:49726932-50226508	1.55E-17
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs4784733;rs11640954;rs9989419;rs12	10	chr16:56691855-57181878	0.00E+00
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs7009673;rs4351435;rs12114418	1	chr8:126442563-126450647	1.27E-59
rs5167;rs146390218	3	chr19:45445495-45541452	5.91E-45
rs10713774	1	chr4:26165077-26436541	6.85E-09
rs1610216;rs282225;rs147056003;rs78	7	chr16:56126899-56643409	4.93E-25
rs13135092	2	chr4:102332443-103352415	1.69E-33
rs1373068;rs78196338	3	chr17:66863433-67138015	9.10E-20
rs78471630	3	chr11:126173647-126310239	3.24E-13
rs174562	4	chr11:61520114-61647626	6.95E-52
rs7933691	6	chr11:55277217-56543682	5.41E-18
rs17585915	1	chr6:139693393-139695757	2.38E-18
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs367070;rs373032	2	chr19:54777675-54809952	1.01E-64
rs4804311	3	chr19:8554941-8642461	6.80E-13
rs1800961	1	chr20:42984340-43060030	1.07E-71
rs429358;rs7412;rs6859;rs11668327;rs	5	chr19:45312338-45422606	7.04E-126
rs116843064;rs12976739	2	chr19:8429011-8469313	7.38E-36
rs56144648	1	chr6:41902671-42018095	6.95E-12
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs2395943	11	chr6:42896938-43129457	1.94E-13
rs6073958;rs435306	3	chr20:44527399-44600833	1.37E-69
rs3802548	4	chr10:45869661-46168228	4.29E-11
rs8078880	4	chr17:45400656-45789427	1.79E-09
rs6073958;rs435306	3	chr20:44527399-44600833	1.37E-69
rs10744826	5	chr12:109826524-110035067	1.33E-29

rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs1154988	4	chr3:135684515-136471220	8.96E-17
rs45490496	2	chr14:105235686-105271049	2.99E-20
rs76127683	2	chr15:63334831-63434260	1.50E-11
rs59781045;rs12280210;rs470898;rs79	8	chr11:116691419-117103241	6.73E-51
rs62133135	2	chr19:54704610-54761167	1.01E-09
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs56960668	1	chr8:144295068-144299044	8.01E-18
rs12965067;rs524925;rs9964735;rs178	10	chr18:46570172-47920543	2.20E-121
rs676210;rs7608123;rs13414987;rs430	1	chr2:21224301-21266945	3.10E-71
rs59781045;rs12280210;rs470898;rs79	8	chr11:116691419-117103241	6.73E-51
rs429358;rs7412;rs6859;rs11668327;rs	5	chr19:45312338-45422606	7.04E-126
rs4804411	1	chr19:7112266-7294011	2.73E-08
rs4688756	10	chr3:49726932-50226508	1.55E-17
rs59781045;rs12280210;rs470898;rs79	8	chr11:116691419-117103241	6.73E-51
rs367070;rs373032	2	chr19:54777675-54809952	1.01E-64
rs1047891	1	chr2:211342406-211543831	3.19E-16
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs540730;rs7303542	4	chr12:57637236-57853063	1.11E-20
rs2315129;rs4708870;rs78822335;rs93	6	chr6:160592093-161174338	1.71E-27
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs1373068;rs78196338	3	chr17:66863433-67138015	9.10E-20
rs836546	4	chr7:6369040-6523873	6.86E-16
rs4820323	3	chr22:38480896-38612518	1.49E-11
rs114165349	15	chr1:27022524-27701315	7.22E-156
rs1128249;rs13410987	1	chr2:165510134-165700189	2.94E-26
rs17575427	11	chr1:109852192-110208118	1.21E-08
rs190737	1	chr1:26856252-26901521	1.92E-08
rs4804311	3	chr19:8554941-8642461	6.80E-13
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs114165349	15	chr1:27022524-27701315	7.22E-156
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs17575427	11	chr1:109852192-110208118	1.21E-08
rs3745683;rs8113156;rs11668537	3	chr19:11274944-11373157	3.93E-65
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs881844	11	chr17:37408897-37903545	6.16E-38
rs4580194	3	chr17:38137050-38210661	2.78E-18
rs57457691	1	chr19:33877855-34012799	1.89E-13
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs59781045;rs12280210;rs470898;rs79	8	chr11:116691419-117103241	6.73E-51
rs429358;rs7412;rs6859;rs11668327;rs	5	chr19:45312338-45422606	7.04E-126
rs6073958;rs435306	3	chr20:44527399-44600833	1.37E-69
rs4418728;rs7068500	1	chr10:94590935-94819250	5.95E-17
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rs1154988	4	chr3:135684515-136471220	8.96E-17
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rs7298909	2	chr12:123773656-123893905	2.38E-31
rs7445	4	chr22:21903736-21998587	1.36E-29
rs4898521	18	chr12:49396057-50158717	1.34E-08
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rs8078880	4	chr17:45400656-45789427	1.79E-09
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rs114165349	15	chr1:27022524-27701315	7.22E-156
rs7137828	16	chr12:111471828-112947717	1.04E-09
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rs10744826	5	chr12:109826524-110035067	1.33E-29
rs1645779	1	chr19:54818353-54824409	2.76E-27
rs4580194	3	chr17:38137050-38210661	2.78E-18
rs2395943	11	chr6:42896938-43129457	1.94E-13

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rs10774579	3	chr12:121416346-121477045	1.66E-13
rs10774579	3	chr12:121416346-121477045	1.66E-13
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rs4688756	10	chr3:49726932-50226508	1.55E-17
rs190528931	16	chr11:63766030-64089283	1.85E-16
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rs836546	4	chr7:6369040-6523873	6.86E-16
rs4580194	3	chr17:38137050-38210661	2.78E-18
rs143361185	7	chr7:938415-1204903	1.01E-08
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rs4898521	18	chr12:49396057-50158717	1.34E-08
rs7137828	16	chr12:111471828-112947717	1.04E-09
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rs4898521	18	chr12:49396057-50158717	1.34E-08
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rs7137828	16	chr12:111471828-112947717	1.04E-09
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rs143361185	7	chr7:938415-1204903	1.01E-08
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rs881844	11	chr17:37408897-37903545	6.16E-38
rs4898521	18	chr12:49396057-50158717	1.34E-08
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rs114165349	15	chr1:27022524-27701315	7.22E-156
rs7137828	16	chr12:111471828-112947717	1.04E-09
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rs114165349	15	chr1:27022524-27701315	7.22E-156
rs4688756	10	chr3:49726932-50226508	1.55E-17
rs2395943	11	chr6:42896938-43129457	1.94E-13
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rs174562	4	chr11:61520114-61647626	6.95E-52
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rs4898521	18	chr12:49396057-50158717	1.34E-08
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rs17575427	11	chr1:109852192-110208118	1.21E-08
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rs114165349	15	chr1:27022524-27701315	7.22E-156
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs9491694	1	chr6:127439749-127518910	1.32E-14
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rs114165349	15	chr1:27022524-27701315	7.22E-156
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rs4847240	5	chr1:93544792-93828149	4.03E-31
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rs190528931	16	chr11:63766030-64089283	1.85E-16
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rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs80080062	2	chr3:185764097-186080026	1.11E-12
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99

rs190528931	16	chr11:63766030-64089283	1.85E-16
rs2395943	11	chr6:42896938-43129457	1.94E-13
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs16872768	1	chr5:74969949-75013313	2.30E-10
rs17575427	11	chr1:109852192-110208118	1.21E-08
rs12753251	1	chr1:178482212-178517734	5.04E-15
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs187929675	1	chr11:117103341-117157161	1.17E-18
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs17451107	1	chr3:156799630-156806336	9.42E-20
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs17575427	11	chr1:109852192-110208118	1.21E-08
rs79355265	1	chr2:21540532-21784185	2.71E-113
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs4660303;rs112646560	4	chr1:39546988-40011859	4.44E-27
rs13247874	5	chr7:72848109-73038873	1.36E-30
rs11236519	4	chr11:75469500-75854239	1.97E-25
rs10530815	1	chr19:44930426-44952665	1.62E-09
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs1610216;rs282225;rs147056003;rs78	7	chr16:56126899-56643409	4.93E-25
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs72729610	2	chr4:154073494-154260472	5.64E-09
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs7445	4	chr22:21903736-21998587	1.36E-29
rs189595952	2	chr18:46065417-46477081	1.43E-10
rs12681175	3	chr8:10581278-10704011	1.52E-08
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs2238689	1	chr19:46171502-46185704	2.15E-13
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs11057413;rs825452;rs707334	3	chr12:124247042-124499974	1.09E-33
rs4847240	5	chr1:93544792-93828149	4.03E-31
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs12965067;rs524925;rs9964735;rs178	10	chr18:46570172-47920543	2.20E-121
rs17575427	11	chr1:109852192-110208118	1.21E-08
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs2972143	1	chr2:227044760-227050087	4.32E-31
rs12965067;rs524925;rs9964735;rs178	10	chr18:46570172-47920543	2.20E-121
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs77231091	1	chr17:67410838-67538451	2.44E-08
rs190528931	16	chr11:63766030-64089283	1.85E-16
rs2737216	1	chr8:116420724-116821899	3.92E-32
rs143361185	7	chr7:938415-1204903	1.01E-08
rs190528931	16	chr11:63766030-64089283	1.85E-16
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99

rs836546	4	chr7:6369040-6523873	6.86E-16
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs881844	11	chr17:37408897-37903545	6.16E-38
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs7528419;rs41279716	1	chr1:109792641-109818377	2.55E-32
rs2315129;rs4708870;rs78822335;rs93	6	chr6:160592093-161174338	1.71E-27
rs34311866	1	chr4:926175-952444	2.07E-08
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs58084604	1	chr18:58038564-58040001	4.97E-15
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs11762784	1	chr7:130417401-130418888	5.65E-37
rs4898521	18	chr12:49396057-50158717	1.34E-08
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs12965067;rs524925;rs9964735;rs178	10	chr18:46570172-47920543	2.20E-121
rs7933691	6	chr11:55277217-56543682	5.41E-18
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs72729610	2	chr4:154073494-154260472	5.64E-09
rs881844	11	chr17:37408897-37903545	6.16E-38
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs4660303;rs112646560	4	chr1:39546988-40011859	4.44E-27
rs113935429	1	chr16:53633824-53737771	7.82E-10
rs7933691	6	chr11:55277217-56543682	5.41E-18
rs114165349	15	chr1:27022524-27701315	7.22E-156
rs4688756	10	chr3:49726932-50226508	1.55E-17
rs7137828	16	chr12:111471828-112947717	1.04E-09
rs1610216;rs282225;rs147056003;rs78	7	chr16:56126899-56643409	4.93E-25
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs2575876;rs4149307;rs73664373;rs13	2	chr9:107543283-107691173	5.93E-162
rs7445	4	chr22:21903736-21998587	1.36E-29
rs658118;rs10769254;rs4491174;rs124	31	chr11:46417964-48192393	4.81E-69
rs80080062	2	chr3:185764097-186080026	1.11E-12
rs3802548	4	chr10:45869661-46168228	4.29E-11
rs9932087;rs142790048;rs255056;rs14	59	chr16:66942025-68732971	2.22E-99
rs149580368;rs1731897	13	chr17:41831103-42201014	1.38E-41
rs150844304;rs138570705;rs14949274	25	chr15:43036550-44955876	3.44E-35
rs17575427	11	chr1:109852192-110208118	1.21E-08
rs190528931	16	chr11:63766030-64089283	1.85E-16

< 5e-8) loci for HDL-cholesterol.

Ensembl gene ID	Gene symbol	Nominal P-value	Gene closest to lead SNP	Top cis eQTL SNP (Westra et al. Nature Genetics 2014)	False discovery rate
ENSG00000135218	*CD36*	8.91E-12	false	rs3211958;rs2272353	**<=0.01**
ENSG00000143641	*GALNT2*	1.38E-11	true	-	**<=0.01**
ENSG00000135821	*GLUL*	9.43E-11	true	rs1925829;rs12022482	**<=0.01**
ENSG00000198670	*LPA*	9.87E-10	true	-	**<=0.01**
ENSG00000124587	*PEX6*	1.19E-09	true	rs2296805	**<=0.01**
ENSG00000167772	*ANGPTL4*	2.21E-09	true	rs11669375	**<=0.01**
ENSG00000141086	*CTRL*	1.43E-08	false	-	**<=0.01**
ENSG00000062282	*DGAT2*	1.81E-08	true	rs7126727	**<=0.01**
ENSG00000073060	*SCARB1*	2.03E-08	true	rs7954697	**<=0.01**
ENSG00000172164	*SNTB1*	2.20E-08	true	rs10099300	**<=0.01**
ENSG00000130173	*C19orf80*	4.01E-08	true	rs12610693	**<=0.01**
ENSG00000196917	*HCAR1*	4.17E-08	true	-	**<=0.01**
ENSG00000149781	*FERMT3*	4.50E-08	false	rs2236648;rs4980525	**<=0.01**
ENSG00000117500	*TMED5*	5.23E-08	false	rs546	**<=0.01**
ENSG00000159461	*AMFR*	6.89E-08	true	rs4924;rs11644679	**<=0.01**
ENSG00000124713	*GNMT*	7.79E-08	false	-	**<=0.01**
ENSG00000112715	*VEGFA*	9.87E-08	true	rs9472113;rs9472113	**<=0.01**
ENSG00000009950	*MLXIPL*	2.03E-07	false	-	**<=0.01**
ENSG00000087237	*CETP*	2.47E-07	true	rs1167742;rs1684575	**<=0.01**
ENSG00000165029	*ABCA1*	2.73E-07	true	rs2472495	**<=0.01**
ENSG00000110243	*APOA5*	5.84E-07	false	-	**<=0.01**
ENSG00000205358	*MT1H*	6.12E-07	true	-	**<=0.01**
ENSG00000088298	*EDEM2*	7.63E-07	false	rs6058194	**<=0.01**
ENSG00000111252	*SH2B3*	9.25E-07	true	rs2239195	**<=0.01**
ENSG00000164849	*GPR146*	1.38E-06	true	rs1997243	**<=0.01**
ENSG00000134824	*FADS2*	1.40E-06	true	rs968567	**<=0.01**
ENSG00000175189	*INHBC*	1.99E-06	false	-	**<=0.01**
ENSG00000069399	*BCL3*	2.23E-06	true	rs846897	**<=0.01**
ENSG00000142748	*FCN3*	2.85E-06	false	-	**<=0.01**
ENSG00000213398	*LCAT*	2.91E-06	false	rs255049	**<=0.01**
ENSG00000169174	*PCSK9*	3.13E-06	true	-	**<=0.01**
ENSG00000186205	*MOSC1*	3.23E-06	true	rs11118598	**<=0.01**
ENSG00000111271	*ACAD10*	3.38E-06	false	rs634389	**<=0.01**
ENSG00000185022	*MAFF*	3.88E-06	true	rs5756968	**<=0.01**
ENSG00000110080	*ST3GAL4*	3.98E-06	false	rs529328	**<=0.01**
ENSG00000172493	*AFF1*	4.02E-06	false	-	**<=0.01**
ENSG00000139644	*TMBIM6*	4.16E-06	false	-	**<=0.01**
ENSG00000161653	*NAGS*	4.49E-06	false	-	**<=0.01**
ENSG00000122194	*PLG*	5.05E-06	false	rs9365237	**<=0.01**
ENSG00000119927	*GPAM*	7.91E-06	true	rs1926559	**<=0.01**
ENSG00000175445	*LPL*	8.59E-06	true	rs11991231	**<=0.01**
ENSG00000066336	*SPI1*	8.68E-06	true	rs1057233;rs326217	**<=0.01**
ENSG00000175003	*SLC22A1*	9.48E-06	true	rs2297372;rs662301	**<=0.01**
ENSG00000141338	*ABCA8*	1.03E-05	true	-	**<=0.01**

ENSG00000167315	*ACAA2*	1.09E-05	true	-	**<=0.01**
ENSG00000159792	*PSKH1*	1.11E-05	false	-	**<=0.01**
ENSG00000025434	*NR1H3*	1.33E-05	false	rs3758673	**<=0.01**
ENSG00000135723	*FHOD1*	1.55E-05	false	rs11639620	**<=0.01**
ENSG00000095015	*MAP3K1*	1.68E-05	true	rs6872807	**<=0.01**
ENSG00000161649	*CD300LG*	1.74E-05	false	-	**<=0.01**
ENSG00000103066	*PLA2G15*	1.78E-05	false	rs7672	**<=0.01**
ENSG00000177575	*CD163*	2.39E-05	true	-	**<=0.01**
ENSG00000166035	*LIPC*	2.45E-05	true	rs12911658	**<=0.01**
ENSG00000187474	*FPR3*	2.48E-05	true	rs12609373	**<=0.01**
ENSG00000101000	*PROCR*	2.74E-05	true	-	**<=0.01**
ENSG00000139428	*MMAB*	3.20E-05	false	rs918106	**<=0.01**
ENSG00000146477	*SLC22A3*	3.71E-05	false	rs316024	**<=0.01**
ENSG00000183955	*SETD8*	4.26E-05	false	rs12366872	**<=0.01**
ENSG00000183255	*PTTG1IP*	6.27E-05	true	rs235266;rs235266	**<=0.01**
ENSG00000104856	*RELB*	6.68E-05	false	-	**<=0.01**
ENSG00000104853	*CLPTM1*	6.76E-05	true	rs10409727	**<=0.01**
ENSG00000142733	*MAP3K6*	6.94E-05	false	rs17340684	**<=0.01**
ENSG00000101670	*LIPG*	6.95E-05	true	-	**<=0.01**
ENSG00000174579	*MSL2*	7.00E-05	true	-	**<=0.01**
ENSG00000164068	*RNF123*	7.18E-05	false	-	**<=0.01**
ENSG00000111275	*ALDH2*	7.32E-05	false	rs16941669	**<=0.01**
ENSG00000051108	*HERPUD1*	7.98E-05	true	rs8044753;rs8044753	**<=0.01**
ENSG00000180210	*F2*	8.74E-05	false	-	**<=0.01**
ENSG00000205250	*E2F4*	8.84E-05	false	rs9932319	**<=0.01**
ENSG00000134575	*ACP2*	9.27E-05	false	rs4752973	**<=0.01**
ENSG00000173334	*TRIB1*	9.55E-05	true	rs4360309	**<=0.01**
ENSG00000224916	*APOC4*	1.03E-04	true	-	**<=0.01**
ENSG00000168214	*RBPJ*	1.04E-04	true	rs13133397;rs4618302	**<=0.01**
ENSG00000125148	*MT2A*	1.10E-04	true	rs1580833	**<=0.01**
ENSG00000138821	*SLC39A8*	1.16E-04	true	rs7655493	**<=0.01**
ENSG00000154262	*ABCA6*	1.20E-04	false	rs1443263	**<=0.01**
ENSG00000247445	-	1.22E-04	true	-	**<=0.01**
ENSG00000149485	*FADS1*	1.35E-04	false	rs968567	**<=0.01**
ENSG00000254576	*OR4A21P*	1.51E-04	false	-	**<=0.01**
ENSG00000164442	*CITED2*	1.53E-04	true	rs4896477	**<=0.01**
ENSG00000161791	*FMNL3*	1.54E-04	false	rs11169109	**<=0.01**
ENSG00000170866	*LILRA3*	1.81E-04	true	-	**<=0.01**
ENSG00000142347	*MYO1F*	1.82E-04	true	rs2042300	**<=0.01**
ENSG00000101076	*HNF4A*	1.94E-04	false	rs17828482	**<=0.01**
ENSG00000130208	*APOC1*	1.96E-04	true	-	**<=0.01**
ENSG00000185236	*RAB11B*	2.02E-04	true	-	**<=0.01**
ENSG00000112576	*CCND3*	2.26E-04	true	rs4130023	**<=0.01**
ENSG00000110497	*AMBRA1*	2.30E-04	false	-	**<=0.01**
ENSG00000137171	*KLC4*	2.46E-04	false	rs6458330;rs7764865	**<=0.01**
ENSG00000198026	*ZNF335*	2.69E-04	false	-	**<=0.01**
ENSG00000012779	*ALOX5*	3.80E-04	false	rs9422650	**<=0.01**
ENSG00000141279	*NPEPPS*	3.96E-04	false	rs16956009	**<=0.01**
ENSG00000100982	*PCIF1*	4.11E-04	false	rs11086985	**<=0.01**
ENSG00000110921	*MVK*	4.22E-04	true	-	**<=0.01**

ENSG00000134571	*MYBPC3*	4.54E-04	true	rs7105851	**<=0.01**
ENSG00000178401	*DNAJC22*	4.77E-04	false	-	**<=0.01**
ENSG00000172831	*CES2*	5.10E-04	false	rs6499106	**<=0.01**
ENSG00000114054	*PCCB*	5.23E-04	false	rs1153877	**<=0.01**
ENSG00000142208	*AKT1*	5.45E-04	false	rs4983559;rs4983559	**<=0.01**
ENSG00000103642	*LACTB*	5.56E-04	true	rs1472631;rs1126308	**<=0.01**
ENSG00000118137	*APOA1*	5.84E-04	false	-	**<=0.01**
ENSG00000105609	*LILRB5*	6.44E-04	true	rs1035829	**<=0.01**
ENSG00000149177	*PTPRJ*	6.48E-04	true	rs17198607	**<=0.01**
ENSG00000182851	*GPIHBP1*	8.29E-04	true	rs2450782;rs10109061	**<=0.01**
ENSG00000141644	*MBD1*	8.53E-04	false	rs17803280	**<=0.01**
ENSG00000084674	*APOB*	8.72E-04	true	-	**<=0.01**
ENSG00000110244	*APOA4*	8.97E-04	false	-	**<=0.01**
ENSG00000130202	*PVRL2*	9.00E-04	true	rs11879589;rs11672399	**<=0.01**
ENSG00000171105	*INSR*	9.00E-04	true	rs459883	**<=0.01**
ENSG00000003756	*RBM5*	1.16E-03	false	rs6776145	**<0.05**
ENSG00000110245	*APOC3*	1.22E-03	false	-	**<0.05**
ENSG00000131042	*LILRB2*	1.30E-03	true	rs11672654	**<0.05**
ENSG00000021826	*CPS1*	1.46E-03	true	-	**<0.05**
ENSG00000103067	*ESRP2*	1.48E-03	false	-	**<0.05**
ENSG00000072736	*NFATC3*	1.50E-03	true	rs12598;rs1125333;rs4783630;r	**<0.05**
ENSG00000139269	*INHBE*	1.70E-03	false	rs11172247	**<0.05**
ENSG00000213071	*LPAL2*	1.82E-03	true	rs415317	**<0.05**
ENSG00000159459	*UBR1*	1.89E-03	false	rs3736054	**<0.05**
ENSG00000154258	*ABCA9*	1.95E-03	false	-	**<0.05**
ENSG00000136240	*KDELR2*	1.99E-03	false	rs6796	**<0.05**
ENSG00000184381	*PLA2G6*	1.99E-03	false	-	**<0.05**
ENSG00000131910	*NR0B2*	2.08E-03	false	-	**<0.05**
ENSG00000082438	*COBLL1*	2.12E-03	false	rs1840326	**<0.05**
ENSG00000065135	*GNAI3*	2.26E-03	false	rs12033376	**<0.05**
ENSG00000117676	*RPS6KA1*	2.33E-03	true	rs17162190	**<0.05**
ENSG00000133250	*ZNF414*	2.39E-03	false	rs2967571	**<0.05**
ENSG00000102974	*CTCF*	2.42E-03	true	-	**<0.05**
ENSG00000117713	*ARID1A*	2.48E-03	true	rs12752833	**<0.05**
ENSG00000167261	*DPEP2*	2.51E-03	false	rs2285912	**<0.05**
ENSG00000166592	*RRAD*	2.57E-03	false	-	**<0.05**
ENSG00000168765	*GSTM4*	2.85E-03	false	rs1010167;rs1010167	**<0.05**
ENSG00000197256	*KANK2*	2.86E-03	true	rs17616620	**<0.05**
ENSG00000179295	*PTPN11*	2.86E-03	false	-	**<0.05**
ENSG00000141738	*GRB7*	2.89E-03	false	rs14050	**<0.05**
ENSG00000108342	*CSF3*	2.93E-03	false	-	**<0.05**
ENSG00000124299	*PEPD*	2.96E-03	false	rs3786913	**<0.05**
ENSG00000166947	*EPB42*	3.23E-03	false	rs3736054	**<0.05**
ENSG00000175220	*ARHGAP1*	3.41E-03	true	rs2070852	**<0.05**
ENSG00000149577	*SIDT2*	3.44E-03	true	rs4938353	**<0.05**
ENSG00000130203	*APOE*	3.63E-03	true	-	**<0.05**
ENSG00000100979	*PLTP*	3.79E-03	true	-	**<0.05**
ENSG00000138190	*EXOC6*	4.21E-03	false	rs2148361	**<0.05**
ENSG00000130158	*DOCK6*	4.33E-03	false	rs317915	**<0.05**
ENSG00000137161	*CNPY3*	4.83E-03	false	-	**<0.05**

ENSG00000117505	*DR1*	4.89E-03	false	rs4847240	**<0.05**
ENSG00000108849	*PPY*	5.02E-03	true	-	**<0.05**
ENSG00000171056	*SOX7*	5.58E-03	true	rs10092781;rs7001281	**<0.05**
ENSG00000160584	*SIK3*	5.68E-03	true	-	**<0.05**
ENSG00000148572	*NRBF2*	6.12E-03	true	-	**<0.05**
ENSG00000067955	*CBFB*	6.38E-03	false	-	**<0.05**
ENSG00000133315	*MACROD1*	6.46E-03	true	-	**<0.05**
ENSG00000009954	*BAZ1B*	6.55E-03	false	rs17145732	**<0.05**
ENSG00000100991	*TRPC4AP*	7.12E-03	false	rs6120819;rs6120777	**<0.05**
ENSG00000125149	*C16orf70*	7.58E-03	false	rs9033	**<0.05**
ENSG00000187193	*MT1X*	7.99E-03	true	rs1599933	**<0.05**
ENSG00000155158	*TTC39B*	8.34E-03	true	-	**<0.05**
ENSG00000172828	*CES3*	8.68E-03	false	-	**<0.05**
ENSG00000139636	*LMBR1L*	8.72E-03	false	-	**<0.05**
ENSG00000243955	*GSTA1*	9.13E-03	true	-	**<0.05**
ENSG00000162402	*USP24*	9.30E-03	false	-	**<0.05**
ENSG00000118007	*STAG1*	9.43E-03	false	rs3931416	**<0.05**
ENSG00000161654	*LSM12*	9.92E-03	false	-	**<0.05**
ENSG00000171988	*JMJD1C*	0.01	false	-	**<0.05**
ENSG00000149182	*ARFGAP2*	0.01	true	rs4647709	**<0.05**
ENSG00000197081	*IGF2R*	0.01	false	rs3798209	**<0.05**
ENSG00000139697	*SBNO1*	0.01	true	rs1790116	<0.20
ENSG00000185651	*UBE2L3*	0.01	false	-	<0.20
ENSG00000167548	*MLL2*	0.01	false	-	<0.20
ENSG00000087157	*PGS1*	0.01	true	rs4969170	<0.20
ENSG00000198382	*UVRAG*	0.02	false	rs11236739	<0.20
ENSG00000143028	*SYPL2*	0.02	false	-	<0.20
ENSG00000075223	*SEMA3C*	0.02	true	-	<0.20
ENSG00000153064	*BANK1*	0.02	false	rs17031974	<0.20
ENSG00000127616	*SMARCA4*	0.02	false	rs12232780	<0.20
ENSG00000106635	*BCL7B*	0.02	false	rs11974409	<0.20
ENSG00000133246	*PRAM1*	0.02	false	-	<0.20
ENSG00000154832	*CXXC1*	0.02	false	rs17660567	<0.20
ENSG00000149782	*PLCB3*	0.02	false	-	<0.20
ENSG00000071189	*SNX13*	0.02	true	rs2723539	<0.20
ENSG00000226645	-	0.02	true	-	<0.20
ENSG00000149187	*CELF1*	0.02	false	rs12419692;rs10838708	<0.20
ENSG00000044090	*CUL7*	0.03	false	-	<0.20
ENSG00000137656	*BUD13*	0.03	true	rs1145187	<0.20
ENSG00000125686	*MED1*	0.03	false	rs11078915	<0.20
ENSG00000178852	*C17orf57*	0.03	false	-	<0.20
ENSG00000124067	*SLC12A4*	0.03	false	-	<0.20
ENSG00000151148	*UBE3B*	0.03	false	rs2241209	<0.20
ENSG00000060642	*PIGV*	0.03	false	rs12742115	<0.20
ENSG00000204842	*ATXN2*	0.03	false	rs3809278	<0.20
ENSG00000165476	*REEP3*	0.03	false	rs7076601	<0.20
ENSG00000174527	*MYO1H*	0.03	false	-	<0.20
ENSG00000187116	*LILRA5*	0.03	true	rs1645784;rs1645784;rs164578	<0.20
ENSG00000008838	*MED24*	0.03	false	rs6503525	<0.20
ENSG00000112640	*PPP2R5D*	0.03	false	rs6458318;rs6903229	<0.20

ENSG00000161395	*PGAP3*	0.03	false	-	<0.20
ENSG00000135100	*HNF1A*	0.03	true	-	<0.20
ENSG00000135114	*OASL*	0.03	false	rs2259693;rs2259693	<0.20
ENSG00000115884	*SDC1*	0.04	true	-	<0.20
ENSG00000167004	*PDIA3*	0.04	false	-	<0.20
ENSG00000179044	*EXOC3L1*	0.04	false	-	<0.20
ENSG00000173511	*VEGFB*	0.04	false	-	<0.20
ENSG00000124702	*KLHDC3*	0.04	false	rs6941129	<0.20
ENSG00000108861	*DUSP3*	0.04	false	rs1230395	<0.20
ENSG00000039523	*FAM65A*	0.04	true	rs6499137	<0.20
ENSG00000128228	*SDF2L1*	0.04	false	rs2599423	<0.20
ENSG00000178381	*ZFAND2A*	0.04	false	rs6973680	<0.20
ENSG00000165912	*PACSIN3*	0.04	true	-	<0.20
ENSG00000109920	*FNBP4*	0.05	false	rs4539273	<0.20
ENSG00000204160	*ZDHHC18*	0.05	false	rs17162315	<0.20
ENSG00000038358	*EDC4*	0.05	false	rs7191129	<0.20
ENSG00000135148	*TRAFD1*	0.05	false	rs10492014	<0.20
ENSG00000125144	*MT1G*	0.05	true	rs1580833	<0.20
ENSG00000185482	*STAC3*	0.05	false	-	<0.20
ENSG00000167258	*CDK12*	0.05	false	-	<0.20
ENSG00000119913	*TECTB*	0.06	false	rs10509961	<0.20
ENSG00000103064	*SLC7A6*	0.06	true	rs11644360;rs3785111	<0.20
ENSG00000187244	*BCAM*	0.06	true	rs203713	<0.20
ENSG00000110906	*KCTD10*	0.06	false	rs6663	<0.20
ENSG00000175793	*SFN*	0.06	false	-	<0.20
ENSG00000102890	*ELMO3*	0.06	true	-	<0.20
ENSG00000187778	*MCRS1*	0.06	false	rs2720295	<0.20
ENSG00000116337	*AMPD2*	0.06	false	-	<0.20
ENSG00000108424	*KPNB1*	0.07	true	-	<0.20
ENSG00000175216	*CKAP5*	0.07	false	-	<0.20
ENSG00000136238	*RAC1*	0.07	false	-	<0.20
ENSG00000143033	*MTF2*	0.07	false	rs2815416	<0.20
ENSG00000172572	*PDE3A*	0.08	true	-	<0.20
ENSG00000102901	*CENPT*	0.08	false	-	<0.20
ENSG00000160613	*PCSK7*	0.08	true	rs7107152	<0.20
ENSG00000257960	-	0.08	false	-	<0.20
ENSG00000173153	*ESRRA*	0.09	false	rs10792436	<0.20
ENSG00000141744	*PNMT*	0.09	false	-	>0.20
ENSG00000170606	*HSPA4*	0.09	false	rs4705986;rs7702889	>0.20
ENSG00000128298	*BAIAP2L2*	0.09	false	-	>0.20
ENSG00000102977	*ACD*	0.1	true	rs12927959	>0.20
ENSG00000175224	*ATG13*	0.1	false	-	>0.20
ENSG00000110536	*PTPMT1*	0.1	false	-	>0.20
ENSG00000168439	*STIP1*	0.1	false	-	>0.20
ENSG00000101665	*SMAD7*	0.1	true	rs11659241	>0.20
ENSG00000137770	*CTDSPL2*	0.1	false	-	>0.20
ENSG00000004534	*RBM6*	0.11	true	rs2245365	>0.20
ENSG00000126432	*PRDX5*	0.12	false	rs7947143;rs7947143	>0.20
ENSG00000078814	*MYH7B*	0.12	false	-	>0.20
ENSG00000102871	*TRADD*	0.12	false	rs1053612	>0.20

ENSG00000108840	*HDAC5*	0.13	false	rs1476512	>0.20
ENSG00000168781	*PPIP5K1*	0.13	false	-	>0.20
ENSG00000153815	*CMIP*	0.13	true	rs1128432;rs12918867	>0.20
ENSG00000205220	*PSMB10*	0.13	false	rs3785100	>0.20
ENSG00000164535	*DAGLB*	0.14	true	rs12537894	>0.20
ENSG00000108344	*PSMD3*	0.15	true	rs8080546	>0.20
ENSG00000229043	-	0.15	false	-	>0.20
ENSG00000173113	*TRMT112*	0.15	false	-	>0.20
ENSG00000100983	*GSS*	0.15	false	-	>0.20
ENSG00000062038	*CDH3*	0.16	false	rs9938842	>0.20
ENSG00000167941	*SOST*	0.16	false	rs1731902	>0.20
ENSG00000165923	*AGBL2*	0.16	false	-	>0.20
ENSG00000108306	*FBXL20*	0.17	false	rs8076462	>0.20
ENSG00000110844	*PRPF40B*	0.17	false	-	>0.20
ENSG00000089234	*BRAP*	0.18	false	-	>0.20
ENSG00000104133	*SPG11*	0.19	false	-	>0.20
ENSG00000167553	*TUBA1C*	0.19	false	-	>0.20
ENSG00000109919	*MTCH2*	0.19	false	rs2242081	>0.20
ENSG00000089022	*MAPKAPK5*	0.19	false	rs12580246;rs12426312	>0.20
ENSG00000102900	*NUP93*	0.2	true	rs12918087	>0.20
ENSG00000149591	*TAGLN*	0.2	false	rs10790177;rs1871757;rs71071	>0.20
ENSG00000240230	*COX19*	0.21	false	-	>0.20
ENSG00000180423	*HARBI1*	0.21	false	-	>0.20
ENSG00000184900	*SUMO3*	0.22	false	rs235359	>0.20
ENSG00000168286	*THAP11*	0.22	false	-	>0.20
ENSG00000165915	*SLC39A13*	0.22	true	-	>0.20
ENSG00000106638	*TBL2*	0.23	true	rs17145813	>0.20
ENSG00000168092	*PAFAH1B2*	0.23	true	-	>0.20
ENSG00000073711	*PPP2R3A*	0.23	false	-	>0.20
ENSG00000184787	*UBE2G2*	0.24	false	rs6518204	>0.20
ENSG00000173991	*TCAP*	0.24	true	-	>0.20
ENSG00000139549	*DHH*	0.24	false	-	>0.20
ENSG00000179627	*ZBTB42*	0.24	true	-	>0.20
ENSG00000182179	*UBA7*	0.24	false	rs1128535	>0.20
ENSG00000141084	*RANBP10*	0.26	false	rs16942887	>0.20
ENSG00000140265	*ZSCAN29*	0.26	false	-	>0.20
ENSG00000110011	*DNAJC4*	0.27	false	-	>0.20
ENSG00000115239	*ASB3*	0.28	false	rs719127;rs2287348	>0.20
ENSG00000171877	*FRMD5*	0.28	false	-	>0.20
ENSG00000142765	*SYTL1*	0.29	false	rs3813795	>0.20
ENSG00000089248	*ERP29*	0.3	false	rs7970397;rs7310545	>0.20
ENSG00000104131	*EIF3J*	0.3	false	-	>0.20
ENSG00000134243	*SORT1*	0.3	false	rs10494041	>0.20
ENSG00000147408	*CSGALNACT1*	0.31	true	rs4481612	>0.20
ENSG00000166589	*CDH16*	0.31	false	-	>0.20
ENSG00000102898	*NUTF2*	0.31	false	-	>0.20
ENSG00000198324	*FAM109A*	0.32	false	rs2239195	>0.20
ENSG00000185614	*C3orf54*	0.32	false	rs7645061	>0.20
ENSG00000165406	*MARCH8*	0.32	false	rs12779637;rs7908745;rs20292	>0.20
ENSG00000140416	*TPM1*	0.33	false	rs11071720;rs4075047	>0.20

ENSG00000256731	-	0.33	false	-	>0.20
ENSG00000229186	*ADAM1*	0.33	false	-	>0.20
ENSG00000142784	*WDTC1*	0.34	false	-	>0.20
ENSG00000164077	*MON1A*	0.34	false	-	>0.20
ENSG00000124541	*RRP36*	0.35	false	rs16896188	>0.20
ENSG00000202093	*SNORD58C*	0.35	true	-	>0.20
ENSG00000159761	*C16orf86*	0.36	false	-	>0.20
ENSG00000170889	*RPS9*	0.36	false	-	>0.20
ENSG00000143942	*CHAC2*	0.36	true	-	>0.20
ENSG00000130204	*TOMM40*	0.36	true	-	>0.20
ENSG00000162650	*ATXN7L2*	0.36	false	-	>0.20
ENSG00000124920	*C11orf9*	0.36	false	rs198462	>0.20
ENSG00000140259	*MFAP1*	0.37	false	rs2470134	>0.20
ENSG00000001617	*SEMA3F*	0.37	false	-	>0.20
ENSG00000109917	*ZNF259*	0.37	false	-	>0.20
ENSG00000167005	*NUDT21*	0.37	false	rs2587881	>0.20
ENSG00000146540	*C7orf50*	0.39	false	-	>0.20
ENSG00000253792	-	0.39	true	-	>0.20
ENSG00000154839	*SKA1*	0.4	false	-	>0.20
ENSG00000135451	*TROAP*	0.4	false	-	>0.20
ENSG00000246379	-	0.4	false	-	>0.20
ENSG00000181929	*PRKAG1*	0.41	false	rs10875910;rs11614738	>0.20
ENSG00000141736	*ERBB2*	0.41	false	-	>0.20
ENSG00000198417	*MT1F*	0.41	false	rs7189840	>0.20
ENSG00000196155	*PLEKHG4*	0.41	false	-	>0.20
ENSG00000092470	*WDR76*	0.41	true	-	>0.20
ENSG00000166946	*CCNDBP1*	0.42	false	rs11070392	>0.20
ENSG00000168496	*FEN1*	0.42	false	rs174469	>0.20
ENSG00000110063	*DCPS*	0.43	false	rs638433	>0.20
ENSG00000149761	*NUDT22*	0.43	false	rs660442	>0.20
ENSG00000254235	-	0.43	false	-	>0.20
ENSG00000159720	*ATP6V0D1*	0.44	false	rs13338993	>0.20
ENSG00000030066	*NUP160*	0.44	true	rs6485788	>0.20
ENSG00000124733	*MEA1*	0.47	false	rs9381225	>0.20
ENSG00000143106	*PSMA5*	0.49	false	-	>0.20
ENSG00000137822	*TUBGCP4*	0.5	true	rs12899865	>0.20
ENSG00000118518	*RNF146*	0.5	true	rs10457487	>0.20
ENSG00000165916	*PSMC3*	0.5	false	rs17726706	>0.20
ENSG00000140848	*CPNE2*	0.51	true	-	>0.20
ENSG00000166595	*FAM96B*	0.51	false	-	>0.20
ENSG00000255507	-	0.51	false	-	>0.20
ENSG00000127603	*MACF1*	0.53	true	rs645061;rs6700698	>0.20
ENSG00000142751	*GPN2*	0.55	false	-	>0.20
ENSG00000111300	*NAA25*	0.55	false	rs16941724	>0.20
ENSG00000146374	*RSPO3*	0.56	true	-	>0.20
ENSG00000087263	*OGFOD1*	0.56	false	rs12447295;rs2301234	>0.20
ENSG00000137842	*TMEM62*	0.56	false	rs999047	>0.20
ENSG00000070915	*SLC12A3*	0.57	true	-	>0.20
ENSG00000179195	*ZNF664*	0.57	false	-	>0.20
ENSG00000159723	*AGRP*	0.57	false	-	>0.20

ENSG00000167264	*DUS2L*	0.57	false	rs6499163	>0.20
ENSG00000110514	*MADD*	0.59	false	rs11570115;rs11570115	>0.20
ENSG00000179523	-	0.6	true	-	>0.20
ENSG00000112651	*MRPL2*	0.6	false	rs9471970	>0.20
ENSG00000141741	*MIEN1*	0.6	false	-	>0.20
ENSG00000123444	*KBTBD4*	0.61	false	rs2305280	>0.20
ENSG00000172824	*CES4A*	0.61	false	-	>0.20
ENSG00000182810	*DDX28*	0.63	false	-	>0.20
ENSG00000123352	*SPATS2*	0.64	true	-	>0.20
ENSG00000090020	*SLC9A1*	0.64	false	rs12751422	>0.20
ENSG00000140853	*NLRC5*	0.64	true	-	>0.20
ENSG00000183763	*TRAIP*	0.65	false	-	>0.20
ENSG00000124900	*SPRYD5*	0.65	false	-	>0.20
ENSG00000068912	*ERLEC1*	0.67	false	-	>0.20
ENSG00000141627	*DYM*	0.67	true	rs2156250	>0.20
ENSG00000166762	*CATSPER2*	0.68	false	-	>0.20
ENSG00000164078	*MST1R*	0.69	false	-	>0.20
ENSG00000103061	*SLC7A6OS*	0.7	false	-	>0.20
ENSG00000181296	-	0.7	false	-	>0.20
ENSG00000254093	*PINX1*	0.71	false	-	>0.20
ENSG00000197653	*DNAH10*	0.71	false	-	>0.20
ENSG00000102878	*HSF4*	0.72	false	rs11639620	>0.20
ENSG00000168676	*KCTD19*	0.72	true	-	>0.20
ENSG00000164850	*GPER*	0.72	false	rs10262070	>0.20
ENSG00000173486	*FKBP2*	0.73	false	rs604203;rs11231684	>0.20
ENSG00000172671	*ANUBL1*	0.73	false	rs2610479	>0.20
ENSG00000174957	*OR5J2*	0.73	true	-	>0.20
ENSG00000184939	*ZFP90*	0.73	false	rs1182968	>0.20
ENSG00000213619	*NDUFS3*	0.75	false	-	>0.20
ENSG00000131096	*PYY*	0.75	false	rs1642592	>0.20
ENSG00000175707	*C1orf172*	0.75	false	-	>0.20
ENSG00000104613	*INTS10*	0.76	true	-	>0.20
ENSG00000067369	*TP53BP1*	0.76	false	-	>0.20
ENSG00000159753	*RLTPR*	0.77	true	-	>0.20
ENSG00000164512	*ANKRD55*	0.77	true	rs10065637;rs10065637	>0.20
ENSG00000236519	-	0.78	false	-	>0.20
ENSG00000255103	*KIAA0754*	0.78	false	-	>0.20
ENSG00000179912	*R3HDM2*	0.79	true	-	>0.20
ENSG00000132600	*PRMT7*	0.8	false	-	>0.20
ENSG00000122483	*CCDC18*	0.82	false	rs2433279	>0.20
ENSG00000198933	*TBKBP1*	0.82	false	rs8075566	>0.20
ENSG00000173264	*GPR137*	0.82	false	rs2244625	>0.20
ENSG00000157895	*C12orf43*	0.83	false	rs2259816;rs2071190	>0.20
ENSG00000128881	*TTBK2*	0.83	false	-	>0.20
ENSG00000186501	*TMEM222*	0.83	false	-	>0.20
ENSG00000158246	*FAM46B*	0.84	false	-	>0.20
ENSG00000135436	*FAM186B*	0.84	false	-	>0.20
ENSG00000176387	*HSD11B2*	0.85	false	-	>0.20
ENSG00000244405	*ETV5*	0.85	true	-	>0.20
ENSG00000141098	*GFOD2*	0.86	false	rs12927959	>0.20

ENSG00000002330	*BAD*	0.86	false	rs487811;rs3741404	>0.20
ENSG00000112655	*PTK7*	0.86	false	-	>0.20
ENSG00000167550	*RHEBL1*	0.87	false	-	>0.20
ENSG00000152359	*POC5*	0.87	true	rs888788	>0.20
ENSG00000134183	*GNAT2*	0.87	false	rs10127988	>0.20
ENSG00000240021	*C1orf49*	0.88	true	-	>0.20
ENSG00000141349	*G6PC3*	0.88	false	rs850856	>0.20
ENSG00000167257	*RNF214*	0.88	true	-	>0.20
ENSG00000231256	*C17orf105*	0.89	true	-	>0.20
ENSG00000241544	-	0.89	true	-	>0.20
ENSG00000165917	*RAPSN*	0.9	false	-	>0.20
ENSG00000174151	*CYB561D1*	0.9	false	-	>0.20
ENSG00000231204	-	0.9	true	-	>0.20
ENSG00000134574	*DDB2*	0.91	false	rs3758674	>0.20
ENSG00000168701	*TMEM208*	0.91	false	-	>0.20
ENSG00000183682	*BMP8A*	0.91	false	-	>0.20
ENSG00000188763	*FZD9*	0.92	false	-	>0.20
ENSG00000247867	-	0.92	false	-	>0.20
ENSG00000167383	*ZNF229*	0.92	true	-	>0.20
ENSG00000168803	*ADAL*	0.92	false	rs7176849	>0.20
ENSG00000125124	*BBS2*	0.92	true	rs4556786	>0.20
ENSG00000175213	*ZNF408*	0.93	false	-	>0.20
ENSG00000141096	*DPEP3*	0.93	true	rs255052	>0.20
ENSG00000213406	*ANXA2P1*	0.94	true	-	>0.20
ENSG00000124074	*C16orf48*	0.94	false	-	>0.20
ENSG00000196123	*KIAA0895L*	0.94	false	-	>0.20
ENSG00000161179	*YDJC*	0.94	true	-	>0.20
ENSG00000134030	*CTIF*	0.94	false	rs299738	>0.20
ENSG00000253695	-	0.94	false	-	>0.20
ENSG00000168806	*LCMT2*	0.94	false	rs3742970	>0.20
ENSG00000010310	*GIPR*	0.95	true	-	>0.20
ENSG00000091947	*TMEM101*	0.95	false	rs16940462	>0.20
ENSG00000237172	*B3GNT9*	0.95	false	-	>0.20
ENSG00000198270	*TMEM116*	0.95	false	rs7295294	>0.20
ENSG00000161647	*MPP3*	0.95	false	-	>0.20
ENSG00000119242	*CCDC92*	0.95	true	rs3768	>0.20
ENSG00000223745	-	0.96	true	-	>0.20
ENSG00000135406	*PRPH*	0.96	false	-	>0.20
ENSG00000172361	*CCDC11*	0.96	false	rs3862691	>0.20
ENSG00000156097	*GPR61*	0.96	false	-	>0.20
ENSG00000173064	*C12orf51*	0.96	false	-	>0.20
ENSG00000235070	-	0.96	true	-	>0.20
ENSG00000177576	*C18orf32*	0.96	false	-	>0.20
ENSG00000159714	*ZDHHC1*	0.96	false	rs8047159	>0.20
ENSG00000108984	*MAP2K6*	0.97	true	rs16974282	>0.20
ENSG00000256116	-	0.97	false	-	>0.20
ENSG00000104447	*TRPS1*	0.97	true	-	>0.20
ENSG00000073067	*CYP2W1*	0.97	false	-	>0.20
ENSG00000149743	*TRPT1*	0.98	false	rs4672	>0.20
ENSG00000159708	*LRRC36*	0.98	true	-	>0.20

ENSG00000178397	*C7orf70*	0.98	false	-	>0.20
ENSG00000102904	*TSNAXIP1*	0.98	false	-	>0.20
ENSG00000125122	*LRRC29*	0.98	false	rs6499119	>0.20
ENSG00000131771	*PPP1R1B*	0.98	false	rs879606	>0.20
ENSG00000134569	*LRP4*	0.98	false	-	>0.20
ENSG00000143126	*CELSR2*	0.98	false	-	>0.20
ENSG00000112499	*SLC22A2*	0.99	false	rs316019;rs10945646	>0.20
ENSG00000127419	*TMEM175*	0.99	true	rs6599389	>0.20
ENSG00000167552	*TUBA1A*	0.99	false	-	>0.20
ENSG00000166603	*MC4R*	0.99	true	-	>0.20
ENSG00000140939	*NOL3*	0.99	false	rs12920590	>0.20
ENSG00000174595	*KLF14*	0.99	true	-	>0.20
ENSG00000135519	*KCNH3*	0.99	false	rs11830144	>0.20
ENSG00000166734	*CASC4*	0.99	false	-	>0.20
ENSG00000159495	*TGM7*	1	false	-	>0.20
ENSG00000167306	*MYO5B*	1	true	rs12604221	>0.20
ENSG00000167825	*OR5I1*	1	false	-	>0.20
ENSG00000149179	*C11orf49*	1	false	rs4494268	>0.20
ENSG00000103056	*SMPD3*	1	false	rs7190307;rs11075686	>0.20
ENSG00000109654	*TRIM2*	1	false	rs13130577	>0.20
ENSG00000171532	*NEUROD2*	1	false	-	>0.20
ENSG00000104055	*TGM5*	1	false	-	>0.20
ENSG00000256746	-	1	false	-	>0.20
ENSG00000111249	*CUX2*	1	false	-	>0.20
ENSG00000182109	-	1	false	-	>0.20
ENSG00000103494	*RPGRIP1L*	1	true	-	>0.20
ENSG00000205030	*OR5L2*	1	false	-	>0.20
ENSG00000253368	*TRNP1*	1	false	-	>0.20
ENSG00000164076	*CAMKV*	1	false	rs11130240	>0.20
ENSG00000234608	*C12orf47*	1	false	-	>0.20
ENSG00000087258	*GNAO1*	1	true	-	>0.20
ENSG00000242866	*STRC*	1	false	-	>0.20
ENSG00000135740	*SLC9A5*	1	false	-	>0.20
ENSG00000226334	-	1	true	-	>0.20
ENSG00000161180	*CCDC116*	1	false	-	>0.20
ENSG00000172247	*C1QTNF4*	1	true	rs7927771	>0.20
ENSG00000058866	*DGKG*	1	false	rs13098259	>0.20
ENSG00000231964	-	1	true	-	>0.20
ENSG00000102981	*PARD6A*	1	false	rs8051587	>0.20
ENSG00000108852	*MPP2*	1	false	-	>0.20
ENSG00000166963	*MAP1A*	1	false	rs2927085	>0.20
ENSG00000181754	*AMIGO1*	1	true	-	>0.20
ENSG00000126500	*FLRT1*	1	false	-	>0.20

Web Table 13: DEPICT Gene prioritization results for the genome-wide significant (2 DF Joint F

Locus	Number of genes in locus	Chromosome and position	GWAS P-value
rs10957054	2	chr8:59323823-59412795	1.76E-30
rs4299376;rs11887534;rs72796745;rs7	2	chr2:44039611-44105605	2.48E-89
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs61941660	1	chr12:125261606-125367214	4.91E-19
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs10176901	1	chr2:169779448-169887832	7.71E-15
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs4299376;rs11887534;rs72796745;rs7	2	chr2:44039611-44105605	2.48E-89
rs1748197;rs4915624	4	chr1:62901968-63176365	3.42E-65
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs11826999;rs180327;rs3135506;rs126	4	chr11:116618886-116663136	2.59E-24
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs2278426;rs56965685	3	chr19:11309973-11437672	2.75E-23
rs55809639	3	chr2:118673054-118943962	4.68E-16
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs75542613	2	chr11:116683920-116694022	2.94E-11
rs7904973	5	chr10:124591665-124757029	1.93E-15
rs11591147;rs499883;rs66679331;rs12	3	chr1:55505221-55683124	3.06E-176
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs4714640	4	chr6:42896938-42980080	2.14E-11
rs662138;rs146203232;rs7750288;rs81	2	chr6:160390131-160579750	3.44E-33
rs8178824	3	chr17:63631656-64801114	1.98E-15
rs183785	1	chr15:58702768-58861151	6.69E-117
rs174554;rs11605884	4	chr11:61520114-61647626	2.85E-54
rs2642438	1	chr1:220960101-220987735	1.54E-22
rs202211262;rs199987224;rs3733907;r	5	chr5:74323289-74896969	0.00E+00
rs486142	1	chr1:234782035-234818922	3.78E-36
rs10066168;rs6866758;rs4704830	3	chr5:156346293-156569880	0.00E+00
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs174554;rs11605884	4	chr11:61520114-61647626	2.85E-54
rs13108218	1	chr4:3443614-3451211	7.82E-10
rs78620068;rs581411;rs934197;rs6547	3	chr2:21059531-21784185	1.60E-249
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs117261169;rs112757114;rs19957987	3	chr19:45445495-45541452	1.97E-126
rs71025174;rs10995527	3	chr10:64893050-65384883	5.40E-108

rs75542613	2	chr11:116683920-116694022	2.94E-11
rs201837204;rs3842409;rs41290120;rs	6	chr19:45281126-45422606	0.00E+00
rs41279633	1	chr7:44552134-44580914	3.70E-23
rs3735810	2	chr8:11653082-11726957	0.00E+00
rs3178166;rs754366	5	chr19:45582530-45685057	2.37E-22
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs4714640	4	chr6:42896938-42980080	2.14E-11
rs9438905;rs76583011	5	chr1:25568740-25826700	9.29E-21
rs9438905;rs76583011	5	chr1:25568740-25826700	9.29E-21
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs13254811	1	chr8:18248755-18258728	3.50E-51
rs67163745	4	chr22:21903736-21998587	3.91E-10
rs3735810	2	chr8:11653082-11726957	0.00E+00
rs1129555	1	chr10:113909624-113975135	1.32E-15
rs11172147	2	chr12:57643392-57845842	0.00E+00
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs535644	6	chr11:126071993-126215644	4.92E-10
rs73006914	3	chr19:19101697-19223704	1.28E-15
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs535644	6	chr11:126071993-126215644	4.92E-10
rs117753190;rs740516	2	chr17:66970629-67138015	3.24E-33
rs1800961	1	chr20:42984340-43060030	1.94E-12
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs12412743	1	chr10:114043493-114064793	3.38E-08
rs138909879	1	chr16:56965748-56977793	1.68E-17
rs76970536	1	chr11:126225535-126310239	3.79E-26
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs72786786;rs5882;rs7499892	1	chr16:56995762-57017757	3.77E-30
rs2244608	3	chr12:121416346-121477045	1.86E-28
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs2088126	6	chr17:37820440-37903545	1.59E-13
rs8088929;rs1970696	1	chr18:47088427-47119278	6.36E-12
rs201837204;rs3842409;rs41290120;rs	6	chr19:45281126-45422606	0.00E+00
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs79966050	2	chr13:32889611-33007091	3.99E-14
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs11826999;rs180327;rs3135506;rs126	4	chr11:116618886-116663136	2.59E-24
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs9931987	28	chr16:67679030-68482591	1.93E-13

rs4714640	4	chr6:42896938-42980080	2.14E-11
rs2487039;rs2575876	1	chr9:107543283-107690518	2.24E-28
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs117261169;rs112757114;rs19957987	3	chr19:45445495-45541452	1.97E-126
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs217381	3	chr7:44605016-44748665	2.41E-38
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs117753190;rs740516	2	chr17:66970629-67138015	3.24E-33
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs201837204;rs3842409;rs41290120;rs	6	chr19:45281126-45422606	0.00E+00
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs2721953;rs148079817;rs1180631	2	chr8:116420724-117337297	7.94E-18
rs535644	6	chr11:126071993-126215644	4.92E-10
rs9411395	1	chr9:136197552-136203235	2.22E-24
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs535644	6	chr11:126071993-126215644	4.92E-10
rs201837204;rs3842409;rs41290120;rs	6	chr19:45281126-45422606	0.00E+00
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs2272021;rs59451830;rs2965156;rs14	2	chr19:45147098-45187631	8.37E-39
rs2278426;rs56965685	3	chr19:11309973-11437672	2.75E-23
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs907866	1	chr2:20400558-20425194	6.06E-12
rs202211262;rs199987224;rs3733907;r	5	chr5:74323289-74896969	0.00E+00
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs13210143	1	chr6:116262693-116381921	2.58E-15
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs11653305	1	chr17:76374735-76420635	4.58E-10
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs8100140	1	chr19:19312224-19314220	6.35E-13
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25

rs11826999;rs180327;rs3135506;rs126	4	chr11:116618886-116663136	2.59E-24
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs10647267	1	chr2:20883803-21022882	2.95E-08
rs535644	6	chr11:126071993-126215644	4.92E-10
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs73006914	3	chr19:19101697-19223704	1.28E-15
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs3178166;rs754366	5	chr19:45582530-45685057	2.37E-22
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs217381	3	chr7:44605016-44748665	2.41E-38
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs1531517;rs2965169;rs11671175;rs55	1	chr19:45250962-45263301	0.00E+00
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs10410204	1	chr19:7112266-7294011	4.66E-47
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs2088126	6	chr17:37820440-37903545	1.59E-13
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2088126	6	chr17:37820440-37903545	1.59E-13
rs62375245	1	chr5:132387654-132442141	4.79E-08
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2244608	3	chr12:121416346-121477045	1.86E-28
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs11870935	4	chr17:45400656-45789427	4.83E-24
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs11826999;rs180327;rs3135506;rs126	4	chr11:116618886-116663136	2.59E-24
rs117261169;rs112757114;rs19957987	3	chr19:45445495-45541452	1.97E-126
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs201445483	3	chr2:17720393-17981509	4.68E-09
rs202211262;rs199987224;rs3733907;r	5	chr5:74323289-74896969	0.00E+00
rs11591147;rs499883;rs66679331;rs12	3	chr1:55505221-55683124	3.06E-176
rs11711419	2	chr3:12598513-12705725	6.04E-12

rs1128249	1	chr2:165510134-165700189	5.50E-17
rs535644	6	chr11:126071993-126215644	4.92E-10
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs11711419	2	chr3:12598513-12705725	6.04E-12
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs11870935	4	chr17:45400656-45789427	4.83E-24
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs1748197;rs4915624	4	chr1:62901968-63176365	3.42E-65
rs201837204;rs3842409;rs41290120;rs	6	chr19:45281126-45422606	0.00E+00
rs7904973	5	chr10:124591665-124757029	1.93E-15
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs117860853	2	chr8:19261672-19709594	1.76E-14
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs3178166;rs754366	5	chr19:45582530-45685057	2.37E-22
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs9438905;rs76583011	5	chr1:25568740-25826700	9.29E-21
rs4841133;rs7012637;rs1461728	1	chr8:9106927-9271224	8.26E-50
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs185539847	1	chr16:56764037-56878862	3.14E-08
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs181765708	1	chr19:45854246-45873876	1.90E-38
rs6029182;rs6029125	1	chr20:39314488-39317880	1.72E-27
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs4722551;rs4719841	1	chr7:26191860-26226745	2.22E-18
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs7717355;rs258496	1	chr5:74969949-75013313	7.32E-20
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs3178166;rs754366	5	chr19:45582530-45685057	2.37E-22
rs2244608	3	chr12:121416346-121477045	1.86E-28
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs360804;rs10206947	5	chr2:62817390-64054977	5.59E-19
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs4418728;rs7068500	1	chr10:94590935-94819250	6.29E-11
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs55809639	3	chr2:118673054-118943962	4.68E-16
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs67163745	4	chr22:21903736-21998587	3.91E-10
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs10832961	2	chr11:18621334-18656338	1.01E-12
rs7124958	28	chr11:46698630-48192393	5.33E-39

rs9931987	28	chr16:67679030-68482591	1.93E-13
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs10066168;rs6866758;rs4704830	3	chr5:156346293-156569880	0.00E+00
rs10957054	2	chr8:59323823-59412795	1.76E-30
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs11870935	4	chr17:45400656-45789427	4.83E-24
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs2272021;rs59451830;rs2965156;rs14	2	chr19:45147098-45187631	8.37E-39
rs2088126	6	chr17:37820440-37903545	1.59E-13
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs1748197;rs4915624	4	chr1:62901968-63176365	3.42E-65
rs2328223;rs1535027	1	chr20:17949556-17971765	2.67E-85
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs1748197;rs4915624	4	chr1:62901968-63176365	3.42E-65
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs9438905;rs76583011	5	chr1:25568740-25826700	9.29E-21
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs79966050	2	chr13:32889611-33007091	3.99E-14
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs200885498	1	chr20:39652845-39653034	5.21E-12
rs7904973	5	chr10:124591665-124757029	1.93E-15
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs71025174;rs10995527	3	chr10:64893050-65384883	5.40E-108
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2911971	1	chr8:6565878-6617184	7.50E-11
rs67163745	4	chr22:21903736-21998587	3.91E-10
rs11810184;rs180683317	1	chr1:63249806-63339980	6.22E-14
rs66476925	1	chr7:21582833-21941457	5.43E-27
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs202211262;rs199987224;rs3733907;r	5	chr5:74323289-74896969	0.00E+00
rs217381	3	chr7:44605016-44748665	2.41E-38
rs71025174;rs10995527	3	chr10:64893050-65384883	5.40E-108
rs4714640	4	chr6:42896938-42980080	2.14E-11
rs9720869;rs12674939;rs7012891;rs11	1	chr8:126442563-126450647	2.22E-162
rs662138;rs146203232;rs7750288;rs81	2	chr6:160390131-160579750	3.44E-33
rs1482852	1	chr3:156799630-156806336	3.00E-25
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs174554;rs11605884	4	chr11:61520114-61647626	2.85E-54
rs2927075	14	chr15:43568479-44487450	9.91E-214

rs31223	1	chr5:156569944-156682201	1.33E-13
rs2278426;rs56965685	3	chr19:11309973-11437672	2.75E-23
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs144439590;rs74747585;rs2722741;rs	7	chr19:44645710-45004574	2.80E-28
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs202211262;rs199987224;rs3733907;r	5	chr5:74323289-74896969	0.00E+00
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs78620068;rs581411;rs934197;rs6547	3	chr2:21059531-21784185	1.60E-249
rs7904973	5	chr10:124591665-124757029	1.93E-15
rs174554;rs11605884	4	chr11:61520114-61647626	2.85E-54
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs11591147;rs499883;rs66679331;rs12	3	chr1:55505221-55683124	3.06E-176
rs73006914	3	chr19:19101697-19223704	1.28E-15
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs55809639	3	chr2:118673054-118943962	4.68E-16
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs10832961	2	chr11:18621334-18656338	1.01E-12
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs201445483	3	chr2:17720393-17981509	4.68E-09
rs360804;rs10206947	5	chr2:62817390-64054977	5.59E-19
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs2088126	6	chr17:37820440-37903545	1.59E-13
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs67546252	1	chr9:78505560-78977255	4.14E-10
rs2283619	1	chr19:19287712-19303400	1.16E-20
rs360804;rs10206947	5	chr2:62817390-64054977	5.59E-19
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69

rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs2088126	6	chr17:37820440-37903545	1.59E-13
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs7904973	5	chr10:124591665-124757029	1.93E-15
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs201837204;rs3842409;rs41290120;rs	6	chr19:45281126-45422606	0.00E+00
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs588918;rs10160754	7	chr11:116700422-117103241	0.00E+00
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2235215;rs2142675	1	chr6:16129356-16148479	1.35E-30
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs17286411;rs3794695;rs77303550;rs9	11	chr16:71660089-72210777	1.10E-69
rs78620068;rs581411;rs934197;rs6547	3	chr2:21059531-21784185	1.60E-249
rs6573778	1	chr14:24867992-24888494	6.02E-21
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs13284665	9	chr9:131464802-131680318	3.33E-10
rs41280463	2	chr4:154073494-154260472	1.54E-08
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs117860853	2	chr8:19261672-19709594	1.76E-14
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs1260326;rs1948922;rs10865493;rs78	23	chr2:27505260-28561768	1.60E-25
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs10066168;rs6866758;rs4704830	3	chr5:156346293-156569880	0.00E+00
rs77231091	1	chr17:67410838-67538451	4.12E-10
rs8178824	3	chr17:63631656-64801114	1.98E-15
rs9496567	1	chr6:100367786-100442114	8.66E-11
rs5014650;rs3120137;rs186696265;rs9	7	chr6:160592093-161551917	1.56E-178
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs360804;rs10206947	5	chr2:62817390-64054977	5.59E-19
rs4804573;rs379309;rs143020224;rs65	16	chr19:10623419-11308243	0.00E+00
rs7310615;rs10735077	16	chr12:111471828-112947717	1.77E-12
rs201445483	3	chr2:17720393-17981509	4.68E-09
rs1584063	1	chr3:12045862-12232907	7.38E-14
rs9931987	28	chr16:67679030-68482591	1.93E-13
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs360804;rs10206947	5	chr2:62817390-64054977	5.59E-19
rs9438905;rs76583011	5	chr1:25568740-25826700	9.29E-21
rs79598313	15	chr1:27022524-27701315	2.12E-17
rs2927075	14	chr15:43568479-44487450	9.91E-214
rs35866622	8	chr19:49141328-49261580	2.68E-30
rs11172147	2	chr12:57643392-57845842	0.00E+00
rs2050058;rs6129820;rs6129753;rs346	8	chr20:39657458-40247133	4.07E-46
rs67163745	4	chr22:21903736-21998587	3.91E-10
rs3178166;rs754366	5	chr19:45582530-45685057	2.37E-22
rs79598313	15	chr1:27022524-27701315	2.12E-17

rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs35434910	1	chr9:136080664-136084630	1.02E-33
rs41280463	2	chr4:154073494-154260472	1.54E-08
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs11870935	4	chr17:45400656-45789427	4.83E-24
rs1337247;rs7528419;rs41279716;rs49	18	chr1:109656301-110306649	0.00E+00
rs56204645	1	chr8:55471729-55682531	3.00E-20
rs2304128;rs2905431	13	chr19:19322782-19791761	0.00E+00
rs8178824	3	chr17:63631656-64801114	1.98E-15
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs495828;rs114820734	1	chr9:136131053-136150617	9.84E-115
rs2721953;rs148079817;rs1180631	2	chr8:116420724-117337297	7.94E-18
rs7124958	28	chr11:46698630-48192393	5.33E-39
rs2927075	14	chr15:43568479-44487450	9.91E-214

› < 5e-8) loci for LDL-cholesterol.

Ensembl gene ID	Gene symbol	Nominal P value	Gene closest to lead SNP	Top cis eQTL SNP (Westra et al. Nature Genetics 2014)	False discovery rate
ENSG00000167910	*CYP7A1*	3.58E-14	false	rs12678010	**<=0.01**
ENSG00000143921	*ABCG8*	1.51E-12	true	-	**<=0.01**
ENSG00000171097	*CCBL1*	2.35E-12	false	rs2259043	**<=0.01**
ENSG00000073060	*SCARB1*	1.12E-11	true	rs7954697	**<=0.01**
ENSG00000171174	*RBKS*	1.61E-11	false	-	**<=0.01**
ENSG00000073734	*ABCB11*	1.69E-11	true	rs487756	**<=0.01**
ENSG00000141086	*CTRL*	5.22E-11	false	-	**<=0.01**
ENSG00000138075	*ABCG5*	2.11E-10	false	-	**<=0.01**
ENSG00000132855	*ANGPTL3*	2.89E-10	true	rs7528963	**<=0.01**
ENSG00000102967	*DHODH*	6.38E-10	true	rs251033	**<=0.01**
ENSG00000084734	*GCKR*	1.04E-09	true	-	**<=0.01**
ENSG00000180210	*F2*	1.52E-09	false	-	**<=0.01**
ENSG00000257017	*HP*	2.31E-09	true	-	**<=0.01**
ENSG00000223522	-	3.11E-09	true	-	**<=0.01**
ENSG00000122194	*PLG*	3.17E-09	true	rs9365237	**<=0.01**
ENSG00000110243	*APOA5*	4.27E-09	true	-	**<=0.01**
ENSG00000198670	*LPA*	4.42E-09	true	-	**<=0.01**
ENSG00000130173	*C19orf80*	6.58E-09	true	rs12610693	**<=0.01**
ENSG00000125629	*INSIG2*	6.95E-09	true	rs17047750	**<=0.01**
ENSG00000234945	-	1.13E-08	false	-	**<=0.01**
ENSG00000236267	-	1.21E-08	true	-	**<=0.01**
ENSG00000138161	*CUZD1*	1.30E-08	false	-	**<=0.01**
ENSG00000169174	*PCSK9*	1.71E-08	true	-	**<=0.01**
ENSG00000110245	*APOC3*	2.16E-08	false	-	**<=0.01**
ENSG00000124713	*GNMT*	5.04E-08	true	-	**<=0.01**
ENSG00000175003	*SLC22A1*	6.73E-08	true	rs2297372;rs662301	**<=0.01**
ENSG00000091583	*APOH*	9.22E-08	true	-	**<=0.01**
ENSG00000166035	*LIPC*	9.52E-08	true	rs12911658	**<=0.01**
ENSG00000134824	*FADS2*	1.07E-07	true	rs968567	**<=0.01**
ENSG00000186205	*MOSC1*	1.13E-07	true	rs11118598	**<=0.01**
ENSG00000113161	*HMGCR*	1.29E-07	true	rs6453133	**<=0.01**
ENSG00000228044	-	1.63E-07	true	-	**<=0.01**
ENSG00000145850	*TIMD4*	2.32E-07	true	-	**<=0.01**
ENSG00000118137	*APOA1*	2.37E-07	false	-	**<=0.01**
ENSG00000149485	*FADS1*	2.50E-07	true	rs968567	**<=0.01**
ENSG00000109758	*HGFAC*	3.14E-07	true	-	**<=0.01**
ENSG00000084674	*APOB*	3.73E-07	true	-	**<=0.01**
ENSG00000160446	*ZDHHC12*	4.71E-07	false	rs2997922	**<=0.01**
ENSG00000213398	*LCAT*	8.66E-07	false	rs255049	**<=0.01**
ENSG00000111271	*ACAD10*	1.11E-06	false	rs634389	**<=0.01**
ENSG00000168765	*GSTM4*	1.14E-06	true	rs1010167;rs1010167	**<=0.01**
ENSG00000025434	*NR1H3*	1.27E-06	false	rs3758673	**<=0.01**
ENSG00000224916	*APOC4*	1.41E-06	false	-	**<=0.01**
ENSG00000148572	*NRBF2*	1.42E-06	false	-	**<=0.01**

ENSG00000110244	*APOA4*	1.43E-06	false	-	**<=0.01**
ENSG00000130208	*APOC1*	1.47E-06	true	-	**<=0.01**
ENSG00000015520	*NPC1L1*	1.74E-06	true	-	**<=0.01**
ENSG00000079459	*FDFT1*	1.86E-06	false	rs1293320;rs1534862	**<=0.01**
ENSG00000007255	*TRAPPC6A*	2.71E-06	false	rs1005451	**<=0.01**
ENSG00000103066	*PLA2G15*	4.21E-06	false	rs7672	**<=0.01**
ENSG00000124587	*PEX6*	4.43E-06	false	rs2296805	**<=0.01**
ENSG00000187010	*RHD*	4.54E-06	false	rs909832	**<=0.01**
ENSG00000188672	*RHCE*	5.63E-06	false	-	**<=0.01**
ENSG00000213996	*TM6SF2*	5.68E-06	false	-	**<=0.01**
ENSG00000110536	*PTPMT1*	5.95E-06	false	-	**<=0.01**
ENSG00000131910	*NR0B2*	6.89E-06	false	-	**<=0.01**
ENSG00000156006	*NAT2*	7.63E-06	true	rs11203964	**<=0.01**
ENSG00000128228	*SDF2L1*	9.40E-06	false	rs2599423	**<=0.01**
ENSG00000164733	*CTSB*	9.51E-06	true	rs1299525;rs7013950	**<=0.01**
ENSG00000119927	*GPAM*	1.02E-05	true	rs1926559	**<=0.01**
ENSG00000175189	*INHBC*	1.33E-05	false	-	**<=0.01**
ENSG00000060642	*PIGV*	1.53E-05	false	rs12742115	**<=0.01**
ENSG00000111275	*ALDH2*	1.60E-05	false	rs16941669	**<=0.01**
ENSG00000110074	*FOXRED1*	1.87E-05	false	rs587891	**<=0.01**
ENSG00000181035	*SLC25A42*	2.28E-05	false	rs7250622;rs10417974	**<=0.01**
ENSG00000213071	*LPAL2*	2.68E-05	true	rs415317	**<=0.01**
ENSG00000099203	*TMED1*	3.21E-05	true	rs3786724	**<=0.01**
ENSG00000182934	*SRPR*	3.55E-05	false	rs512577	**<=0.01**
ENSG00000154262	*ABCA6*	4.65E-05	true	rs1443263	**<=0.01**
ENSG00000101076	*HNF4A*	7.08E-05	false	rs17828482	**<=0.01**
ENSG00000109919	*MTCH2*	7.68E-05	false	rs2242081	**<=0.01**
ENSG00000119913	*TECTB*	9.42E-05	true	rs10509961	**<=0.01**
ENSG00000051108	*HERPUD1*	9.57E-05	true	rs8044753;rs8044753	**<=0.01**
ENSG00000110080	*ST3GAL4*	1.01E-04	true	rs529328	**<=0.01**
ENSG00000167136	*ENDOG*	1.59E-04	false	rs3115874	**<=0.01**
ENSG00000142748	*FCN3*	1.91E-04	false	-	**<=0.01**
ENSG00000165923	*AGBL2*	2.20E-04	false	-	**<=0.01**
ENSG00000167261	*DPEP2*	2.35E-04	false	rs2285912	**<=0.01**
ENSG00000134575	*ACP2*	2.71E-04	false	rs4752973	**<=0.01**
ENSG00000159792	*PSKH1*	2.84E-04	false	-	**<=0.01**
ENSG00000087237	*CETP*	2.93E-04	true	rs1167742;rs1684575	**<=0.01**
ENSG00000135100	*HNF1A*	2.97E-04	true	-	**<=0.01**
ENSG00000130164	*LDLR*	3.21E-04	true	rs12459603	**<=0.01**
ENSG00000141738	*GRB7*	4.13E-04	false	rs14050	**<=0.01**
ENSG00000101670	*LIPG*	6.19E-04	true	-	**<=0.01**
ENSG00000142273	*CBLC*	6.40E-04	true	-	**<=0.01**
ENSG00000167264	*DUS2L*	8.47E-04	false	rs6499163	**<=0.01**
ENSG00000139597	*N4BP2L1*	8.54E-04	true	rs8002690	**<=0.01**
ENSG00000158019	*BRE*	8.88E-04	false	rs2002406	**<=0.01**
ENSG00000109917	*ZNF259*	1.49E-03	false	-	**<=0.01**
ENSG00000105726	*ATP13A1*	2.20E-03	false	rs2304130	**<0.05**
ENSG00000149182	*ARFGAP2*	2.59E-03	false	rs4647709	**<0.05**
ENSG00000166762	*CATSPER2*	2.71E-03	true	-	**<0.05**
ENSG00000182810	*DDX28*	2.82E-03	false	-	**<0.05**

ENSG00000137161	*CNPY3*	3.02E-03	false	-	**<0.05**
ENSG00000165029	*ABCA1*	3.42E-03	false	rs2472495	**<0.05**
ENSG00000131115	*ZNF227*	3.59E-03	false	-	**<0.05**
ENSG00000104853	*CLPTM1*	4.80E-03	true	rs10409727	**<0.05**
ENSG00000105550	*FGF21*	5.57E-03	false	-	**<0.05**
ENSG00000103067	*ESRP2*	5.99E-03	true	-	**<0.05**
ENSG00000142733	*MAP3K6*	6.68E-03	false	rs17340684	**<0.05**
ENSG00000111300	*NAA25*	7.11E-03	false	rs16941724	**<0.05**
ENSG00000136271	*DDX56*	7.93E-03	true	rs217372	**<0.05**
ENSG00000146477	*SLC22A3*	8.29E-03	true	rs316024	**<0.05**
ENSG00000154258	*ABCA9*	8.69E-03	true	-	**<0.05**
ENSG00000167004	*PDIA3*	9.15E-03	false	-	**<0.05**
ENSG00000130203	*APOE*	0.01	false	-	**<0.05**
ENSG00000142751	*GPN2*	0.01	false	-	**<0.05**
ENSG00000249917	-	0.01	false	-	**<0.05**
ENSG00000110063	*DCPS*	0.01	false	rs638433	**<0.05**
ENSG00000148296	*SURF6*	0.01	true	rs3739890	<0.20
ENSG00000129347	*KRI1*	0.01	false	-	<0.20
ENSG00000165526	*RPUSD4*	0.01	false	rs612592	<0.20
ENSG00000130204	*TOMM40*	0.02	true	-	<0.20
ENSG00000143106	*PSMA5*	0.02	false	-	<0.20
ENSG00000115211	*EIF2B4*	0.02	false	rs1260345;rs7602534	<0.20
ENSG00000167380	*ZNF226*	0.02	false	-	<0.20
ENSG00000256731	-	0.02	false	-	<0.20
ENSG00000073008	*PVR*	0.02	true	-	<0.20
ENSG00000130167	*TSPAN16*	0.02	false	rs7417	<0.20
ENSG00000205220	*PSMB10*	0.02	false	rs3785100	<0.20
ENSG00000089022	*MAPKAPK5*	0.02	false	rs12580246;rs12426312	<0.20
ENSG00000115884	*SDC1*	0.02	true	-	<0.20
ENSG00000176928	*GCNT4*	0.02	true	-	<0.20
ENSG00000141096	*DPEP3*	0.02	false	rs255052	<0.20
ENSG00000229186	*ADAM1*	0.02	false	-	<0.20
ENSG00000132793	*LPIN3*	0.03	true	rs6072412	<0.20
ENSG00000111816	*FRK*	0.03	true	-	<0.20
ENSG00000175793	*SFN*	0.03	false	-	<0.20
ENSG00000127616	*SMARCA4*	0.03	true	rs12232780	<0.20
ENSG00000129933	*MAU2*	0.03	false	rs2301668	<0.20
ENSG00000087157	*PGS1*	0.03	true	rs4969170	<0.20
ENSG00000168803	*ADAL*	0.03	false	rs7176849	<0.20
ENSG00000103061	*SLC7A6OS*	0.04	false	-	<0.20
ENSG00000072736	*NFATC3*	0.04	false	rs12598;rs1125333;rs4783630;rs	<0.20
ENSG00000140829	*DHX38*	0.04	false	rs2240243	<0.20
ENSG00000089234	*BRAP*	0.04	false	-	<0.20
ENSG00000115207	*GTF3C2*	0.04	false	-	<0.20
ENSG00000184162	*NR2C2AP*	0.04	true	-	<0.20
ENSG00000031698	*SARS*	0.04	true	rs2477363	<0.20
ENSG00000109920	*FNBP4*	0.04	false	rs4539273	<0.20
ENSG00000140259	*MFAP1*	0.05	false	rs2470134	<0.20
ENSG00000213339	*QTRT1*	0.05	true	-	<0.20
ENSG00000157992	*KRTCAP3*	0.05	false	-	<0.20

ENSG00000226645	-	0.05	false	-	<0.20
ENSG00000198522	*GPN1*	0.05	false	-	<0.20
ENSG00000129351	*ILF3*	0.05	false	rs4804519;rs2043305	<0.20
ENSG00000118961	*C2orf43*	0.05	true	rs10182643	<0.20
ENSG00000150455	*TIRAP*	0.05	false	rs588361;rs3104589	<0.20
ENSG00000141098	*GFOD2*	0.06	false	rs12927959	<0.20
ENSG00000105705	*SUGP1*	0.06	false	-	<0.20
ENSG00000165912	*PACSIN3*	0.06	false	-	<0.20
ENSG00000105538	*RASIP1*	0.06	false	rs281377	<0.20
ENSG00000213619	*NDUFS3*	0.06	false	-	<0.20
ENSG00000198917	*C9orf114*	0.06	false	-	<0.20
ENSG00000141084	*RANBP10*	0.06	false	rs16942887	<0.20
ENSG00000105676	*ARMC6*	0.07	false	rs4808171	<0.20
ENSG00000140265	*ZSCAN29*	0.07	false	-	<0.20
ENSG00000140830	*TXNL4B*	0.08	true	rs10492814	<0.20
ENSG00000142252	*GEMIN7*	0.09	false	rs12978931	>0.20
ENSG00000182149	*IST1*	0.09	true	-	>0.20
ENSG00000102898	*NUTF2*	0.09	false	-	>0.20
ENSG00000158604	*TMED4*	0.09	false	rs217373	>0.20
ENSG00000149577	*SIDT2*	0.09	false	rs4938353	>0.20
ENSG00000069399	*BCL3*	0.09	true	rs846897	>0.20
ENSG00000198900	*TOP1*	0.09	false	rs8121001;rs2207309	>0.20
ENSG00000186501	*TMEM222*	0.1	false	-	>0.20
ENSG00000171105	*INSR*	0.1	true	rs459883	>0.20
ENSG00000166747	*AP1G1*	0.1	false	rs17356316	>0.20
ENSG00000119760	*SUPT7L*	0.1	true	-	>0.20
ENSG00000161395	*PGAP3*	0.1	false	-	>0.20
ENSG00000134571	*MYBPC3*	0.11	true	rs7105851	>0.20
ENSG00000141744	*PNMT*	0.11	false	-	>0.20
ENSG00000170606	*HSPA4*	0.11	false	rs4705986;rs7702889	>0.20
ENSG00000038358	*EDC4*	0.11	false	rs7191129	>0.20
ENSG00000165916	*PSMC3*	0.12	false	rs17726706	>0.20
ENSG00000135114	*OASL*	0.12	false	rs2259693;rs2259693	>0.20
ENSG00000130733	*YIPF2*	0.12	false	rs11085749	>0.20
ENSG00000132600	*PRMT7*	0.12	false	-	>0.20
ENSG00000108424	*KPNB1*	0.13	true	-	>0.20
ENSG00000137822	*TUBGCP4*	0.13	false	rs12899865	>0.20
ENSG00000102977	*ACD*	0.14	false	rs12927959	>0.20
ENSG00000137656	*BUD13*	0.14	true	rs1145187	>0.20
ENSG00000104856	*RELB*	0.14	true	-	>0.20
ENSG00000243943	*ZNF512*	0.14	false	-	>0.20
ENSG00000167491	*GATAD2A*	0.15	true	rs6909;rs7259773	>0.20
ENSG00000085511	*MAP3K4*	0.15	false	rs1488	>0.20
ENSG00000102904	*TSNAXIP1*	0.15	false	-	>0.20
ENSG00000143028	*SYPL2*	0.15	false	-	>0.20
ENSG00000065135	*GNAI3*	0.15	false	rs12033376	>0.20
ENSG00000163029	*SMC6*	0.15	false	-	>0.20
ENSG00000113163	*COL4A3BP*	0.16	false	rs6896136	>0.20
ENSG00000162402	*USP24*	0.16	true	-	>0.20
ENSG00000075975	*MKRN2*	0.16	false	rs11710163	>0.20

ENSG00000082438	*COBLL1*	0.16	false	rs1840326	>0.20
ENSG00000197798	*FAM118B*	0.16	true	-	>0.20
ENSG00000168781	*PPIP5K1*	0.17	false	-	>0.20
ENSG00000132155	*RAF1*	0.17	true	rs2442807	>0.20
ENSG00000030066	*NUP160*	0.18	false	rs6485788	>0.20
ENSG00000178852	*C17orf57*	0.19	false	-	>0.20
ENSG00000115216	*NRBP1*	0.19	false	rs11684134	>0.20
ENSG00000235545	-	0.19	true	-	>0.20
ENSG00000130202	*PVRL2*	0.19	true	rs11879589;rs11672399	>0.20
ENSG00000119965	*C10orf88*	0.19	false	-	>0.20
ENSG00000062370	*ZNF285*	0.2	true	-	>0.20
ENSG00000104613	*INTS10*	0.2	false	-	>0.20
ENSG00000064547	*LPAR2*	0.2	true	rs880090	>0.20
ENSG00000189114	*BLOC1S3*	0.2	false	-	>0.20
ENSG00000115226	*FNDC4*	0.21	false	-	>0.20
ENSG00000117616	*C1orf63*	0.21	false	rs592372;rs630931	>0.20
ENSG00000254235	-	0.21	false	-	>0.20
ENSG00000115241	*PPM1G*	0.21	false	-	>0.20
ENSG00000103064	*SLC7A6*	0.22	false	rs11644360;rs3785111	>0.20
ENSG00000163795	*ZNF513*	0.22	false	-	>0.20
ENSG00000118557	*PMFBP1*	0.22	true	-	>0.20
ENSG00000102900	*NUP93*	0.22	true	rs12918087	>0.20
ENSG00000198758	*EPS8L3*	0.22	false	rs11102006	>0.20
ENSG00000115234	*SNX17*	0.23	false	rs3739095	>0.20
ENSG00000179295	*PTPN11*	0.23	false	-	>0.20
ENSG00000089248	*ERP29*	0.23	false	rs7970397;rs7310545	>0.20
ENSG00000104884	*ERCC2*	0.23	true	-	>0.20
ENSG00000204103	*MAFB*	0.24	true	rs2902941	>0.20
ENSG00000232493	*RPL12P11*	0.24	false	-	>0.20
ENSG00000050344	*NFE2L3*	0.24	true	-	>0.20
ENSG00000134201	*GSTM5*	0.24	false	-	>0.20
ENSG00000152359	*POC5*	0.25	true	rs888788	>0.20
ENSG00000079805	*DNM2*	0.26	true	-	>0.20
ENSG00000179846	*NKPD1*	0.27	true	-	>0.20
ENSG00000157895	*C12orf43*	0.27	false	rs2259816;rs2071190	>0.20
ENSG00000168806	*LCMT2*	0.27	false	rs3742970	>0.20
ENSG00000226622	-	0.28	false	-	>0.20
ENSG00000181896	*ZNF101*	0.28	false	rs247775	>0.20
ENSG00000138190	*EXOC6*	0.28	false	rs2148361	>0.20
ENSG00000134183	*GNAT2*	0.29	false	rs10127988	>0.20
ENSG00000125633	*CCDC93*	0.29	false	rs17819632	>0.20
ENSG00000167383	*ZNF229*	0.29	true	-	>0.20
ENSG00000135148	*TRAFD1*	0.3	false	rs10492014	>0.20
ENSG00000116337	*AMPD2*	0.3	false	-	>0.20
ENSG00000168286	*THAP11*	0.3	false	-	>0.20
ENSG00000185651	*UBE2L3*	0.3	false	-	>0.20
ENSG00000204842	*ATXN2*	0.3	false	rs3809278	>0.20
ENSG00000142453	*CARM1*	0.32	false	rs11670365	>0.20
ENSG00000179119	*SPTY2D1*	0.32	true	-	>0.20
ENSG00000175213	*ZNF408*	0.32	false	-	>0.20

ENSG00000124074	*C16orf48*	0.34	false	-	>0.20
ENSG00000176920	*FUT2*	0.35	false	-	>0.20
ENSG00000135077	*HAVCR2*	0.35	false	rs2033475	>0.20
ENSG00000215114	*UBXN2B*	0.36	true	-	>0.20
ENSG00000117713	*ARID1A*	0.36	false	rs12752833	>0.20
ENSG00000175216	*CKAP5*	0.36	false	-	>0.20
ENSG00000124067	*SLC12A4*	0.36	false	-	>0.20
ENSG00000141279	*NPEPPS*	0.37	false	rs16956009	>0.20
ENSG00000243147	*MRPL33*	0.38	false	-	>0.20
ENSG00000186567	*CEACAM19*	0.38	true	-	>0.20
ENSG00000141741	*MIEN1*	0.38	true	-	>0.20
ENSG00000115204	*MPV17*	0.39	false	rs1275510	>0.20
ENSG00000162607	*USP1*	0.39	false	rs1168089	>0.20
ENSG00000125871	*C20orf72*	0.39	true	rs8120495	>0.20
ENSG00000102901	*CENPT*	0.41	false	-	>0.20
ENSG00000067369	*TP53BP1*	0.41	false	-	>0.20
ENSG00000066336	*SPI1*	0.41	false	rs1057233;rs326217	>0.20
ENSG00000116641	*DOCK7*	0.42	false	rs11207957	>0.20
ENSG00000175220	*ARHGAP1*	0.44	false	rs2070852	>0.20
ENSG00000138002	*IFT172*	0.45	false	-	>0.20
ENSG00000149187	*CELF1*	0.45	false	rs12419692;rs10838708	>0.20
ENSG00000204178	*TMEM57*	0.45	true	rs2986161	>0.20
ENSG00000159761	*C16orf86*	0.45	false	-	>0.20
ENSG00000139618	*BRCA2*	0.45	false	rs1081796	>0.20
ENSG00000223478	-	0.46	false	-	>0.20
ENSG00000222612	-	0.48	true	-	>0.20
ENSG00000203795	*FAM24A*	0.49	false	-	>0.20
ENSG00000167384	*ZNF180*	0.5	true	-	>0.20
ENSG00000159917	*ZNF235*	0.51	false	rs2125579	>0.20
ENSG00000171988	*JMJD1C*	0.52	true	-	>0.20
ENSG00000123444	*KBTBD4*	0.53	false	rs2305280	>0.20
ENSG00000155189	*AGPAT5*	0.53	true	rs2980679	>0.20
ENSG00000161179	*YDJC*	0.54	true	-	>0.20
ENSG00000125703	*ATG4C*	0.55	true	-	>0.20
ENSG00000105877	*DNAH11*	0.56	true	-	>0.20
ENSG00000187664	*HAPLN4*	0.57	false	-	>0.20
ENSG00000182264	*IZUMO1*	0.58	false	-	>0.20
ENSG00000134574	*DDB2*	0.59	false	rs3758674	>0.20
ENSG00000122008	*POLK*	0.59	true	-	>0.20
ENSG00000105953	*OGDH*	0.61	false	rs10951768;rs10951768	>0.20
ENSG00000165476	*REEP3*	0.63	false	rs7076601	>0.20
ENSG00000112640	*PPP2R5D*	0.67	false	rs6458318;rs6903229	>0.20
ENSG00000173334	*TRIB1*	0.67	true	rs4360309	>0.20
ENSG00000197081	*IGF2R*	0.69	true	rs3798209	>0.20
ENSG00000241544	-	0.69	true	-	>0.20
ENSG00000040199	*PHLPP2*	0.7	false	-	>0.20
ENSG00000162650	*ATXN7L2*	0.7	false	-	>0.20
ENSG00000142765	*SYTL1*	0.71	false	rs3813795	>0.20
ENSG00000168496	*FEN1*	0.71	false	rs174469	>0.20
ENSG00000092470	*WDR76*	0.71	false	-	>0.20

ENSG00000113263	*ITK*	0.71	false	rs6876898	>0.20
ENSG00000130158	*DOCK6*	0.71	true	rs317915	>0.20
ENSG00000124177	*CHD6*	0.71	true	-	>0.20
ENSG00000174951	*FUT1*	0.72	false	rs281377	>0.20
ENSG00000159495	*TGM7*	0.73	false	-	>0.20
ENSG00000168092	*PAFAH1B2*	0.73	false	-	>0.20
ENSG00000159915	*ZNF233*	0.73	false	-	>0.20
ENSG00000111252	*SH2B3*	0.73	true	rs2239195	>0.20
ENSG00000165915	*SLC39A13*	0.76	false	-	>0.20
ENSG00000171877	*FRMD5*	0.77	false	-	>0.20
ENSG00000130734	*ATG4D*	0.77	false	-	>0.20
ENSG00000160584	*SIK3*	0.78	true	-	>0.20
ENSG00000224470	*ATXN1L*	0.78	false	-	>0.20
ENSG00000134222	*PSRC1*	0.78	true	-	>0.20
ENSG00000145700	*ANKRD31*	0.79	true	-	>0.20
ENSG00000136802	*LRRC8A*	0.8	false	rs7854319	>0.20
ENSG00000236436	-	0.8	true	-	>0.20
ENSG00000213185	*FAM24B*	0.8	false	rs12251443	>0.20
ENSG00000124920	*C11orf9*	0.81	false	rs198462	>0.20
ENSG00000160445	*ZER1*	0.82	true	rs2259043	>0.20
ENSG00000244861	-	0.82	true	-	>0.20
ENSG00000064607	*SUGP2*	0.82	true	rs8106146	>0.20
ENSG00000149177	*PTPRJ*	0.83	false	rs17198607	>0.20
ENSG00000176909	*MAMSTR*	0.83	true	-	>0.20
ENSG00000089639	*GMIP*	0.84	false	rs1476459	>0.20
ENSG00000138100	*TRIM54*	0.84	false	rs780090	>0.20
ENSG00000160613	*PCSK7*	0.84	false	rs7107152	>0.20
ENSG00000226856	-	0.85	false	-	>0.20
ENSG00000142444	*C19orf52*	0.85	false	rs11085752	>0.20
ENSG00000221843	*C2orf16*	0.85	false	-	>0.20
ENSG00000197256	*KANK2*	0.86	true	rs17616620	>0.20
ENSG00000204160	*ZDHHC18*	0.86	false	rs17162315	>0.20
ENSG00000107021	*TBC1D13*	0.87	false	rs1572912	>0.20
ENSG00000142784	*WDTC1*	0.88	false	-	>0.20
ENSG00000102981	*PARD6A*	0.88	false	rs8051587	>0.20
ENSG00000247595	-	0.89	false	-	>0.20
ENSG00000198324	*FAM109A*	0.89	false	rs2239195	>0.20
ENSG00000178295	*GEN1*	0.89	true	-	>0.20
ENSG00000115504	*EHBP1*	0.9	true	-	>0.20
ENSG00000175707	*C1orf172*	0.9	true	-	>0.20
ENSG00000173991	*TCAP*	0.9	false	-	>0.20
ENSG00000178093	*TSSK6*	0.91	false	-	>0.20
ENSG00000174151	*CYB561D1*	0.92	true	-	>0.20
ENSG00000156097	*GPR61*	0.92	false	-	>0.20
ENSG00000134202	*GSTM3*	0.92	true	-	>0.20
ENSG00000163794	*UCN*	0.93	false	-	>0.20
ENSG00000099139	*PCSK5*	0.93	true	rs7850358	>0.20
ENSG00000254901	*MEF2BNB*	0.93	false	-	>0.20
ENSG00000143951	*WDPCP*	0.95	false	-	>0.20
ENSG00000140832	*MARVELD3*	0.95	false	-	>0.20

ENSG00000124181	*PLCG1*	0.95	true	rs6093416	>0.20
ENSG00000141736	*ERBB2*	0.95	false	-	>0.20
ENSG00000111249	*CUX2*	0.96	false	-	>0.20
ENSG00000198270	*TMEM116*	0.96	true	rs7295294	>0.20
ENSG00000149179	*C11orf49*	0.96	false	rs4494268	>0.20
ENSG00000179988	*PSTK*	0.96	true	rs7902802	>0.20
ENSG00000159753	*RLTPR*	0.97	false	-	>0.20
ENSG00000134243	*SORT1*	0.97	true	rs10494041	>0.20
ENSG00000187244	*BCAM*	0.97	true	rs203713	>0.20
ENSG00000234608	*C12orf47*	0.97	false	-	>0.20
ENSG00000149591	*TAGLN*	0.98	false	rs10790177;rs1871757;rs710715	>0.20
ENSG00000226648	-	0.98	false	-	>0.20
ENSG00000110514	*MADD*	0.98	false	rs11570115;rs11570115	>0.20
ENSG00000007944	*MYLIP*	0.98	true	rs2021900	>0.20
ENSG00000158246	*FAM46B*	0.98	false	-	>0.20
ENSG00000102984	*ZNF821*	0.99	false	-	>0.20
ENSG00000231204	-	0.99	true	-	>0.20
ENSG00000205978	*NYNRIN*	0.99	true	-	>0.20
ENSG00000174306	*ZHX3*	0.99	true	rs1000410	>0.20
ENSG00000160447	*PKN3*	0.99	false	rs9697210	>0.20
ENSG00000213406	*ANXA2P1*	0.99	true	-	>0.20
ENSG00000232871	-	0.99	false	-	>0.20
ENSG00000147408	*CSGALNACT1*	0.99	false	rs4481612	>0.20
ENSG00000129355	*CDKN2D*	0.99	false	rs3745249;rs12720356	>0.20
ENSG00000176714	*CCDC121*	0.99	false	-	>0.20
ENSG00000129354	*AP1M2*	0.99	false	rs4371270	>0.20
ENSG00000113249	*HAVCR1*	0.99	true	-	>0.20
ENSG00000108984	*MAP2K6*	0.99	true	rs16974282	>0.20
ENSG00000154240	*CEP112*	0.99	false	-	>0.20
ENSG00000152034	*MCHR2*	0.99	true	-	>0.20
ENSG00000112499	*SLC22A2*	0.99	false	rs316019;rs10945646	>0.20
ENSG00000160161	*CILP2*	0.99	false	-	>0.20
ENSG00000129353	*SLC44A2*	1	true	rs892078	>0.20
ENSG00000242412	*DBIL5P2*	1	true	-	>0.20
ENSG00000180739	*S1PR5*	1	false	rs7251213	>0.20
ENSG00000173064	*C12orf51*	1	false	-	>0.20
ENSG00000163032	*VSNL1*	1	false	rs4832399	>0.20
ENSG00000157152	*SYN2*	1	false	rs310758	>0.20
ENSG00000103056	*SMPD3*	1	false	rs7190307;rs11075686	>0.20
ENSG00000165917	*RAPSN*	1	false	-	>0.20
ENSG00000115507	*OTX1*	1	false	rs17407696	>0.20
ENSG00000183726	*TMEM50A*	1	false	rs1293259	>0.20
ENSG00000090020	*SLC9A1*	1	false	rs12751422	>0.20
ENSG00000242866	*STRC*	1	false	-	>0.20
ENSG00000142233	*NTN5*	1	false	-	>0.20
ENSG00000179912	*R3HDM2*	1	false	-	>0.20
ENSG00000183798	*EMILIN3*	1	false	-	>0.20
ENSG00000161180	*CCDC116*	1	false	-	>0.20
ENSG00000104866	*PPP1R37*	1	true	-	>0.20
ENSG00000253368	*TRNP1*	1	false	-	>0.20

ENSG00000130287	*NCAN*	1	false	-	>0.20
ENSG00000171102	*OBP2B*	1	false	-	>0.20
ENSG00000109654	*TRIM2*	1	false	rs13130577	>0.20
ENSG00000116299	*KIAA1324*	1	false	rs565751	>0.20
ENSG00000134569	*LRP4*	1	false	-	>0.20
ENSG00000143126	*CELSR2*	1	true	-	>0.20
ENSG00000198933	*TBKBP1*	1	false	rs8075566	>0.20
ENSG00000181754	*AMIGO1*	1	true	-	>0.20
ENSG00000104237	*RP1*	1	true	rs16920316	>0.20
ENSG00000105717	*PBX4*	1	false	rs12611058	>0.20
ENSG00000154229	*PRKCA*	1	false	rs12938937	>0.20
ENSG00000172247	*C1QTNF4*	1	false	rs7927771	>0.20
ENSG00000175164	*ABO*	1	true	rs9411463	>0.20
ENSG00000104447	*TRPS1*	1	true	-	>0.20
ENSG00000256746	-	1	false	-	>0.20
ENSG00000166963	*MAP1A*	1	false	rs2927085	>0.20

Web Table 14: DEPICT Gene prioritization results for the genome-wide significant (2 DF Joint F

Locus	Number of genes in locus	Chromosome and position	GWAS P-value
rs3124784;rs73014164;rs41272086	5	chr6:160769300-161174338	1.37E-14
rs79624003;rs66579735;rs56127649	6	chr7:72742167-73038873	9.03E-203
rs7350481;rs3135506;rs61905084;rs62	4	chr11:116618886-116663136	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs116843064;rs34833485	2	chr19:8429011-8469313	2.00E-23
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs12445401;rs12925078	6	chr16:71919136-72210777	1.08E-13
rs3124784;rs73014164;rs41272086	5	chr6:160769300-161174338	1.37E-14
rs12460346	2	chr19:45445495-45496598	2.13E-09
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs4495740;rs4915624;rs72929768	4	chr1:62901968-63176365	3.02E-130
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs1077835;rs261291;rs56903760;rs756	1	chr15:58702768-58861151	4.29E-76
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs2278426	2	chr19:11309973-11373157	1.85E-12
rs13108218	1	chr4:3443614-3451211	7.76E-29
rs75627662;rs484195;rs283810;rs1166	4	chr19:45349393-45422606	3.85E-157
rs10787429;rs4573621	2	chr10:113909624-114064793	1.82E-13
rs1090107;rs4320509	4	chr8:11534468-11696818	2.20E-13
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs2281721	1	chr1:230193536-230417870	9.97E-35
rs8103840	6	chr19:49199228-49261580	6.07E-13
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs2678379;rs6547409;rs7608123;rs344	1	chr2:21224301-21266945	1.33E-82
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs8103840	6	chr19:49199228-49261580	6.07E-13
rs2642439	1	chr1:220960101-220987735	2.03E-10
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs6882345	2	chr5:156346293-156486130	9.97E-29
rs1580180	4	chr8:59323823-59572403	1.57E-10
rs3124784;rs73014164;rs41272086	5	chr6:160769300-161174338	1.37E-14
rs174566	4	chr11:61520114-61647626	4.65E-68
rs247616;rs289713;rs289719	1	chr16:56995762-57017757	5.24E-33
rs2749008	1	chr6:52656462-52668708	8.98E-14
rs61352607	2	chr12:57643392-57845842	3.86E-14
rs174566	4	chr11:61520114-61647626	4.65E-68
rs112201728	2	chr6:160390131-160579750	2.62E-13
rs1495743;rs13257339	1	chr8:18248755-18258728	3.08E-29

rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs1711171	4	chr3:135684515-136471220	1.29E-14
rs11967262	1	chr6:43737921-43754224	5.99E-34
rs3124784;rs73014164;rs41272086	5	chr6:160769300-161174338	1.37E-14
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs8103728	1	chr19:33877855-34012799	5.71E-09
rs2575876	1	chr9:107543283-107690518	7.22E-11
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs75627662;rs484195;rs283810;rs1166	4	chr19:45349393-45422606	3.85E-157
rs74637035	1	chr11:116683920-116684719	1.38E-34
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs9687832	1	chr5:56111401-56191979	9.39E-17
rs71171277	1	chr19:45147098-45169429	4.03E-24
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4820325	3	chr22:38480896-38612518	7.63E-15
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs287;rs263;rs6999158;rs117604010;rs	1	chr8:19759228-19824770	0.00E+00
rs6995541	3	chr8:10581278-10704011	1.89E-09
rs2278426	2	chr19:11309973-11373157	1.85E-12
rs12460346	2	chr19:45445495-45496598	2.13E-09
rs2896635	1	chr11:13298199-13408813	4.22E-15
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs4804411	1	chr19:7112266-7294011	7.96E-12
rs60695258;rs7698284;4:88226868	2	chr4:87856154-88141760	4.68E-36
rs75627662;rs484195;rs283810;rs1166	4	chr19:45349393-45422606	3.85E-157
rs1090107;rs4320509	4	chr8:11534468-11696818	2.20E-13
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs2954021;rs6470361;rs62521034;rs72	1	chr8:126442563-126450647	9.35E-179
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs907866	1	chr2:20400558-20425194	1.39E-15
rs10761716;rs10740138;10:65114437	3	chr10:64893050-65384883	1.93E-29
19:49109712	2	chr19:49055429-49116694	9.56E-09
rs6073958;rs435306	3	chr20:44527399-44600833	8.02E-44
rs12445401;rs12925078	6	chr16:71919136-72210777	1.08E-13
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs10787429;rs4573621	2	chr10:113909624-114064793	1.82E-13
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs10761716;rs10740138;10:65114437	3	chr10:64893050-65384883	1.93E-29
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35

rs6029604	5	chr20:39657458-39989222	1.06E-08
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs4820325	3	chr22:38480896-38612518	7.63E-15
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs12445401;rs12925078	6	chr16:71919136-72210777	1.08E-13
rs6073958;rs435306	3	chr20:44527399-44600833	8.02E-44
rs2967767	3	chr19:8554941-8642461	7.16E-14
rs7350481;rs3135506;rs61905084;rs62	4	chr11:116618886-116663136	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs13389219	1	chr2:165510134-165700189	3.16E-19
rs56226803	4	chr17:45400656-45789427	7.76E-10
rs1111336	1	chr2:28680012-28866654	3.02E-13
rs3124784;rs73014164;rs41272086	5	chr6:160769300-161174338	1.37E-14
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs2908522	1	chr6:139693393-139695757	2.23E-26
rs2967767	3	chr19:8554941-8642461	7.16E-14
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs10761716;rs10740138;10:65114437	3	chr10:64893050-65384883	1.93E-29
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs7350481;rs3135506;rs61905084;rs62	4	chr11:116618886-116663136	0.00E+00
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs112201728	2	chr6:160390131-160579750	2.62E-13
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs4841132;rs7012814	1	chr8:9106927-9271224	1.89E-15
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs116843064;rs34833485	2	chr19:8429011-8469313	2.00E-23
rs62129551	1	chr2:26915558-26956288	1.21E-14
rs4495740;rs4915624;rs72929768	4	chr1:62901968-63176365	3.02E-130
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs7140110	1	chr13:114523524-114567046	3.38E-12
rs6073958;rs435306	3	chr20:44527399-44600833	8.02E-44
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs9491696;rs4580892	1	chr6:127439749-127518910	4.72E-31
rs1711171	4	chr3:135684515-136471220	1.29E-14
rs4820325	3	chr22:38480896-38612518	7.63E-15
rs174566	4	chr11:61520114-61647626	4.65E-68
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs79624003;rs66579735;rs56127649	6	chr7:72742167-73038873	9.03E-203

rs6995541	3	chr8:10581278-10704011	1.89E-09
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs12445401;rs12925078	6	chr16:71919136-72210777	1.08E-13
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4418728;rs7068500	1	chr10:94590935-94819250	7.15E-27
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs2967767	3	chr19:8554941-8642461	7.16E-14
rs6029604	5	chr20:39657458-39989222	1.06E-08
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs2292642	1	chr17:76374735-76420635	1.78E-10
rs12445401;rs12925078	6	chr16:71919136-72210777	1.08E-13
rs56226803	4	chr17:45400656-45789427	7.76E-10
rs2963472	1	chr5:157600609-157603430	1.80E-11
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs1580180	4	chr8:59323823-59572403	1.57E-10
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs4722551;rs4719841	1	chr7:26191860-26226745	4.36E-12
rs1711171	4	chr3:135684515-136471220	1.29E-14
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs79624003;rs66579735;rs56127649	6	chr7:72742167-73038873	9.03E-203
rs56076449	1	chr5:132387654-132442141	3.16E-11
rs56226803	4	chr17:45400656-45789427	7.76E-10
rs6995541	3	chr8:10581278-10704011	1.89E-09
rs75627662;rs484195;rs283810;rs1166	4	chr19:45349393-45422606	3.85E-157
rs8103840	6	chr19:49199228-49261580	6.07E-13
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs7350481;rs3135506;rs61905084;rs62	4	chr11:116618886-116663136	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs256903	1	chr5:55395507-55529186	1.02E-17
rs6029604	5	chr20:39657458-39989222	1.06E-08
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs2921097	1	chr8:8175258-8244008	6.83E-12
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs1090107;rs4320509	4	chr8:11534468-11696818	2.20E-13
rs4495740;rs4915624;rs72929768	4	chr1:62901968-63176365	3.02E-130
rs2925979	1	chr16:81478775-81745367	4.77E-21

rs79624003;rs66579735;rs56127649	6	chr7:72742167-73038873	9.03E-203
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs7966192;rs825453	3	chr12:124247042-124499974	4.41E-17
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs1711171	4	chr3:135684515-136471220	1.29E-14
rs1580180	4	chr8:59323823-59572403	1.57E-10
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs61352607	2	chr12:57643392-57845842	3.86E-14
rs1580180	4	chr8:59323823-59572403	1.57E-10
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs8103840	6	chr19:49199228-49261580	6.07E-13
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs1090107;rs4320509	4	chr8:11534468-11696818	2.20E-13
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs56164803;rs142342247	1	chr8:19674651-19709594	3.98E-31
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs79624003;rs66579735;rs56127649	6	chr7:72742167-73038873	9.03E-203
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs4921675;rs2006476	1	chr8:19261672-19615540	2.72E-25
rs56226803	4	chr17:45400656-45789427	7.76E-10
rs60695258;rs7698284;4:88226868	2	chr4:87856154-88141760	4.68E-36
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs4495740;rs4915624;rs72929768	4	chr1:62901968-63176365	3.02E-130
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs2854117;rs7946390;rs7943608;rs236	8	chr11:116691419-117103241	9.89E-106
rs77198935	1	chr2:20883803-21022882	1.67E-09
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs116987336	2	chr11:117156402-117283984	7.88E-50
rs7661844	2	chr4:86936276-87736324	6.90E-14
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs12445401;rs12925078	6	chr16:71919136-72210777	1.08E-13
rs174566	4	chr11:61520114-61647626	4.65E-68
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs7966192;rs825453	3	chr12:124247042-124499974	4.41E-17
rs116987336	2	chr11:117156402-117283984	7.88E-50
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28

rs1913657	1	chr2:227044760-227050087	9.20E-24
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs79624003;rs66579735;rs56127649	6	chr7:72742167-73038873	9.03E-203
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs6029604	5	chr20:39657458-39989222	1.06E-08
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs8103840	6	chr19:49199228-49261580	6.07E-13
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs7807870	1	chr7:73082155-73086442	7.30E-15
rs6029604	5	chr20:39657458-39989222	1.06E-08
19:49109712	2	chr19:49055429-49116694	9.56E-09
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs8103840	6	chr19:49199228-49261580	6.07E-13
rs12129919;rs180683317	1	chr1:63249806-63339980	1.84E-27
rs550057	1	chr9:136131053-136150617	1.12E-09
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs7966192;rs825453	3	chr12:124247042-124499974	4.41E-17
rs6063050	1	chr20:45523263-45817492	2.93E-08
rs6974288	1	chr7:130417401-130418888	5.74E-25
rs34311866	1	chr4:926175-952444	1.45E-11
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs58542926;rs7247263	12	chr19:19322782-19774502	2.59E-102
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs34633411	1	chr18:58038564-58040001	4.60E-08
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs6882345	2	chr5:156346293-156486130	9.97E-29
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs7661844	2	chr4:86936276-87736324	6.90E-14
rs3136458;rs7109203	17	chr11:46417964-47374253	1.04E-11
rs56271783	16	chr11:63766030-64089283	3.01E-12
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00
rs190543502;rs138570705;rs14949274	25	chr15:43036550-44955876	9.24E-35
rs77697917;rs1731897	13	chr17:41831103-42201014	6.11E-28
rs4665972;rs62141290;rs2305929;rs62	39	chr2:27070615-28561768	0.00E+00

› < 5e-8) loci for Triglycerides.

Ensembl gene ID	Gene symbol	Nominal P value	Gene closest to lead SNP	Top cis eQTL SNP (Westra et al. Nature Genetics 2014)	False discovery rate
ENSG00000198670	*LPA*	1.02E-10	false	-	**<=0.01**
ENSG00000009950	*MLXIPL*	1.08E-09	false	-	**<=0.01**
ENSG00000110243	*APOA5*	2.64E-09	true	-	**<=0.01**
ENSG00000084734	*GCKR*	3.68E-09	true	-	**<=0.01**
ENSG00000161653	*NAGS*	4.71E-09	false	-	**<=0.01**
ENSG00000167772	*ANGPTL4*	1.05E-08	true	rs11669375	**<=0.01**
ENSG00000180210	*F2*	1.15E-08	true	-	**<=0.01**
ENSG00000257017	*HP*	1.81E-08	true	-	**<=0.01**
ENSG00000122194	*PLG*	3.59E-08	false	rs9365237	**<=0.01**
ENSG00000224916	*APOC4*	6.22E-08	false	-	**<=0.01**
ENSG00000118137	*APOA1*	6.57E-08	true	-	**<=0.01**
ENSG00000132855	*ANGPTL3*	7.36E-08	false	rs7528963	**<=0.01**
ENSG00000138030	*KHK*	9.44E-08	false	rs11680096;rs2011616	**<=0.01**
ENSG00000166035	*LIPC*	1.09E-07	true	rs12911658	**<=0.01**
ENSG00000110245	*APOC3*	1.50E-07	true	-	**<=0.01**
ENSG00000130173	*C19orf80*	1.95E-07	true	rs12610693	**<=0.01**
ENSG00000109758	*HGFAC*	2.09E-07	true	-	**<=0.01**
ENSG00000130208	*APOC1*	4.79E-07	true	-	**<=0.01**
ENSG00000119927	*GPAM*	6.14E-07	true	rs1926559	**<=0.01**
ENSG00000136574	*GATA4*	6.35E-07	true	-	**<=0.01**
ENSG00000223522	-	9.24E-07	true	-	**<=0.01**
ENSG00000143641	*GALNT2*	9.46E-07	true	-	**<=0.01**
ENSG00000105550	*FGF21*	1.12E-06	false	-	**<=0.01**
ENSG00000110244	*APOA4*	1.12E-06	false	-	**<=0.01**
ENSG00000084674	*APOB*	1.28E-06	true	-	**<=0.01**
ENSG00000213996	*TM6SF2*	1.54E-06	true	-	**<=0.01**
ENSG00000138074	*SLC5A6*	1.70E-06	false	-	**<=0.01**
ENSG00000105538	*RASIP1*	2.16E-06	false	rs281377	**<=0.01**
ENSG00000186205	*MOSC1*	2.38E-06	true	rs11118598	**<=0.01**
ENSG00000025434	*NR1H3*	2.67E-06	true	rs3758673	**<=0.01**
ENSG00000145850	*TIMD4*	2.95E-06	true	-	**<=0.01**
ENSG00000167910	*CYP7A1*	3.10E-06	true	rs12678010	**<=0.01**
ENSG00000146477	*SLC22A3*	3.93E-06	false	rs316024	**<=0.01**
ENSG00000134824	*FADS2*	4.21E-06	true	rs968567	**<=0.01**
ENSG00000087237	*CETP*	4.84E-06	true	rs1167742;rs1684575	**<=0.01**
ENSG00000243955	*GSTA1*	6.32E-06	true	-	**<=0.01**
ENSG00000175189	*INHBC*	8.37E-06	false	-	**<=0.01**
ENSG00000149485	*FADS1*	1.46E-05	false	rs968567	**<=0.01**
ENSG00000175003	*SLC22A1*	1.47E-05	true	rs2297372;rs662301	**<=0.01**
ENSG00000156006	*NAT2*	2.16E-05	true	rs11203964	**<=0.01**

ENSG00000161649	*CD300LG*	2.30E-05	false	-	**<=0.01**
ENSG00000149781	*FERMT3*	2.82E-05	false	rs2236648;rs4980525	**<=0.01**
ENSG00000114054	*PCCB*	3.26E-05	true	rs1153877	**<=0.01**
ENSG00000112715	*VEGFA*	5.67E-05	true	rs9472113;rs9472113	**<=0.01**
ENSG00000213071	*LPAL2*	9.66E-05	true	rs415317	**<=0.01**
ENSG00000138073	*PREB*	1.24E-04	false	-	**<=0.01**
ENSG00000124299	*PEPD*	2.10E-04	false	rs3786913	**<=0.01**
ENSG00000165029	*ABCA1*	2.27E-04	false	rs2472495	**<=0.01**
ENSG00000171174	*RBKS*	2.54E-04	true	-	**<=0.01**
ENSG00000130202	*PVRL2*	3.44E-04	true	rs11879589;rs11672399	**<=0.01**
ENSG00000236267	-	3.45E-04	true	-	**<=0.01**
ENSG00000149577	*SIDT2*	4.09E-04	false	rs4938353	**<=0.01**
ENSG00000095015	*MAP3K1*	4.99E-04	true	rs6872807	**<=0.01**
ENSG00000073008	*PVR*	5.10E-04	true	-	**<=0.01**
ENSG00000143994	*ABHD1*	5.19E-04	false	-	**<=0.01**
ENSG00000184381	*PLA2G6*	5.73E-04	false	-	**<=0.01**
ENSG00000138080	*EMILIN1*	7.52E-04	false	-	**<=0.01**
ENSG00000175445	*LPL*	7.90E-04	true	rs11991231	**<=0.01**
ENSG00000171056	*SOX7*	1.06E-03	true	rs10092781;rs7001281	**<=0.01**
ENSG00000130158	*DOCK6*	1.35E-03	false	rs317915	**<=0.01**
ENSG00000104853	*CLPTM1*	1.37E-03	true	rs10409727	**<=0.01**
ENSG00000133794	*ARNTL*	1.57E-03	true	-	**<=0.01**
ENSG00000134575	*ACP2*	1.58E-03	false	rs4752973	**<=0.01**
ENSG00000171105	*INSR*	1.59E-03	true	rs459883	**<=0.01**
ENSG00000172493	*AFF1*	1.83E-03	false	-	**<=0.01**
ENSG00000130203	*APOE*	1.91E-03	true	-	**<=0.01**
ENSG00000079459	*FDFT1*	2.12E-03	false	rs1293320;rs1534862	**<=0.01**
ENSG00000140265	*ZSCAN29*	3.34E-03	false	-	**<0.05**
ENSG00000173334	*TRIB1*	3.59E-03	true	rs4360309	**<0.05**
ENSG00000134571	*MYBPC3*	4.43E-03	false	rs7105851	**<0.05**
ENSG00000115884	*SDC1*	4.68E-03	true	-	**<0.05**
ENSG00000148572	*NRBF2*	4.71E-03	true	-	**<0.05**
ENSG00000088002	*SULT2B1*	5.70E-03	false	rs2665584	**<0.05**
ENSG00000100979	*PLTP*	6.14E-03	true	-	**<0.05**
ENSG00000102967	*DHODH*	7.24E-03	false	rs251033	**<0.05**
ENSG00000157992	*KRTCAP3*	8.04E-03	false	-	**<0.05**
ENSG00000175220	*ARHGAP1*	9.37E-03	false	rs2070852	**<0.05**
ENSG00000138085	*C2orf28*	9.62E-03	false	-	**<0.05**
ENSG00000115226	*FNDC4*	0.01	false	-	**<0.05**
ENSG00000119913	*TECTB*	0.01	false	rs10509961	**<0.05**
ENSG00000133315	*MACROD1*	0.01	false	-	**<0.05**
ENSG00000234945	-	0.01	false	-	**<0.05**
ENSG00000165912	*PACSIN3*	0.01	false	-	**<0.05**
ENSG00000165476	*REEP3*	0.01	true	rs7076601	**<0.05**
ENSG00000167004	*PDIA3*	0.01	false	-	**<0.05**
ENSG00000163795	*ZNF513*	0.02	false	-	**<0.05**
ENSG00000166947	*EPB42*	0.02	false	rs3736054	**<0.05**

ENSG00000198900	*TOP1*	0.02	false	rs8121001;rs2207309	<0.20
ENSG00000110497	*AMBRA1*	0.02	false	-	<0.20
ENSG00000180423	*HARBI1*	0.02	false	-	<0.20
ENSG00000185022	*MAFF*	0.02	true	rs5756968	<0.20
ENSG00000108849	*PPY*	0.02	true	-	<0.20
ENSG00000140829	*DHX38*	0.03	false	rs2240243	<0.20
ENSG00000198026	*ZNF335*	0.03	false	-	<0.20
ENSG00000142347	*MYO1F*	0.03	false	rs2042300	<0.20
ENSG00000226645	-	0.03	false	-	<0.20
ENSG00000115216	*NRBP1*	0.04	false	rs11684134	<0.20
ENSG00000137842	*TMEM62*	0.04	false	rs999047	<0.20
ENSG00000082438	*COBLL1*	0.04	false	rs1840326	<0.20
ENSG00000141279	*NPEPPS*	0.04	false	rs16956009	<0.20
ENSG00000163803	*PLB1*	0.05	true	rs11127152	<0.20
ENSG00000256731	-	0.05	false	-	<0.20
ENSG00000161654	*LSM12*	0.05	false	-	<0.20
ENSG00000167491	*GATAD2A*	0.05	false	rs6909;rs7259773	<0.20
ENSG00000164442	*CITED2*	0.06	true	rs4896477	<0.20
ENSG00000133246	*PRAM1*	0.06	false	-	<0.20
ENSG00000167941	*SOST*	0.07	true	rs1731902	<0.20
ENSG00000171988	*JMJD1C*	0.07	true	-	<0.20
ENSG00000110011	*DNAJC4*	0.08	false	-	<0.20
ENSG00000109917	*ZNF259*	0.08	false	-	<0.20
ENSG00000173511	*VEGFB*	0.08	true	-	>0.20
ENSG00000197081	*IGF2R*	0.08	false	rs3798209	>0.20
ENSG00000149782	*PLCB3*	0.08	false	-	>0.20
ENSG00000254235	-	0.09	false	-	>0.20
ENSG00000173153	*ESRRA*	0.09	false	rs10792436	>0.20
ENSG00000185236	*RAB11B*	0.1	true	-	>0.20
ENSG00000171303	*KCNK3*	0.1	true	-	>0.20
ENSG00000116641	*DOCK7*	0.11	true	rs11207957	>0.20
ENSG00000105726	*ATP13A1*	0.11	false	rs2304130	>0.20
ENSG00000149182	*ARFGAP2*	0.11	false	rs4647709	>0.20
ENSG00000173113	*TRMT112*	0.12	false	-	>0.20
ENSG00000183087	*GAS6*	0.12	true	rs7338868	>0.20
ENSG00000100982	*PCIF1*	0.12	false	rs11086985	>0.20
ENSG00000126432	*PRDX5*	0.12	false	rs7947143;rs7947143	>0.20
ENSG00000160584	*SIK3*	0.12	true	-	>0.20
ENSG00000146374	*RSPO3*	0.13	true	-	>0.20
ENSG00000174579	*MSL2*	0.13	false	-	>0.20
ENSG00000128298	*BAIAP2L2*	0.13	false	-	>0.20
ENSG00000124920	*C11orf9*	0.13	false	rs198462	>0.20
ENSG00000159459	*UBR1*	0.14	false	rs3736054	>0.20
ENSG00000171877	*FRMD5*	0.14	false	-	>0.20
ENSG00000186143	*C2orf53*	0.14	true	-	>0.20
ENSG00000119777	*TMEM214*	0.16	true	rs1275510	>0.20
ENSG00000106638	*TBL2*	0.16	true	rs17145813	>0.20

ENSG00000253695	-	0.18	false	-	>0.20
ENSG00000108861	*DUSP3*	0.18	false	rs1230395	>0.20
ENSG00000182149	*IST1*	0.19	false	-	>0.20
ENSG00000115207	*GTF3C2*	0.19	false	-	>0.20
ENSG00000138190	*EXOC6*	0.2	false	rs2148361	>0.20
ENSG00000168781	*PPIP5K1*	0.2	false	-	>0.20
ENSG00000133250	*ZNF414*	0.2	true	rs2967571	>0.20
ENSG00000132793	*LPIN3*	0.22	false	rs6072412	>0.20
ENSG00000115241	*PPM1G*	0.23	true	-	>0.20
ENSG00000168439	*STIP1*	0.23	false	-	>0.20
ENSG00000087157	*PGS1*	0.24	true	rs4969170	>0.20
ENSG00000118557	*PMFBP1*	0.24	false	-	>0.20
ENSG00000178852	*C17orf57*	0.24	false	-	>0.20
ENSG00000253792	-	0.25	true	-	>0.20
ENSG00000166762	*CATSPER2*	0.25	false	-	>0.20
ENSG00000104131	*EIF3J*	0.27	false	-	>0.20
ENSG00000137575	*SDCBP*	0.27	false	-	>0.20
ENSG00000064547	*LPAR2*	0.27	false	rs880090	>0.20
ENSG00000187664	*HAPLN4*	0.28	false	-	>0.20
ENSG00000149591	*TAGLN*	0.28	true	rs10790177;rs1871757;rs71071	>0.20
ENSG00000050344	*NFE2L3*	0.29	true	-	>0.20
ENSG00000118007	*STAG1*	0.29	false	rs3931416	>0.20
ENSG00000084774	*CAD*	0.3	false	-	>0.20
ENSG00000104133	*SPG11*	0.3	false	-	>0.20
ENSG00000009954	*BAZ1B*	0.32	true	rs17145732	>0.20
ENSG00000170606	*HSPA4*	0.34	false	rs4705986;rs7702889	>0.20
ENSG00000108424	*KPNB1*	0.34	true	-	>0.20
ENSG00000254093	*PINX1*	0.35	false	-	>0.20
ENSG00000130204	*TOMM40*	0.36	true	-	>0.20
ENSG00000174951	*FUT1*	0.37	true	rs281377	>0.20
ENSG00000108840	*HDAC5*	0.38	false	rs1476512	>0.20
ENSG00000137656	*BUD13*	0.39	true	rs1145187	>0.20
ENSG00000168803	*ADAL*	0.39	false	rs7176849	>0.20
ENSG00000129933	*MAU2*	0.4	true	rs2301668	>0.20
ENSG00000164512	*ANKRD55*	0.4	true	rs10065637;rs10065637	>0.20
ENSG00000124181	*PLCG1*	0.42	false	rs6093416	>0.20
ENSG00000159495	*TGM7*	0.42	false	-	>0.20
ENSG00000138100	*TRIM54*	0.42	true	rs780090	>0.20
ENSG00000182319	-	0.45	true	rs867757	>0.20
ENSG00000084693	*AGBL5*	0.45	false	-	>0.20
ENSG00000089639	*GMIP*	0.46	false	rs1476459	>0.20
ENSG00000115211	*EIF2B4*	0.46	true	rs1260345;rs7602534	>0.20
ENSG00000119760	*SUPT7L*	0.46	false	-	>0.20
ENSG00000231256	*C17orf105*	0.46	false	-	>0.20
ENSG00000255394	*C8orf49*	0.47	false	-	>0.20
ENSG00000162607	*USP1*	0.49	true	rs1168089	>0.20
ENSG00000153815	*CMIP*	0.49	true	rs1128432;rs12918867	>0.20

ENSG00000106635	*BCL7B*	0.5	true	rs11974409	>0.20
ENSG00000115234	*SNX17*	0.5	true	rs3739095	>0.20
ENSG00000105705	*SUGP1*	0.51	false	-	>0.20
ENSG00000158019	*BRE*	0.51	false	rs2002406	>0.20
ENSG00000160613	*PCSK7*	0.51	true	rs7107152	>0.20
ENSG00000197653	*DNAH10*	0.52	false	-	>0.20
ENSG00000175224	*ATG13*	0.54	false	-	>0.20
ENSG00000179523	-	0.54	true	-	>0.20
ENSG00000073711	*PPP2R3A*	0.55	false	-	>0.20
ENSG00000215114	*UBXN2B*	0.59	false	-	>0.20
ENSG00000163794	*UCN*	0.61	false	-	>0.20
ENSG00000179912	*R3HDM2*	0.61	false	-	>0.20
ENSG00000035681	*NSMAF*	0.63	false	rs2279460	>0.20
ENSG00000140259	*MFAP1*	0.63	false	rs2470134	>0.20
ENSG00000175216	*CKAP5*	0.63	false	-	>0.20
ENSG00000176920	*FUT2*	0.63	false	-	>0.20
ENSG00000198522	*GPN1*	0.65	false	-	>0.20
ENSG00000243943	*ZNF512*	0.65	false	-	>0.20
ENSG00000166946	*CCNDBP1*	0.67	false	rs11070392	>0.20
ENSG00000154328	*NEIL2*	0.67	true	-	>0.20
ENSG00000138002	*IFT172*	0.67	true	-	>0.20
ENSG00000137770	*CTDSPL2*	0.69	false	-	>0.20
ENSG00000104613	*INTS10*	0.69	true	-	>0.20
ENSG00000137822	*TUBGCP4*	0.69	false	rs12899865	>0.20
ENSG00000188763	*FZD9*	0.7	false	-	>0.20
ENSG00000173486	*FKBP2*	0.7	false	rs604203;rs11231684	>0.20
ENSG00000147408	*CSGALNACT1*	0.7	true	rs4481612	>0.20
ENSG00000198933	*TBKBP1*	0.72	false	rs8075566	>0.20
ENSG00000145332	*KLHL8*	0.73	true	rs13145898;rs10433937	>0.20
ENSG00000178093	*TSSK6*	0.74	false	-	>0.20
ENSG00000235545	-	0.74	true	-	>0.20
ENSG00000141349	*G6PC3*	0.74	false	rs850856	>0.20
ENSG00000115204	*MPV17*	0.75	false	rs1275510	>0.20
ENSG00000168092	*PAFAH1B2*	0.75	true	-	>0.20
ENSG00000118961	*C2orf43*	0.75	true	rs10182643	>0.20
ENSG00000149761	*NUDT22*	0.75	false	rs660442	>0.20
ENSG00000110274	*CEP164*	0.77	true	rs897837	>0.20
ENSG00000163629	*PTPN13*	0.8	false	rs1471251	>0.20
ENSG00000104055	*TGM5*	0.81	false	-	>0.20
ENSG00000140830	*TXNL4B*	0.83	true	rs10492814	>0.20
ENSG00000168496	*FEN1*	0.83	false	rs174469	>0.20
ENSG00000002330	*BAD*	0.84	false	rs487811;rs3741404	>0.20
ENSG00000091947	*TMEM101*	0.86	false	rs16940462	>0.20
ENSG00000179195	*ZNF664*	0.86	true	-	>0.20
ENSG00000186318	*BACE1*	0.87	false	rs10790180	>0.20
ENSG00000228474	*OST4*	0.87	false	-	>0.20
ENSG00000131096	*PYY*	0.88	false	rs1642592	>0.20

ENSG00000235070	-	0.88	true	-	>0.20
ENSG00000067369	*TP53BP1*	0.89	true	-	>0.20
ENSG00000160161	*CILP2*	0.89	false	-	>0.20
ENSG00000077800	*FKBP6*	0.89	false	-	>0.20
ENSG00000256116	-	0.9	false	-	>0.20
ENSG00000092470	*WDR76*	0.9	true	-	>0.20
ENSG00000110514	*MADD*	0.91	false	rs11570115;rs11570115	>0.20
ENSG00000173264	*GPR137*	0.92	false	rs2244625	>0.20
ENSG00000161647	*MPP3*	0.92	false	-	>0.20
ENSG00000221843	*C2orf16*	0.92	true	-	>0.20
ENSG00000149743	*TRPT1*	0.92	false	rs4672	>0.20
ENSG00000175213	*ZNF408*	0.92	false	-	>0.20
ENSG00000174306	*ZHX3*	0.93	true	rs1000410	>0.20
ENSG00000138028	*CGREF1*	0.93	false	-	>0.20
ENSG00000182264	*IZUMO1*	0.93	false	-	>0.20
ENSG00000168806	*LCMT2*	0.95	false	rs3742970	>0.20
ENSG00000176428	*VPS37D*	0.95	true	rs867500	>0.20
ENSG00000226648	-	0.95	false	-	>0.20
ENSG00000105523	*FAM83E*	0.95	false	rs2544795	>0.20
ENSG00000243147	*MRPL33*	0.96	true	-	>0.20
ENSG00000176909	*MAMSTR*	0.96	false	-	>0.20
ENSG00000125703	*ATG4C*	0.97	true	-	>0.20
ENSG00000175164	*ABO*	0.97	true	rs9411463	>0.20
ENSG00000134569	*LRP4*	0.97	false	-	>0.20
ENSG00000084764	*MAPRE3*	0.97	true	rs10203050	>0.20
ENSG00000119242	*CCDC92*	0.98	true	rs3768	>0.20
ENSG00000064655	*EYA2*	0.98	true	rs947079;rs6066138	>0.20
ENSG00000174595	*KLF14*	0.98	true	-	>0.20
ENSG00000127419	*TMEM175*	0.98	true	rs6599389	>0.20
ENSG00000256746	-	0.99	false	-	>0.20
ENSG00000130287	*NCAN*	0.99	false	-	>0.20
ENSG00000105717	*PBX4*	0.99	false	rs12611058	>0.20
ENSG00000134574	*DDB2*	0.99	false	rs3758674	>0.20
ENSG00000166603	*MC4R*	0.99	true	-	>0.20
ENSG00000166734	*CASC4*	1	false	-	>0.20
ENSG00000113249	*HAVCR1*	1	false	-	>0.20
ENSG00000128881	*TTBK2*	1	false	-	>0.20
ENSG00000115194	*SLC30A3*	1	false	rs2304713	>0.20
ENSG00000163793	*DNAJC5G*	1	true	-	>0.20
ENSG00000242866	*STRC*	1	false	-	>0.20
ENSG00000109339	*MAPK10*	1	true	-	>0.20
ENSG00000149179	*C11orf49*	1	false	rs4494268	>0.20
ENSG00000126500	*FLRT1*	1	false	-	>0.20
ENSG00000176714	*CCDC121*	1	false	-	>0.20
ENSG00000166963	*MAP1A*	1	false	rs2927085	>0.20
ENSG00000108852	*MPP2*	1	false	-	>0.20
ENSG00000157851	*DPYSL5*	1	false	-	>0.20

Web Table 15: Results from the four DEPICT gene set enrichment analyses on HDL-C, LDL-C and TG. The table is lir
enrichment (FDR<0.05) in at least one of the three separate analyses.

		HDL-C	
Original gene set ID	**Original gene set description**	**P-value**	**FDR**
MP:0005278	abnormal cholesterol homeostasis	7.94E-06	<0.01
MP:0005311	abnormal circulating amino acid level	9.09E-05	<0.01
MP:0000180	abnormal circulating cholesterol level	3.47E-06	<0.01
MP:0005319	abnormal enzyme/ coenzyme level	2.07E-07	<0.01
MP:0002078	abnormal glucose homeostasis	1.57E-06	<0.01
MP:0000607	abnormal hepatocyte morphology	1.33E-05	<0.01
MP:0001764	abnormal homeostasis	1.15E-05	<0.01
MP:0002118	abnormal lipid homeostasis	5.20E-07	<0.01
MP:0001547	abnormal lipid level	0.000234	<0.01
MP:0000598	abnormal liver morphology	2.36E-07	<0.01
MP:0000609	abnormal liver physiology	1.87E-06	<0.01
MP:0001711	abnormal placenta morphology	4.30E-08	<0.01
MP:0000187	abnormal triglyceride level	0.000191	<0.01
GO:0006639	acylglycerol metabolic process	7.84E-06	<0.01
GO:0016051	carbohydrate biosynthetic process	1.62E-06	<0.01
GO:0031406	carboxylic acid binding	0.000113	<0.01
GO:0052689	carboxylic ester hydrolase activity	5.33E-05	<0.01
GO:0034637	cellular carbohydrate biosynthetic process	1.25E-07	<0.01
GO:0044242	cellular lipid catabolic process	0.000327	<0.01
GO:0044264	cellular polysaccharide metabolic process	5.78E-06	<0.01
GO:0042632	cholesterol homeostasis	0.000113	<0.01
GO:0030301	cholesterol transport	0.00011	<0.01
MP:0005179	decreased circulating cholesterol level	9.99E-08	<0.01
MP:0002702	decreased circulating free fatty acid level	2.94E-07	<0.01
MP:0000186	decreased circulating HDL cholesterol level	5.27E-05	<0.01
MP:0000183	decreased circulating LDL cholesterol level	3.34E-05	<0.01
MP:0005668	decreased circulating leptin level	8.93E-06	<0.01
MP:0002644	decreased circulating triglyceride level	1.47E-06	<0.01
MP:0005146	decreased circulating VLDL cholesterol level	5.95E-05	<0.01
MP:0005439	decreased glycogen level	2.86E-06	<0.01
MP:0005659	decreased susceptibility to diet-induced obesity	1.89E-05	<0.01
MP:0010025	decreased total body fat amount	1.67E-09	<0.01
ENSG00000197561	ELANE PPI subnetwork	9.72E-05	<0.01
MP:0000599	enlarged liver	3.02E-05	<0.01
ENSG00000211949	ENSG00000211949 PPI subnetwork	2.00E-04	<0.01
ENSG00000180210	F2 PPI subnetwork	0.000321	<0.01
GO:0050660	flavin adenine dinucleotide binding	0.000326	<0.01
ENSG00000160282	FTCD PPI subnetwork	4.92E-09	<0.01
GO:0006662	glycerol ether metabolic process	4.94E-06	<0.01
GO:0046486	glycerolipid metabolic process	0.000194	<0.01
GO:0020037	heme binding	0.000289	<0.01

MP:0002628	hepatic steatosis	1.01E-05	<0.01
GO:0019318	hexose metabolic process	7.99E-09	<0.01
ENSG00000019991	HGF PPI subnetwork	2.32E-05	<0.01
ENSG00000017427	IGF1 PPI subnetwork	7.72E-06	<0.01
MP:0005178	increased circulating cholesterol level	1.42E-07	<0.01
MP:0005559	increased circulating glucose level	5.78E-06	<0.01
MP:0000182	increased circulating LDL cholesterol level	6.90E-05	<0.01
MP:0001552	increased circulating triglyceride level	6.32E-07	<0.01
MP:0005145	increased circulating VLDL cholesterol level	6.51E-05	<0.01
MP:0009355	increased liver triglyceride level	6.78E-05	<0.01
MP:0002981	increased liver weight	9.26E-05	<0.01
MP:0005339	increased susceptibility to atherosclerosis	0.000125	<0.01
GO:0005506	iron ion binding	6.38E-05	<0.01
KEGG_COMPLEMENT_AND_C	KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	0.000115	<0.01
KEGG_LYSINE_DEGRADATION	KEGG_LYSINE_DEGRADATION	0.000138	<0.01
KEGG_PPAR_SIGNALING_PAT	KEGG_PPAR_SIGNALING_PATHWAY	0.000108	<0.01
ENSG00000164344	KLKB1 PPI subnetwork	0.000277	<0.01
GO:0008289	lipid binding	6.73E-06	<0.01
GO:0008610	lipid biosynthetic process	9.13E-05	<0.01
GO:0016042	lipid catabolic process	0.000198	<0.01
GO:0055088	lipid homeostasis	6.85E-07	<0.01
GO:0010876	lipid localization	4.03E-05	<0.01
GO:0006869	lipid transport	0.000112	<0.01
GO:0071813	lipoprotein particle binding	6.05E-05	<0.01
MP:0001860	liver inflammation	1.28E-05	<0.01
GO:0005537	mannose binding	0.000218	<0.01
GO:0005792	microsome	5.62E-05	<0.01
GO:0033293	monocarboxylic acid binding	7.47E-05	<0.01
GO:0048029	monosaccharide binding	2.76E-06	<0.01
GO:0005996	monosaccharide metabolic process	3.64E-08	<0.01
GO:0006638	neutral lipid metabolic process	8.95E-06	<0.01
GO:0008374	O-acyltransferase activity	3.67E-05	<0.01
GO:0018904	organic ether metabolic process	1.14E-06	<0.01
MP:0000603	pale liver	1.96E-08	<0.01
GO:0005543	phospholipid binding	2.59E-05	<0.01
GO:0034358	plasma lipoprotein particle	5.59E-05	<0.01
ENSG00000122861	PLAU PPI subnetwork	0.000286	<0.01
GO:0005976	polysaccharide metabolic process	8.37E-07	<0.01
GO:0032994	protein-lipid complex	5.59E-05	<0.01
GO:0071814	protein-lipid complex binding	6.05E-05	<0.01
GO:0042803	protein homodimerization activity	4.00E-08	<0.01
REACTOME_CHYLOMICRON:M	REACTOME_CHYLOMICRON:MEDIATED_LIPID_TRANSPORT	2.00E-04	<0.01
REACTOME_FATTY_ACID_TRI	REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_	1.57E-05	<0.01
REACTOME_INNATE_IMMUNI	REACTOME_INNATE_IMMUNE_SYSTEM	4.87E-05	<0.01
REACTOME_LIPID_DIGESTION	REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSP	1.30E-06	<0.01
REACTOME_LIPOPROTEIN_MI	REACTOME_LIPOPROTEIN_METABOLISM	2.75E-05	<0.01
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	1.31E-06	<0.01

REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS	0.000179	<0.01
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_WATER:SOLUBLE_VITAMINS_	0.000179	<0.01
REACTOME_PPARA_ACTIVATE	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	3.47E-05	<0.01
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PERC	4.60E-05	<0.01
GO:0032374	regulation of cholesterol transport	0.000318	<0.01
GO:0019216	regulation of lipid metabolic process	1.50E-08	<0.01
GO:0032368	regulation of lipid transport	0.000183	<0.01
GO:0097006	regulation of plasma lipoprotein particle levels	1.94E-05	<0.01
GO:0032371	regulation of sterol transport	0.000318	<0.01
GO:0009749	response to glucose stimulus	4.42E-06	<0.01
GO:0009746	response to hexose stimulus	4.39E-06	<0.01
GO:0034284	response to monosaccharide stimulus	9.81E-06	<0.01
MP:0004259	small placenta	2.56E-05	<0.01
GO:0005625	soluble fraction	3.14E-07	<0.01
GO:0055092	sterol homeostasis	0.000113	<0.01
GO:0015918	sterol transport	6.94E-05	<0.01
GO:0016746	transferase activity, transferring acyl groups	0.00014	<0.01
GO:0016747	transferase activity, transferring acyl groups other than amin	0.000101	<0.01
GO:0006641	triglyceride metabolic process	7.25E-06	<0.01
GO:0042598	vesicular fraction	4.56E-05	<0.01
GO:0019842	vitamin binding	0.000217	<0.01
MP:0002551	abnormal blood coagulation	9.27E-05	<0.01
GO:0046463	acylglycerol biosynthetic process	9.73E-05	<0.01
ENSG00000144908	ALDH1L1 PPI subnetwork	7.53E-07	<0.01
GO:0045334	clathrin-coated endocytic vesicle	8.64E-05	<0.01
MP:0004151	decreased circulating iron level	1.79E-05	<0.01
MP:0009289	decreased epididymal fat pad weight	3.23E-06	<0.01
MP:0000208	decreased hematocrit	1.29E-06	<0.01
MP:0000691	enlarged spleen	8.26E-06	<0.01
GO:0046504	glycerol ether biosynthetic process	0.000224	<0.01
ENSG00000146674	IGFBP3 PPI subnetwork	0.000174	<0.01
MP:0002599	increased mean platelet volume	0.000261	<0.01
GO:0046460	neutral lipid biosynthetic process	9.73E-05	<0.01
ENSG00000131910	NR0B2 PPI subnetwork	9.05E-07	<0.01
GO:0034381	plasma lipoprotein particle clearance	6.06E-05	<0.01
GO:0045834	positive regulation of lipid metabolic process	6.70E-06	<0.01
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_CARBOHYDRATES	1.64E-05	<0.01
GO:0019432	triglyceride biosynthetic process	0.000145	<0.01
GO:0019200	carbohydrate kinase activity	0.000151	<0.01
MP:0008808	decreased spleen iron level	7.78E-05	<0.01
GO:0046890	regulation of lipid biosynthetic process	0.000273	<0.01
GO:0009991	response to extracellular stimulus	1.79E-05	<0.01
GO:0031667	response to nutrient levels	3.61E-05	<0.01
MP:0002874	decreased hemoglobin content	2.86E-06	<0.01
MP:0002640	reticulocytosis	6.28E-05	<0.01
MP:0005584	abnormal enzyme/coenzyme activity	1.16E-06	<0.01
GO:0046464	acylglycerol catabolic process	0.000258	<0.01

ENSG00000164733	CTSB PPI subnetwork	3.26E-05	<0.01
MP:0005560	decreased circulating glucose level	2.11E-05	<0.01
MP:0002727	decreased circulating insulin level	1.15E-05	<0.01
MP:0009356	decreased liver triglyceride level	3.12E-06	<0.01
MP:0006396	decreased long bone epiphyseal plate size	4.24E-05	<0.01
MP:0005318	decreased triglyceride level	0.000141	<0.01
GO:0044269	glycerol ether catabolic process	0.000258	<0.01
MP:0001654	hepatic necrosis	1.62E-06	<0.01
GO:0032452	histone demethylase activity	0.000394	<0.01
MP:0005292	improved glucose tolerance	1.26E-06	<0.01
MP:0002079	increased circulating insulin level	0.000132	<0.01
MP:0008596	increased circulating interleukin-6 level	6.82E-05	<0.01
MP:0005289	increased oxygen consumption	0.000363	<0.01
MP:0009763	increased sensitivity to induced morbidity/mortality	8.48E-07	<0.01
MP:0005331	insulin resistance	4.44E-05	<0.01
ENSG00000130164	LDLR PPI subnetwork	2.91E-06	<0.01
GO:0046461	neutral lipid catabolic process	0.000258	<0.01
MP:0011108	partial embryonic lethality during organogenesis	3.21E-05	<0.01
GO:0043434	response to peptide hormone stimulus	1.52E-07	<0.01
GO:0031983	vesicle lumen	5.82E-05	<0.01
MP:0002971	abnormal brown adipose tissue morphology	0.000211	<0.01
GO:0033692	cellular polysaccharide biosynthetic process	0.000325	<0.01
MP:0011091	complete prenatal lethality	2.17E-05	<0.01
ENSG00000117984	CTSD PPI subnetwork	2.67E-05	<0.01
GO:0006006	glucose metabolic process	1.11E-08	<0.01
MP:0008705	increased interleukin-6 secretion	6.33E-05	<0.01
GO:0000271	polysaccharide biosynthetic process	1.13E-05	<0.01
ENSG00000115718	PROC PPI subnetwork	0.000281	<0.01
REACTOME_GLUCOSE_METAE	REACTOME_GLUCOSE_METABOLISM	7.97E-07	<0.01
ENSG00000042832	TG PPI subnetwork	0.000326	<0.01
MP:0002419	abnormal innate immunity	2.94E-05	<0.01
MP:0005637	abnormal iron homeostasis	1.35E-05	<0.01
MP:0001577	anemia	5.44E-07	<0.01
ENSG00000128272	ATF4 PPI subnetwork	0.00014	<0.01
GO:0043498	cell surface binding	0.00031	<0.01
GO:0030131	clathrin adaptor complex	9.29E-05	<0.01
MP:0008597	decreased circulating interleukin-6 level	0.000227	<0.01
MP:0002875	decreased erythrocyte cell number	2.39E-05	<0.01
MP:0005606	increased bleeding time	0.000181	<0.01
MP:0002575	increased circulating ketone body level	0.000247	<0.01
ENSG00000126934	MAP2K2 PPI subnetwork	0.000173	<0.01
MP:0005025	abnormal response to infection	0.000196	<0.01
MP:0008706	decreased interleukin-6 secretion	0.000125	<0.01
MP:0002591	decreased mean corpuscular volume	0.000249	<0.01
KEGG_ADIPOCYTOKINE_SIGN/	KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	0.000105	<0.01
ENSG00000065154	OAT PPI subnetwork	0.00019	<0.01
MP:0005048	thrombosis	0.000255	<0.01

MP:0009642	abnormal blood homeostasis	2.53E-05	<0.01
MP:0004255	abnormal spongiotrophoblast layer morphology	7.74E-08	<0.01
MP:0003229	abnormal vitelline vasculature morphology	6.57E-07	<0.01
MP:0009674	decreased birth weight	0.000195	<0.01
MP:0005459	decreased percent body fat	1.10E-06	<0.01
MP:0001783	decreased white adipose tissue amount	3.68E-05	<0.01
MP:0003909	increased eating behavior	0.000175	<0.01
MP:0005281	increased fatty acid level	2.35E-05	<0.01
MP:0008735	increased susceptibility to endotoxin shock	6.62E-06	<0.01
GO:0019433	triglyceride catabolic process	0.00036	<0.01
MP:0003566	abnormal cell adhesion	1.25E-06	<0.01
GO:0019203	carbohydrate phosphatase activity	0.000363	<0.01
GO:0005905	coated pit	9.98E-06	<0.01
GO:0060205	cytoplasmic membrane-bounded vesicle lumen	7.54E-05	<0.01
MP:0003179	decreased platelet cell number	0.000252	<0.01
MP:0002412	increased susceptibility to bacterial infection	0.000187	<0.01
MP:0001915	intracranial hemorrhage	3.47E-08	<0.01
KEGG_INSULIN_SIGNALING_P	KEGG_INSULIN_SIGNALING_PATHWAY	8.46E-06	<0.01
GO:0005811	lipid particle	9.76E-05	<0.01
ENSG00000088833	NSFL1C PPI subnetwork	1.06E-05	<0.01
MP:0001722	pale yolk sac	1.01E-05	<0.01
GO:0031091	platelet alpha granule	0.000116	<0.01
GO:0031093	platelet alpha granule lumen	8.95E-05	<0.01
ENSG00000119414	PPP6C PPI subnetwork	0.000401	<0.01
ENSG00000162409	PRKAA2 PPI subnetwork	1.92E-07	<0.01
GO:0010906	regulation of glucose metabolic process	1.09E-05	<0.01
GO:0032868	response to insulin stimulus	5.05E-06	<0.01
ENSG00000186350	RXRA PPI subnetwork	3.77E-06	<0.01
GO:0034774	secretory granule lumen	9.93E-05	<0.01
GO:0050308	sugar-phosphatase activity	0.000363	<0.01
MP:0001716	abnormal placenta labyrinth morphology	1.05E-06	<0.01
GO:0033500	carbohydrate homeostasis	7.54E-06	<0.01
ENSG00000012124	CD22 PPI subnetwork	0.000252	<0.01
GO:0032870	cellular response to hormone stimulus	1.13E-05	<0.01
GO:0006094	gluconeogenesis	0.000184	<0.01
GO:0042593	glucose homeostasis	7.54E-06	<0.01
GO:0019319	hexose biosynthetic process	0.000133	<0.01
GO:0046364	monosaccharide biosynthetic process	0.000298	<0.01
MP:0000601	small liver	6.50E-06	<0.01
ENSG00000120156	TEK PPI subnetwork	0.000316	<0.01
MP:0004229	abnormal embryonic erythropoiesis	9.64E-06	<0.01
MP:0002451	abnormal macrophage physiology	0.000106	<0.01
MP:0005087	decreased acute inflammation	0.000356	<0.01
MP:0005562	decreased mean corpuscular hemoglobin	0.000311	<0.01
MP:0008561	decreased tumor necrosis factor secretion	0.000411	<0.01
MP:0001585	hemolytic anemia	0.000222	<0.01
REACTOME_GLUCONEOGENE	REACTOME_GLUCONEOGENESIS	0.000298	<0.01

REACTOME_GLYCOLYSIS	REACTOME_GLYCOLYSIS	0.000253	<0.01
ENSG00000115415	STAT1 PPI subnetwork	0.000166	<0.01
MP:0011098	complete embryonic lethality during organogenesis	2.90E-08	<0.01
ENSG00000198646	NCOA6 PPI subnetwork	4.34E-07	<0.01
MP:0002086	abnormal extraembryonic tissue morphology	0.000228	<0.01
MP:0004130	abnormal muscle cell glucose uptake	7.85E-05	<0.01
MP:0000259	abnormal vascular development	6.47E-06	<0.01
MP:0001622	abnormal vasculogenesis	5.07E-05	<0.01
MP:0001698	decreased embryo size	1.04E-05	<0.01
MP:0001785	edema	0.000376	<0.01
GO:0006897	endocytosis	4.00E-05	<0.01
MP:0001914	hemorrhage	6.63E-06	<0.01
MP:0005293	impaired glucose tolerance	0.000404	<0.01
ENSG00000171105	INSR PPI subnetwork	2.85E-09	<0.01
MP:0001861	lung inflammation	0.000215	<0.01
GO:0010324	membrane invagination	4.00E-05	<0.01
REACTOME_PLATELET_DEGRA	REACTOME_PLATELET_DEGRANULATION	1.45E-05	<0.01
REACTOME_RESPONSE_TO_EL	REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC	1.51E-05	<0.01
GO:0071495	cellular response to endogenous stimulus	8.41E-05	<0.01
GO:0071375	cellular response to peptide hormone stimulus	5.61E-06	<0.01
MP:0011099	complete lethality throughout fetal growth and development	3.10E-06	<0.01
ENSG00000005339	CREBBP PPI subnetwork	0.000265	<0.01
ENSG00000120063	GNA13 PPI subnetwork	0.000327	<0.01
MP:0002192	hydrops fetalis	0.000192	<0.01
ENSG00000166333	ILK PPI subnetwork	0.000306	<0.01
MP:0002891	increased insulin sensitivity	9.38E-06	<0.01
ENSG00000096968	JAK2 PPI subnetwork	2.78E-05	<0.01
ENSG00000213625	LEPROT PPI subnetwork	0.000123	<0.01
MP:0003674	oxidative stress	0.000376	<0.01
ENSG00000068976	PYGM PPI subnetwork	1.78E-06	<0.01
REACTOME_HEMOSTASIS	REACTOME_HEMOSTASIS	1.29E-06	<0.01
REACTOME_TRANSCRIPTIONA	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_AD	6.52E-05	<0.01
GO:0006109	regulation of carbohydrate metabolic process	7.15E-05	<0.01
GO:0042974	retinoic acid receptor binding	2.01E-05	<0.01
GO:0046965	retinoid X receptor binding	6.31E-05	<0.01
ENSG00000160691	SHC1 PPI subnetwork	3.41E-06	<0.01
ENSG00000166949	SMAD3 PPI subnetwork	0.000381	<0.01
MP:0002652	thin myocardium	6.58E-05	<0.01
ENSG00000174123	TLR10 PPI subnetwork	0.00021	<0.01
MP:0000295	trabecula carnea hypoplasia	0.000242	<0.01
MP:0002458	abnormal B cell number	0.000297	<0.01
MP:0000358	abnormal cell morphology	0.000201	<0.01
MP:0008721	abnormal chemokine level	0.000271	<0.01
MP:0000245	abnormal erythropoiesis	0.000253	<0.01
MP:0008803	abnormal placental labyrinth vasculature morphology	0.000212	<0.01
ENSG00000142208	AKT1 PPI subnetwork	0.000119	<0.01
GO:0007596	blood coagulation	2.41E-05	<0.01

GO:0050817	coagulation	3.88E-05	<0.01
ENSG00000141736	ERBB2 PPI subnetwork	2.35E-05	<0.01
ENSG00000091831	ESR1 PPI subnetwork	6.87E-06	<0.01
MP:0000240	extramedullary hematopoiesis	8.50E-05	<0.01
ENSG00000183386	FHL3 PPI subnetwork	0.000192	<0.01
ENSG00000146535	GNA12 PPI subnetwork	0.000392	<0.01
GO:0007599	hemostasis	1.35E-05	<0.01
GO:0051427	hormone receptor binding	4.03E-05	<0.01
ENSG00000140443	IGF1R PPI subnetwork	4.10E-05	<0.01
MP:0002833	increased heart weight	6.83E-05	<0.01
ENSG00000169047	IRS1 PPI subnetwork	9.91E-06	<0.01
GO:0019900	kinase binding	4.21E-05	<0.01
ENSG00000100030	MAPK1 PPI subnetwork	0.000158	<0.01
ENSG00000105976	MET PPI subnetwork	8.99E-05	<0.01
ENSG00000140992	PDPK1 PPI subnetwork	0.000352	<0.01
ENSG00000127445	PIN1 PPI subnetwork	0.000398	<0.01
GO:0019901	protein kinase binding	0.000154	<0.01
GO:0004713	protein tyrosine kinase activity	0.000124	<0.01
ENSG00000179295	PTPN11 PPI subnetwork	0.000339	<0.01
REACTOME_CELL_SURFACE_II	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCUI	6.51E-05	<0.01
REACTOME_PLATELET_ACTIV/	REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGR	0.000339	<0.01
REACTOME_PLATELET_SENSIT	REACTOME_PLATELET_SENSITIZATION_BY_LDL	0.000331	<0.01
REACTOME_SIGNALING_BY_S	REACTOME_SIGNALING_BY_SCF:KIT	0.000132	<0.01
GO:0010675	regulation of cellular carbohydrate metabolic process	9.65E-05	<0.01
ENSG00000126561	STAT5A PPI subnetwork	0.000376	<0.01
ENSG00000173757	STAT5B PPI subnetwork	0.000186	<0.01
ENSG00000109906	ZBTB16 PPI subnetwork	0.000151	<0.01
MP:0004774	abnormal bile salt level	0.00329	<0.05
MP:0005416	abnormal circulating protein level	0.00166	<0.05
ENSG00000163631	ALB PPI subnetwork	0.000792	<0.05
ENSG00000106804	C5 PPI subnetwork	0.000439	<0.05
GO:0015485	cholesterol binding	0.0026	<0.05
GO:0017127	cholesterol transporter activity	0.00176	<0.05
GO:0050662	coenzyme binding	0.000535	<0.05
GO:0048037	cofactor binding	0.000944	<0.05
GO:0032451	demethylase activity	0.000524	<0.05
GO:0051213	dioxygenase activity	0.00198	<0.05
GO:0005504	fatty acid binding	0.000447	<0.05
GO:0034364	high-density lipoprotein particle	0.000611	<0.05
GO:0034375	high-density lipoprotein particle remodeling	0.00308	<0.05
MP:0002941	increased circulating alanine transaminase level	0.000554	<0.05
MP:0005309	increased circulating ammonia level	0.00208	<0.05
KEGG_GLYCINE_SERINE_AND_	KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	0.00321	<0.05
KEGG_PEROXISOME	KEGG_PEROXISOME	0.00185	<0.05
KEGG_TRYPTOPHAN_METABC	KEGG_TRYPTOPHAN_METABOLISM	0.000808	<0.05
GO:0070325	lipoprotein particle receptor binding	0.000615	<0.05
GO:0032787	monocarboxylic acid metabolic process	0.00135	<0.05

GO:0016705	oxidoreductase activity, acting on paired donors, with incorp	0.00317	<0.05
GO:0016701	oxidoreductase activity, acting on single donors with incorpo	0.00127	<0.05
GO:0016702	oxidoreductase activity, acting on single donors with incorpo	0.00258	<0.05
GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	0.00258	<0.05
GO:0071827	plasma lipoprotein particle organization	0.00164	<0.05
GO:0071825	protein-lipid complex subunit organization	0.00164	<0.05
REACTOME_HDL:MEDIATED_I	REACTOME_HDL:MEDIATED_LIPID_TRANSPORT	0.00085	<0.05
GO:0090207	regulation of triglyceride metabolic process	0.000867	<0.05
GO:0044282	small molecule catabolic process	0.000615	<0.05
GO:0015248	sterol transporter activity	0.00173	<0.05
GO:0046906	tetrapyrrole binding	0.000421	<0.05
GO:0034385	triglyceride-rich lipoprotein particle	0.0016	<0.05
GO:0070328	triglyceride homeostasis	0.000507	<0.05
GO:0034361	very-low-density lipoprotein particle	0.0016	<0.05
GO:0051183	vitamin transporter activity	0.00202	<0.05
MP:0004773	abnormal bile composition	0.00349	<0.05
ENSG00000084674	APOB PPI subnetwork	0.00144	<0.05
ENSG00000125730	C3 PPI subnetwork	0.00086	<0.05
GO:0033344	cholesterol efflux	0.0028	<0.05
GO:0008203	cholesterol metabolic process	0.000814	<0.05
GO:0030669	clathrin-coated endocytic vesicle membrane	0.0015	<0.05
GO:0004866	endopeptidase inhibitor activity	0.00169	<0.05
GO:0061135	endopeptidase regulator activity	0.00133	<0.05
ENSG00000204319	ENSG00000204319 PPI subnetwork	0.00296	<0.05
GO:0004857	enzyme inhibitor activity	0.001	<0.05
ENSG00000088926	F11 PPI subnetwork	0.000539	<0.05
MP:0001556	increased circulating HDL cholesterol level	0.00057	<0.05
KEGG_PRION_DISEASES	KEGG_PRION_DISEASES	0.000944	<0.05
GO:0034362	low-density lipoprotein particle	0.000516	<0.05
GO:0034367	macromolecular complex remodeling	0.00342	<0.05
ENSG00000182446	NPLOC4 PPI subnetwork	0.000979	<0.05
GO:0031100	organ regeneration	0.00319	<0.05
GO:0030414	peptidase inhibitor activity	0.00184	<0.05
GO:0061134	peptidase regulator activity	0.00348	<0.05
GO:0034369	plasma lipoprotein particle remodeling	0.00342	<0.05
GO:0034368	protein-lipid complex remodeling	0.00342	<0.05
REACTOME_COMPLEMENT_C	REACTOME_COMPLEMENT_CASCADE	0.00149	<0.05
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASC	0.000703	<0.05
REACTOME_INTRINSIC_PATH\	REACTOME_INTRINSIC_PATHWAY	0.00336	<0.05
REACTOME_TRIGLYCERIDE_BI	REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	0.000419	<0.05
GO:0009743	response to carbohydrate stimulus	0.000659	<0.05
GO:0044283	small molecule biosynthetic process	0.000747	<0.05
GO:0008202	steroid metabolic process	0.00265	<0.05
GO:0016125	sterol metabolic process	0.00163	<0.05
ENSG00000154582	TCEB1 PPI subnetwork	0.000772	<0.05
ENSG00000175899	A2M PPI subnetwork	0.000943	<0.05
GO:0016052	carbohydrate catabolic process	0.000939	<0.05

GO:0038024	cargo receptor activity	0.00098	<0.05
ENSG00000131187	F12 PPI subnetwork	0.000582	<0.05
ENSG00000185010	F8 PPI subnetwork	0.00271	<0.05
ENSG00000171564	FGB PPI subnetwork	0.000842	<0.05
ENSG00000171557	FGG PPI subnetwork	0.000516	<0.05
GO:0016798	hydrolase activity, acting on glycosyl bonds	0.00267	<0.05
MP:0003887	increased hepatocyte apoptosis	0.00121	<0.05
ENSG00000168918	INPP5D PPI subnetwork	0.00169	<0.05
KEGG_SULFUR_METABOLISM	KEGG_SULFUR_METABOLISM	0.000633	<0.05
ENSG00000025800	KPNA6 PPI subnetwork	0.000879	<0.05
ENSG00000170486	KRT72 PPI subnetwork	0.00334	<0.05
ENSG00000004799	PDK4 PPI subnetwork	0.00156	<0.05
REACTOME_COMMON_PATH'	REACTOME_COMMON_PATHWAY	0.000579	<0.05
GO:0010565	regulation of cellular ketone metabolic process	0.000532	<0.05
GO:0019217	regulation of fatty acid metabolic process	0.000612	<0.05
GO:0052547	regulation of peptidase activity	0.00303	<0.05
GO:0019218	regulation of steroid metabolic process	0.00118	<0.05
ENSG00000196954	CASP4 PPI subnetwork	0.000821	<0.05
ENSG00000132464	ENAM PPI subnetwork	0.00223	<0.05
ENSG00000196911	KPNA5 PPI subnetwork	0.00162	<0.05
GO:0007584	response to nutrient	0.000472	<0.05
MP:0004948	abnormal neuronal precursor proliferation	0.00345	<0.05
ENSG00000132703	APCS PPI subnetwork	0.000938	<0.05
ENSG00000132693	CRP PPI subnetwork	0.000554	<0.05
ENSG00000100448	CTSG PPI subnetwork	0.000768	<0.05
GO:0005542	folic acid binding	0.0013	<0.05
GO:0046503	glycerolipid catabolic process	0.000819	<0.05
ENSG00000115461	IGFBP5 PPI subnetwork	0.000648	<0.05
GO:0016638	oxidoreductase activity, acting on the CH-NH2 group of dono	0.00259	<0.05
GO:0004806	triglyceride lipase activity	0.00263	<0.05
MP:0002723	abnormal immune serum protein physiology	0.00133	<0.05
MP:0005282	decreased fatty acid level	0.00172	<0.05
MP:0003436	decreased susceptibility to induced arthritis	0.000484	<0.05
ENSG00000198780	FAM169A PPI subnetwork	0.00248	<0.05
GO:0005529	GO:0005529	0.00213	<0.05
ENSG00000187837	HIST1H1C PPI subnetwork	0.00104	<0.05
MP:0005533	increased body temperature	0.00265	<0.05
MP:0001554	increased circulating free fatty acid level	0.00127	<0.05
ENSG00000196365	LONP1 PPI subnetwork	0.00317	<0.05
GO:0030169	low-density lipoprotein particle binding	0.000455	<0.05
GO:0008329	pattern recognition receptor activity	0.00289	<0.05
ENSG00000163586	FABP1 PPI subnetwork	0.000863	<0.05
MP:0008553	increased circulating tumor necrosis factor level	0.000717	<0.05
MP:0004952	increased spleen weight	0.000547	<0.05
MP:0008537	increased susceptibility to induced colitis	0.00107	<0.05
KEGG_GALACTOSE_METABOL	KEGG_GALACTOSE_METABOLISM	0.00266	<0.05
GO:0019915	lipid storage	0.000563	<0.05

ENSG00000181929	PRKAG1 PPI subnetwork	0.00298	<0.05
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_4_TLR4_CASCADE	0.00295	<0.05
REACTOME_TOLL_RECEPTOR_	REACTOME_TOLL_RECEPTOR_CASCADES	0.00303	<0.05
ENSG00000154134	ROBO3 PPI subnetwork	0.00156	<0.05
ENSG00000103363	TCEB2 PPI subnetwork	0.000677	<0.05
ENSG00000006715	VPS41 PPI subnetwork	0.000987	<0.05
MP:0002447	abnormal erythrocyte morphology	0.00153	<0.05
MP:0000229	abnormal megakaryocyte differentiation	0.00128	<0.05
GO:0044275	cellular carbohydrate catabolic process	0.00145	<0.05
MP:0008809	increased spleen iron level	0.000499	<0.05
ENSG00000164077	MON1A PPI subnetwork	0.00174	<0.05
ENSG00000106617	PRKAG2 PPI subnetwork	0.00194	<0.05
GO:0032496	response to lipopolysaccharide	0.00272	<0.05
ENSG00000174175	SELP PPI subnetwork	0.00123	<0.05
MP:0002743	glomerulonephritis	0.000426	<0.05
MP:0001718	abnormal visceral yolk sac morphology	0.000635	<0.05
GO:0016209	antioxidant activity	0.00322	<0.05
GO:0030246	carbohydrate binding	0.00194	<0.05
MP:0004921	decreased placenta weight	0.000452	<0.05
MP:0000292	distended pericardium	0.00198	<0.05
MP:0001559	hyperglycemia	0.00122	<0.05
MP:0000189	hypoglycemia	0.000638	<0.05
MP:0001846	increased inflammatory response	0.000653	<0.05
MP:0001859	kidney inflammation	0.00201	<0.05
GO:0034440	lipid oxidation	0.00229	<0.05
GO:0072593	reactive oxygen species metabolic process	0.00334	<0.05
MP:0002421	abnormal cell-mediated immunity	0.00141	<0.05
MP:0005621	abnormal cell physiology	0.000517	<0.05
MP:0005201	abnormal retinal pigment epithelium morphology	0.00301	<0.05
GO:0006073	cellular glucan metabolic process	0.000459	<0.05
ENSG00000101266	CSNK2A1 PPI subnetwork	0.00205	<0.05
MP:0001780	decreased brown adipose tissue amount	0.00158	<0.05
MP:0009549	decreased platelet aggregation	0.00275	<0.05
GO:0030139	endocytic vesicle	0.00171	<0.05
GO:0043499	eukaryotic cell surface binding	0.00145	<0.05
GO:0044042	glucan metabolic process	0.000459	<0.05
GO:0005977	glycogen metabolic process	0.000495	<0.05
ENSG00000044574	HSPA5 PPI subnetwork	0.000674	<0.05
GO:0016836	hydro-lyase activity	0.0031	<0.05
MP:0001242	hyperkeratosis	0.00244	<0.05
MP:0000322	increased granulocyte number	0.000705	<0.05
MP:0003724	increased susceptibility to induced arthritis	0.000566	<0.05
MP:0001634	internal hemorrhage	0.00217	<0.05
ENSG00000169896	ITGAM PPI subnetwork	0.00264	<0.05
GO:0043202	lysosomal lumen	0.00225	<0.05
ENSG00000135341	MAP3K7 PPI subnetwork	0.00155	<0.05
ENSG00000013364	MVP PPI subnetwork	0.0017	<0.05

MP:0001651	necrosis	0.000806	<0.05
GO:0051241	negative regulation of multicellular organismal process	0.00201	<0.05
ENSG00000100311	PDGFB PPI subnetwork	0.00287	<0.05
ENSG00000119630	PGF PPI subnetwork	0.00328	<0.05
REACTOME_PLATELET_AGGRE	REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	0.00188	<0.05
GO:0006898	receptor-mediated endocytosis	0.000487	<0.05
ENSG00000173039	RELA PPI subnetwork	0.00324	<0.05
ENSG00000100934	SEC23A PPI subnetwork	0.000514	<0.05
ENSG00000143379	SETDB1 PPI subnetwork	0.00342	<0.05
MP:0001209	spontaneous skin ulceration	0.0015	<0.05
ENSG00000104980	TIMM44 PPI subnetwork	0.00325	<0.05
MP:0005670	abnormal white adipose tissue physiology	0.00219	<0.05
GO:0046165	alcohol biosynthetic process	0.000539	<0.05
MP:0000414	alopecia	0.000674	<0.05
MP:0002642	anisocytosis	0.00253	<0.05
GO:0030119	AP-type membrane coat adaptor complex	0.000447	<0.05
MP:0008554	decreased circulating tumor necrosis factor level	0.00105	<0.05
ENSG00000066044	ELAVL1 PPI subnetwork	0.00246	<0.05
ENSG00000165197	FIGF PPI subnetwork	0.00331	<0.05
MP:0001798	impaired macrophage phagocytosis	0.000676	<0.05
MP:0008663	increased interleukin-12 secretion	0.000415	<0.05
GO:0006954	inflammatory response	0.000774	<0.05
GO:0044419	interspecies interaction between organisms	0.00263	<0.05
ENSG00000005961	ITGA2B PPI subnetwork	0.00159	<0.05
ENSG00000160255	ITGB2 PPI subnetwork	0.00266	<0.05
ENSG00000002834	LASP1 PPI subnetwork	0.00158	<0.05
ENSG00000125686	MED1 PPI subnetwork	0.00131	<0.05
GO:0005741	mitochondrial outer membrane	0.00254	<0.05
ENSG00000034971	MYOC PPI subnetwork	0.00118	<0.05
ENSG00000067225	PKM2 PPI subnetwork	0.000882	<0.05
GO:0009896	positive regulation of catabolic process	0.00314	<0.05
GO:0010885	regulation of cholesterol storage	0.00262	<0.05
GO:0031347	regulation of defense response	0.00284	<0.05
ENSG00000116030	SUMO1 PPI subnetwork	0.000866	<0.05
ENSG00000173511	VEGFB PPI subnetwork	0.00229	<0.05
ENSG00000173207	CKS1B PPI subnetwork	0.00103	<0.05
MP:0003355	decreased ovulation rate	0.00109	<0.05
MP:0009657	failure of chorioallantoic fusion	0.00295	<0.05
ENSG00000123384	LRP1 PPI subnetwork	0.00255	<0.05
MP:0001712	abnormal placenta development	0.00315	<0.05
ENSG00000050820	BCAR1 PPI subnetwork	0.00164	<0.05
MP:0005558	decreased creatinine clearance	0.000687	<0.05
MP:0008770	decreased survivor rate	0.00156	<0.05
ENSG00000150907	FOXO1 PPI subnetwork	0.000664	<0.05
MP:0000600	liver hypoplasia	0.000671	<0.05
MP:0011101	partial prenatal lethality	0.00231	<0.05
GO:0042277	peptide binding	0.00184	<0.05

REACTOME_DARPP:32_EVENT	REACTOME_DARPP:32_EVENTS	0.00131	<0.05
MP:0002397	abnormal bone marrow morphology	0.00228	<0.05
MP:0005076	abnormal cell differentiation	0.000444	<0.05
MP:0001685	abnormal endoderm development	0.00131	<0.05
MP:0009115	abnormal fat cell morphology	0.000714	<0.05
MP:0003383	abnormal gluconeogenesis	0.00089	<0.05
MP:0000266	abnormal heart morphology	0.000661	<0.05
MP:0002109	abnormal limb morphology	0.00157	<0.05
MP:0000596	abnormal liver development	0.00145	<0.05
MP:0000136	abnormal microglial cell morphology	0.00301	<0.05
MP:0004883	abnormal vascular wound healing	0.00116	<0.05
MP:0001613	abnormal vasodilation	0.000664	<0.05
MP:0001719	absent vitelline blood vessels	0.00205	<0.05
ENSG00000137486	ARRB1 PPI subnetwork	0.000916	<0.05
ENSG00000105401	CDC37 PPI subnetwork	0.00104	<0.05
MP:0004810	decreased hematopoietic stem cell number	0.000766	<0.05
MP:0008844	decreased subcutaneous adipose tissue amount	0.000632	<0.05
MP:0006264	decreased systemic arterial systolic blood pressure	0.000651	<0.05
ENSG00000004975	DVL2 PPI subnetwork	0.00331	<0.05
ENSG00000138798	EGF PPI subnetwork	0.00313	<0.05
MP:0003984	embryonic growth retardation	0.000778	<0.05
MP:0008034	enhanced lipolysis	0.00325	<0.05
ENSG00000157557	ETS2 PPI subnetwork	0.00337	<0.05
GO:0042800	histone methyltransferase activity (H3-K4 specific)	0.00157	<0.05
ENSG00000167244	IGF2 PPI subnetwork	0.00178	<0.05
MP:0008033	impaired lipolysis	0.00348	<0.05
MP:0000218	increased leukocyte cell number	0.000989	<0.05
ENSG00000185950	IRS2 PPI subnetwork	0.00151	<0.05
ENSG00000144668	ITGA9 PPI subnetwork	0.000501	<0.05
KEGG_ACUTE_MYELOID_LEUK	KEGG_ACUTE_MYELOID_LEUKEMIA	0.000498	<0.05
GO:0000287	magnesium ion binding	0.00323	<0.05
ENSG00000169967	MAP3K2 PPI subnetwork	0.00242	<0.05
GO:0051051	negative regulation of transport	0.000578	<0.05
ENSG00000180530	NRIP1 PPI subnetwork	0.00056	<0.05
MP:0001787	pericardial edema	0.0017	<0.05
ENSG00000168490	PHYHIP PPI subnetwork	0.00166	<0.05
ENSG00000188313	PLSCR1 PPI subnetwork	0.00309	<0.05
ENSG00000080815	PSEN1 PPI subnetwork	0.00192	<0.05
ENSG00000111679	PTPN6 PPI subnetwork	0.00209	<0.05
REACTOME_INTEGRIN_ALPHA	REACTOME_INTEGRIN_ALPHAIIB_BETA3_SIGNALING	0.000603	<0.05
REACTOME_INTEGRIN_CELL_S	REACTOME_INTEGRIN_CELL_SURFACE_INTERACTIONS	0.000597	<0.05
GO:0001666	response to hypoxia	0.00154	<0.05
ENSG00000175387	SMAD2 PPI subnetwork	0.000693	<0.05
ENSG00000141646	SMAD4 PPI subnetwork	0.00313	<0.05
ENSG00000120693	SMAD9 PPI subnetwork	0.000764	<0.05
ENSG00000096063	SRPK1 PPI subnetwork	0.00164	<0.05
ENSG00000168610	STAT3 PPI subnetwork	0.000413	<0.05

MP:0002954	abnormal aerobic energy metabolism	0.00227	<0.05
MP:0002896	abnormal bone mineralization	0.00285	<0.05
MP:0003795	abnormal bone structure	0.00299	<0.05
MP:0009858	abnormal cellular extravasation	0.00211	<0.05
MP:0008722	abnormal chemokine secretion	0.000495	<0.05
MP:0005334	abnormal fat pad morphology	0.000549	<0.05
MP:0005438	abnormal glycogen homeostasis	0.00173	<0.05
MP:0001601	abnormal myelopoiesis	0.000691	<0.05
MP:0002463	abnormal neutrophil physiology	0.00274	<0.05
MP:0003957	abnormal nitric oxide homeostasis	0.000555	<0.05
MP:0002416	abnormal proerythroblast morphology	0.00178	<0.05
MP:0000689	abnormal spleen morphology	0.00081	<0.05
MP:0008752	abnormal tumor necrosis factor level	0.00279	<0.05
MP:0005023	abnormal wound healing	0.00239	<0.05
ENSG00000072778	ACADVL PPI subnetwork	0.000739	<0.05
ENSG00000078061	ARAF PPI subnetwork	0.00201	<0.05
ENSG00000002330	BAD PPI subnetwork	0.00324	<0.05
ENSG00000177951	BET1L PPI subnetwork	0.00147	<0.05
ENSG00000139637	C12orf10 PPI subnetwork	0.00339	<0.05
ENSG00000110931	CAMKK2 PPI subnetwork	0.0013	<0.05
GO:0005901	caveola	0.00308	<0.05
GO:0032869	cellular response to insulin stimulus	0.000671	<0.05
ENSG00000173575	CHD2 PPI subnetwork	0.00275	<0.05
MP:0002499	chronic inflammation	0.00336	<0.05
ENSG00000176444	CLK2 PPI subnetwork	0.00142	<0.05
ENSG00000103653	CSK PPI subnetwork	0.00218	<0.05
ENSG00000163599	CTLA4 PPI subnetwork	0.00194	<0.05
ENSG00000121966	CXCR4 PPI subnetwork	0.000474	<0.05
ENSG00000172115	CYCS PPI subnetwork	0.00101	<0.05
ENSG00000198563	DDX39B PPI subnetwork	0.00122	<0.05
ENSG00000215425	DDX39B PPI subnetwork	0.00122	<0.05
ENSG00000167658	EEF2 PPI subnetwork	0.00206	<0.05
ENSG00000103319	EEF2K PPI subnetwork	0.000797	<0.05
MP:0001730	embryonic growth arrest	0.0011	<0.05
ENSG00000056345	ENSG00000056345 PPI subnetwork	0.00127	<0.05
ENSG00000147507	ENSG00000147507 PPI subnetwork	0.00139	<0.05
ENSG00000215412	ENSG00000215412 PPI subnetwork	0.00122	<0.05
ENSG00000100393	EP300 PPI subnetwork	0.002	<0.05
ENSG00000000938	FGR PPI subnetwork	0.00123	<0.05
ENSG00000170345	FOS PPI subnetwork	0.00261	<0.05
ENSG00000077809	GTF2I PPI subnetwork	0.00118	<0.05
ENSG00000104812	GYS1 PPI subnetwork	0.001	<0.05
GO:0030097	hemopoiesis	0.0024	<0.05
ENSG00000080824	HSP90AA1 PPI subnetwork	0.00042	<0.05
MP:0008720	impaired neutrophil chemotaxis	0.00162	<0.05
MP:0003131	increased erythrocyte cell number	0.00307	<0.05
MP:0008657	increased interleukin-1 beta secretion	0.00312	<0.05

ENSG00000115232	ITGA4 PPI subnetwork	0.00328	<0.05
ENSG00000077943	ITGA8 PPI subnetwork	0.00161	<0.05
ENSG00000082781	ITGB5 PPI subnetwork	0.00292	<0.05
KEGG_BLADDER_CANCER	KEGG_BLADDER_CANCER	0.00134	<0.05
KEGG_FRUCTOSE_AND_MANI	KEGG_FRUCTOSE_AND_MANNOSE_METABOLISM	0.000432	<0.05
KEGG_MTOR_SIGNALING_PA	KEGG_MTOR_SIGNALING_PATHWAY	0.000603	<0.05
ENSG00000198909	MAP3K3 PPI subnetwork	0.00173	<0.05
ENSG00000102882	MAPK3 PPI subnetwork	0.00158	<0.05
ENSG00000198793	MTOR PPI subnetwork	0.00207	<0.05
ENSG00000136997	MYC PPI subnetwork	0.00292	<0.05
GO:0030099	myeloid cell differentiation	0.000939	<0.05
GO:0051248	negative regulation of protein metabolic process	0.00159	<0.05
ENSG00000147140	NONO PPI subnetwork	0.00308	<0.05
ENSG00000113580	NR3C1 PPI subnetwork	0.00336	<0.05
GO:0000790	nuclear chromatin	0.0015	<0.05
GO:0035257	nuclear hormone receptor binding	0.000749	<0.05
GO:0051170	nuclear import	0.00293	<0.05
MP:0003717	pallor	0.000668	<0.05
ENSG00000113721	PDGFRB PPI subnetwork	0.00326	<0.05
ENSG00000123836	PFKFB2 PPI subnetwork	0.0034	<0.05
ENSG00000145675	PIK3R1 PPI subnetwork	0.00174	<0.05
ENSG00000197943	PLCG2 PPI subnetwork	0.00199	<0.05
GO:0046777	protein autophosphorylation	0.00195	<0.05
GO:0046982	protein heterodimerization activity	0.00195	<0.05
GO:0017038	protein import	0.00314	<0.05
GO:0033365	protein localization to organelle	0.00207	<0.05
GO:0006605	protein targeting	0.000599	<0.05
ENSG00000197746	PSAP PPI subnetwork	0.000625	<0.05
ENSG00000127947	PTPN12 PPI subnetwork	0.00304	<0.05
ENSG00000179950	PUF60 PPI subnetwork	0.00122	<0.05
ENSG00000144566	RAB5A PPI subnetwork	0.00122	<0.05
REACTOME_ACTIVATED_AMP	REACTOME_ACTIVATED_AMPK_STIMULATES_FATTY:ACID_O	0.00074	<0.05
REACTOME_DIABETES_PATHV	REACTOME_DIABETES_PATHWAYS	0.00153	<0.05
REACTOME_ERKMAPK_TARGE	REACTOME_ERKMAPK_TARGETS	0.00188	<0.05
REACTOME_GAB1_SIGNALOS	REACTOME_GAB1_SIGNALOSOME	0.00189	<0.05
REACTOME_GROWTH_HORM	REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	0.00151	<0.05
REACTOME_NUCLEAR_EVENT	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTIO	0.00266	<0.05
REACTOME_SIGNALING_BY_E	REACTOME_SIGNALING_BY_ERBB4	0.00129	<0.05
MP:0001923	reduced female fertility	0.000887	<0.05
GO:0009894	regulation of catabolic process	0.00195	<0.05
GO:0070201	regulation of establishment of protein localization	0.00143	<0.05
GO:0032386	regulation of intracellular transport	0.00136	<0.05
GO:0046822	regulation of nucleocytoplasmic transport	0.000469	<0.05
GO:0051223	regulation of protein transport	0.00299	<0.05
GO:0070482	response to oxygen levels	0.0033	<0.05
ENSG00000119335	SET PPI subnetwork	0.000642	<0.05
MP:0004947	skin inflammation	0.0032	<0.05

ENSG00000197122	SRC PPI subnetwork	0.00199	<0.05
ENSG00000138768	USO1 PPI subnetwork	0.000855	<0.05
ENSG00000141968	VAV1 PPI subnetwork	0.00255	<0.05
ENSG00000164924	YWHAZ PPI subnetwork	0.000866	<0.05
MP:0004777	abnormal phospholipid level	0.00718	<0.20
ENSG00000118137	APOA1 PPI subnetwork	0.01	<0.20
ENSG00000158874	APOA2 PPI subnetwork	0.00853	<0.20
ENSG00000110245	APOC3 PPI subnetwork	0.03	<0.20
GO:0046395	carboxylic acid catabolic process	0.01	<0.20
ENSG00000211896	ENSG00000211896 PPI subnetwork	0.00663	<0.20
ENSG00000215754	ENSG00000215754 PPI subnetwork	0.01	<0.20
ENSG00000215755	ENSG00000215755 PPI subnetwork	0.03	<0.20
ENSG00000215756	ENSG00000215756 PPI subnetwork	0.01	<0.20
GO:0000062	fatty-acyl-CoA binding	0.01	<0.20
MP:0003982	increased cholesterol level	0.01	<0.20
KEGG_ARGININE_AND_PROLI	KEGG_ARGININE_AND_PROLINE_METABOLISM	0.0073	<0.20
KEGG_FATTY_ACID_METABOL	KEGG_FATTY_ACID_METABOLISM	0.00638	<0.20
GO:0016298	lipase activity	0.01	<0.20
GO:0005319	lipid transporter activity	0.00409	<0.20
MP:0003333	liver fibrosis	0.00484	<0.20
GO:0031907	microbody lumen	0.00555	<0.20
GO:0016054	organic acid catabolic process	0.01	<0.20
GO:0005782	peroxisomal matrix	0.00555	<0.20
GO:0050997	quaternary ammonium group binding	0.00904	<0.20
GO:0043691	reverse cholesterol transport	0.00687	<0.20
GO:0017171	serine hydrolase activity	0.00547	<0.20
GO:0032934	sterol binding	0.00565	<0.20
MP:0005332	abnormal amino acid level	0.0039	<0.20
MP:0001881	abnormal mammary gland physiology	0.02	<0.20
MP:0008875	abnormal xenobiotic pharmacokinetics	0.02	<0.20
ENSG00000136250	AOAH PPI subnetwork	0.00791	<0.20
GO:0051635	bacterial cell surface binding	0.01	<0.20
ENSG00000127022	CANX PPI subnetwork	0.00408	<0.20
GO:0044106	cellular amine metabolic process	0.02	<0.20
ENSG00000204359	CFB PPI subnetwork	0.00363	<0.20
ENSG00000000971	CFH PPI subnetwork	0.00765	<0.20
GO:0009055	electron carrier activity	0.00395	<0.20
ENSG00000166285	ENSG00000166285 PPI subnetwork	0.00363	<0.20
ENSG00000213044	ENSG00000213044 PPI subnetwork	0.00372	<0.20
GO:0006631	fatty acid metabolic process	0.00377	<0.20
GO:0045017	glycerolipid biosynthetic process	0.00462	<0.20
GO:0005796	Golgi lumen	0.00659	<0.20
MP:0010027	increased liver cholesterol level	0.0039	<0.20
MP:0008478	increased spleen white pulp amount	0.00591	<0.20
ENSG00000186832	KRT16 PPI subnetwork	0.02	<0.20
ENSG00000101680	LAMA1 PPI subnetwork	0.01	<0.20
GO:0042157	lipoprotein metabolic process	0.02	<0.20

GO:0016829	lyase activity	0.00843	<0.20
GO:0042579	microbody	0.01	<0.20
GO:0044438	microbody part	0.00795	<0.20
GO:0072329	monocarboxylic acid catabolic process	0.01	<0.20
GO:0071702	organic substance transport	0.00714	<0.20
GO:0016706	oxidoreductase activity, acting on paired donors, with incorp	0.02	<0.20
GO:0044439	peroxisomal part	0.00795	<0.20
GO:0005777	peroxisome	0.01	<0.20
GO:0046470	phosphatidylcholine metabolic process	0.00838	<0.20
GO:0004623	phospholipase A2 activity	0.00416	<0.20
GO:0002020	protease binding	0.01	<0.20
REACTOME_GAMMA:CARBOX	REACTOME_GAMMA:CARBOXYLATION_TRANSPORT_AND_AI	0.00806	<0.20
REACTOME_GLUCOSE_TRANS	REACTOME_GLUCOSE_TRANSPORT	0.03	<0.20
REACTOME_GLYCOSPHINGOL	REACTOME_GLYCOSPHINGOLIPID_METABOLISM	0.02	<0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVA	0.02	<0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_	0.02	<0.20
REACTOME_PHASE_1_:_FUNC	REACTOME_PHASE_1_:_FUNCTIONALIZATION_OF_COMPOU	0.01	<0.20
REACTOME_SYNTHESIS_OF_B	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS_V	0.01	<0.20
ENSG00000181827	RFX7 PPI subnetwork	0.00459	<0.20
ENSG00000148965	SAA4 PPI subnetwork	0.00888	<0.20
GO:0004252	serine-type endopeptidase activity	0.00623	<0.20
GO:0004867	serine-type endopeptidase inhibitor activity	0.01	<0.20
GO:0008236	serine-type peptidase activity	0.0055	<0.20
ENSG00000188488	SERPINA5 PPI subnetwork	0.0052	<0.20
ENSG00000167711	SERPINF2 PPI subnetwork	0.00483	<0.20
ENSG00000038002	AGA PPI subnetwork	0.0069	<0.20
ENSG00000133805	AMPD3 PPI subnetwork	0.0075	<0.20
ENSG00000145692	BHMT PPI subnetwork	0.00518	<0.20
ENSG00000206340	C4A PPI subnetwork	0.00621	<0.20
ENSG00000007402	CACNA2D2 PPI subnetwork	0.01	<0.20
GO:0046394	carboxylic acid biosynthetic process	0.02	<0.20
ENSG00000197766	CFD PPI subnetwork	0.00791	<0.20
GO:0006732	coenzyme metabolic process	0.00633	<0.20
GO:0051186	cofactor metabolic process	0.00583	<0.20
ENSG00000150527	CTAGE5 PPI subnetwork	0.02	<0.20
MP:0008734	decreased susceptibility to endotoxin shock	0.00529	<0.20
MP:0001511	disheveled coat	0.00707	<0.20
GO:0005788	endoplasmic reticulum lumen	0.01	<0.20
ENSG00000205813	ENSG00000205813 PPI subnetwork	0.00697	<0.20
ENSG00000126218	F10 PPI subnetwork	0.00866	<0.20
ENSG00000198734	F5 PPI subnetwork	0.00694	<0.20
ENSG00000057593	F7 PPI subnetwork	0.02	<0.20
GO:0061008	hepaticobiliary system development	0.00865	<0.20
ENSG00000110169	HPX PPI subnetwork	0.00818	<0.20
ENSG00000166598	HSP90B1 PPI subnetwork	0.00538	<0.20
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	0.00436	<0.20
ENSG00000103742	IGDCC4 PPI subnetwork	0.006	<0.20

GO:0016853	isomerase activity	0.00577	<0.20
ENSG00000055957	ITIH1 PPI subnetwork	0.00787	<0.20
KEGG_GLYCEROPHOSPHOLIPI	KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	0.00669	<0.20
KEGG_TYROSINE_METABOLIS	KEGG_TYROSINE_METABOLISM	0.02	<0.20
ENSG00000170871	KIAA0232 PPI subnetwork	0.00593	<0.20
ENSG00000142515	KLK3 PPI subnetwork	0.00355	<0.20
ENSG00000171401	KRT13 PPI subnetwork	0.00403	<0.20
ENSG00000185479	KRT6B PPI subnetwork	0.02	<0.20
GO:0001889	liver development	0.02	<0.20
GO:0008170	N-methyltransferase activity	0.02	<0.20
GO:0050661	NADP binding	0.01	<0.20
GO:0010951	negative regulation of endopeptidase activity	0.00518	<0.20
GO:0010466	negative regulation of peptidase activity	0.00613	<0.20
ENSG00000124006	OBSL1 PPI subnetwork	0.00679	<0.20
ENSG00000197263	OR8D2 PPI subnetwork	0.01	<0.20
GO:0016053	organic acid biosynthetic process	0.02	<0.20
GO:0019825	oxygen binding	0.02	<0.20
ENSG00000109272	PF4V1 PPI subnetwork	0.00697	<0.20
ENSG00000168907	PLA2G4F PPI subnetwork	0.00661	<0.20
GO:0072376	protein activation cascade	0.03	<0.20
ENSG00000204983	PRSS1 PPI subnetwork	0.00653	<0.20
REACTOME_PTM_GAMMA_C/	REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FOI	0.01	<0.20
GO:0052548	regulation of endopeptidase activity	0.00577	<0.20
ENSG00000117601	SERPINC1 PPI subnetwork	0.00407	<0.20
GO:0005496	steroid binding	0.00464	<0.20
GO:0006694	steroid biosynthetic process	0.02	<0.20
ENSG00000003436	TFPI PPI subnetwork	0.00758	<0.20
ENSG00000106636	YKT6 PPI subnetwork	0.00583	<0.20
ENSG00000188994	ZNF292 PPI subnetwork	0.008	<0.20
MP:0003657	abnormal erythrocyte osmotic lysis	0.00635	<0.20
ENSG00000133935	C14orf1 PPI subnetwork	0.00887	<0.20
ENSG00000001630	CYP51A1 PPI subnetwork	0.02	<0.20
MP:0005642	decreased mean corpuscular hemoglobin concentration	0.00505	<0.20
GO:0030145	manganese ion binding	0.02	<0.20
ENSG00000143627	PKLR PPI subnetwork	0.00704	<0.20
ENSG00000081237	PTPRC PPI subnetwork	0.02	<0.20
ENSG00000170348	TMED10 PPI subnetwork	0.01	<0.20
ENSG00000165280	VCP PPI subnetwork	0.03	<0.20
MP:0000639	abnormal adrenal gland morphology	0.01	<0.20
MP:0001882	abnormal lactation	0.00956	<0.20
GO:0016411	acylglycerol O-acyltransferase activity	0.00365	<0.20
MP:0005185	decreased circulating progesterone level	0.00521	<0.20
KEGG_BETA_ALANINE_METAE	KEGG_BETA_ALANINE_METABOLISM	0.01	<0.20
KEGG_GLYCEROLIPID_METAB	KEGG_GLYCEROLIPID_METABOLISM	0.00538	<0.20
GO:0016878	acid-thiol ligase activity	0.00757	<0.20
ENSG00000130203	APOE PPI subnetwork	0.00722	<0.20
ENSG00000118690	ARMC2 PPI subnetwork	0.00745	<0.20

ENSG00000112936	C7 PPI subnetwork	0.01	<0.20
MP:0002665	decreased circulating corticosterone level	0.0049	<0.20
GO:0009062	fatty acid catabolic process	0.02	<0.20
ENSG00000099860	GADD45B PPI subnetwork	0.01	<0.20
ENSG00000136110	LECT1 PPI subnetwork	0.00383	<0.20
GO:0005759	mitochondrial matrix	0.00626	<0.20
GO:0042645	mitochondrial nucleoid	0.02	<0.20
GO:0051346	negative regulation of hydrolase activity	0.00437	<0.20
GO:0009295	nucleoid	0.02	<0.20
ENSG00000122194	PLG PPI subnetwork	0.00579	<0.20
REACTOME_INITIAL_TRIGGER	REACTOME_INITIAL_TRIGGERING_OF_COMPLEMENT	0.00633	<0.20
REACTOME_STEROID_HORMO	REACTOME_STEROID_HORMONES	0.01	<0.20
GO:0051384	response to glucocorticoid stimulus	0.00424	<0.20
ENSG00000182010	RTKN2 PPI subnetwork	0.00982	<0.20
MP:0001510	abnormal coat appearance	0.02	<0.20
ENSG00000076555	ACACB PPI subnetwork	0.02	<0.20
ENSG00000161618	ALDH16A1 PPI subnetwork	0.01	<0.20
GO:0004177	aminopeptidase activity	0.02	<0.20
GO:0071216	cellular response to biotic stimulus	0.01	<0.20
ENSG00000136108	CKAP2 PPI subnetwork	0.01	<0.20
GO:0030128	clathrin coat of endocytic vesicle	0.00964	<0.20
ENSG00000107611	CUBN PPI subnetwork	0.01	<0.20
MP:0006058	decreased cerebral infarction size	0.00464	<0.20
MP:0009789	decreased susceptibility to bacterial infection induced morbi	0.00401	<0.20
GO:0005793	endoplasmic reticulum-Golgi intermediate compartment	0.02	<0.20
ENSG00000125998	FAM83C PPI subnetwork	0.00697	<0.20
ENSG00000171560	FGA PPI subnetwork	0.01	<0.20
ENSG00000107623	GDF10 PPI subnetwork	0.03	<0.20
ENSG00000206172	HBA1 PPI subnetwork	0.00652	<0.20
ENSG00000188536	HBA2 PPI subnetwork	0.00652	<0.20
ENSG00000103942	HOMER2 PPI subnetwork	0.02	<0.20
ENSG00000106348	IMPDH1 PPI subnetwork	0.00406	<0.20
KEGG_STARCH_AND_SUCROS	KEGG_STARCH_AND_SUCROSE_METABOLISM	0.00856	<0.20
KEGG_STEROID_BIOSYNTHESI	KEGG_STEROID_BIOSYNTHESIS	0.02	<0.20
ENSG00000113889	KNG1 PPI subnetwork	0.02	<0.20
GO:0016877	ligase activity, forming carbon-sulfur bonds	0.02	<0.20
ENSG00000146701	MDH2 PPI subnetwork	0.02	<0.20
ENSG00000171497	PPID PPI subnetwork	0.02	<0.20
REACTOME_CREATION_OF_C4	REACTOME_CREATION_OF_C4_AND_C2_ACTIVATORS	0.01	<0.20
REACTOME_NUCLEAR_RECEP	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWA	0.00357	<0.20
GO:0042493	response to drug	0.00983	<0.20
GO:0033993	response to lipid	0.00947	<0.20
GO:0019841	retinol binding	0.02	<0.20
ENSG00000171150	SOCS5 PPI subnetwork	0.02	<0.20
ENSG00000116754	SRSF11 PPI subnetwork	0.01	<0.20
ENSG00000137561	TTPA PPI subnetwork	0.00601	<0.20
ENSG00000139719	VPS33A PPI subnetwork	0.01	<0.20

GO:0006953	acute-phase response	0.00936	<0.20
GO:0046164	alcohol catabolic process	0.00728	<0.20
ENSG00000171793	CTPS PPI subnetwork	0.00506	<0.20
ENSG00000115866	DARS PPI subnetwork	0.01	<0.20
MP:0008617	increased circulating interleukin-12 level	0.02	<0.20
GO:0045087	innate immune response	0.02	<0.20
KEGG_GLYCOSAMINOGLYCAN	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	0.02	<0.20
GO:0004879	ligand-activated sequence-specific DNA binding RNA polymer	0.00392	<0.20
GO:0005764	lysosome	0.00828	<0.20
GO:0000323	lytic vacuole	0.00828	<0.20
GO:0046365	monosaccharide catabolic process	0.01	<0.20
ENSG00000066933	MYO9A PPI subnetwork	0.00753	<0.20
GO:0031968	organelle outer membrane	0.00695	<0.20
GO:0019867	outer membrane	0.00381	<0.20
GO:0045923	positive regulation of fatty acid metabolic process	0.02	<0.20
ENSG00000111725	PRKAB1 PPI subnetwork	0.00496	<0.20
ENSG00000148334	PTGES2 PPI subnetwork	0.00903	<0.20
GO:0030193	regulation of blood coagulation	0.02	<0.20
GO:0050994	regulation of lipid catabolic process	0.02	<0.20
GO:0050810	regulation of steroid biosynthetic process	0.02	<0.20
GO:0061041	regulation of wound healing	0.00987	<0.20
GO:0002237	response to molecule of bacterial origin	0.00444	<0.20
ENSG00000180879	SSR4 PPI subnetwork	0.03	<0.20
GO:0003707	steroid hormone receptor activity	0.00452	<0.20
ENSG00000174125	TLR1 PPI subnetwork	0.02	<0.20
ENSG00000137462	TLR2 PPI subnetwork	0.03	<0.20
GO:0005773	vacuole	0.00714	<0.20
MP:0005325	abnormal renal glomerulus morphology	0.00387	<0.20
MP:0000221	decreased leukocyte cell number	0.02	<0.20
GO:0001701	in utero embryonic development	0.00919	<0.20
MP:0001879	abnormal lymphatic vessel morphology	0.02	<0.20
MP:0002357	abnormal spleen white pulp morphology	0.00354	<0.20
GO:0019395	fatty acid oxidation	0.00502	<0.20
ENSG00000115414	FN1 PPI subnetwork	0.01	<0.20
ENSG00000116717	GADD45A PPI subnetwork	0.00636	<0.20
ENSG00000124151	NCOA3 PPI subnetwork	0.00396	<0.20
REACTOME_PEROXISOMAL_LI	REACTOME_PEROXISOMAL_LIPID_METABOLISM	0.02	<0.20
ENSG00000154262	ABCA6 PPI subnetwork	0.00611	<0.20
MP:0000681	abnormal thyroid gland morphology	0.01	<0.20
MP:0009643	abnormal urine homeostasis	0.01	<0.20
ENSG00000120500	ARR3 PPI subnetwork	0.01	<0.20
GO:0016835	carbon-oxygen lyase activity	0.01	<0.20
GO:0005507	copper ion binding	0.01	<0.20
ENSG00000175197	DDIT3 PPI subnetwork	0.00732	<0.20
MP:0008664	decreased interleukin-12 secretion	0.02	<0.20
MP:0001935	decreased litter size	0.00368	<0.20
ENSG00000150768	DLAT PPI subnetwork	0.0054	<0.20

MP:0000465	gastrointestinal hemorrhage	0.00591	<0.20
MP:0003725	increased autoantibody level	0.01	<0.20
MP:0005317	increased triglyceride level	0.02	<0.20
KEGG_PYRUVATE_METABOLIS	KEGG_PYRUVATE_METABOLISM	0.00354	<0.20
GO:0030258	lipid modification	0.01	<0.20
ENSG00000075643	MOCOS PPI subnetwork	0.00896	<0.20
GO:0070403	NAD+ binding	0.02	<0.20
GO:0043086	negative regulation of catalytic activity	0.0065	<0.20
GO:0015932	nucleobase-containing compound transmembrane transport	0.01	<0.20
ENSG00000109819	PPARGC1A PPI subnetwork	0.02	<0.20
ENSG00000173281	PPP1R3B PPI subnetwork	0.00446	<0.20
REACTOME_CLASSICAL_ANTIE	REACTOME_CLASSICAL_ANTIBODY:MEDIATED_COMPLEMEN	0.03	<0.20
MP:0001190	reddish skin	0.00634	<0.20
GO:0031960	response to corticosteroid stimulus	0.00995	<0.20
ENSG00000185338	SOCS1 PPI subnetwork	0.00676	<0.20
ENSG00000137642	SORL1 PPI subnetwork	0.00365	<0.20
MP:0000693	spleen hyperplasia	0.00407	<0.20
ENSG00000165409	TSHR PPI subnetwork	0.00557	<0.20
ENSG00000168454	TXNDC2 PPI subnetwork	0.02	<0.20
GO:0005775	vacuolar lumen	0.00518	<0.20
ENSG00000150630	VEGFC PPI subnetwork	0.00389	<0.20
MP:0008751	abnormal interleukin level	0.00823	<0.20
MP:0004047	abnormal milk composition	0.01	<0.20
MP:0006298	abnormal platelet activation	0.02	<0.20
GO:0002526	acute inflammatory response	0.02	<0.20
GO:0045178	basal part of cell	0.02	<0.20
ENSG00000156127	BATF PPI subnetwork	0.00891	<0.20
ENSG00000004660	CAMKK1 PPI subnetwork	0.00865	<0.20
ENSG00000153879	CEBPG PPI subnetwork	0.01	<0.20
GO:0010878	cholesterol storage	0.00495	<0.20
ENSG00000072832	CRMP1 PPI subnetwork	0.00877	<0.20
ENSG00000176102	CSTF3 PPI subnetwork	0.03	<0.20
ENSG00000173406	DAB1 PPI subnetwork	0.00509	<0.20
MP:0002411	decreased susceptibility to bacterial infection	0.01	<0.20
ENSG00000074800	ENO1 PPI subnetwork	0.02	<0.20
ENSG00000185637	ENSG00000185637 PPI subnetwork	0.01	<0.20
GO:0008238	exopeptidase activity	0.02	<0.20
MP:0001195	flaky skin	0.02	<0.20
GO:0009250	glucan biosynthetic process	0.00744	<0.20
GO:0005978	glycogen biosynthetic process	0.00744	<0.20
ENSG00000185245	GP1BA PPI subnetwork	0.01	<0.20
GO:0019320	hexose catabolic process	0.01	<0.20
ENSG00000169813	HNRNPF PPI subnetwork	0.01	<0.20
MP:0008388	hypochromic microcytic anemia	0.00368	<0.20
ENSG00000196083	IL1RAP PPI subnetwork	0.02	<0.20
MP:0010375	increased kidney iron level	0.02	<0.20
MP:0009766	increased sensitivity to xenobiotic induced morbidity/mortali	0.01	<0.20

MP:0008560	increased tumor necrosis factor secretion	0.00402	<0.20
KEGG_LYSOSOME	KEGG_LYSOSOME	0.00899	<0.20
ENSG00000088247	KHSRP PPI subnetwork	0.00991	<0.20
ENSG00000166484	MAPK7 PPI subnetwork	0.02	<0.20
ENSG00000100714	MTHFD1 PPI subnetwork	0.01	<0.20
ENSG00000136937	NCBP1 PPI subnetwork	0.0091	<0.20
GO:0010745	negative regulation of macrophage derived foam cell differer	0.01	<0.20
ENSG00000197111	PCBP2 PPI subnetwork	0.02	<0.20
ENSG00000145431	PDGFC PPI subnetwork	0.01	<0.20
ENSG00000170962	PDGFD PPI subnetwork	0.01	<0.20
GO:0031331	positive regulation of cellular catabolic process	0.00882	<0.20
GO:0051259	protein oligomerization	0.00676	<0.20
GO:0008565	protein transporter activity	0.00775	<0.20
ENSG00000174231	PRPF8 PPI subnetwork	0.03	<0.20
REACTOME_ACTIVATED_TLR4	REACTOME_ACTIVATED_TLR4_SIGNALLING	0.00608	<0.20
REACTOME_FATTY_ACYL:COA	REACTOME_FATTY_ACYL:COA_BIOSYNTHESIS	0.01	<0.20
REACTOME_MYD88:INDEPENI	REACTOME_MYD88:INDEPENDENT_CASCADE_INITIATED_ON	0.02	<0.20
GO:0010874	regulation of cholesterol efflux	0.00807	<0.20
GO:0051917	regulation of fibrinolysis	0.02	<0.20
GO:0060334	regulation of interferon-gamma-mediated signaling pathway	0.00783	<0.20
GO:0051004	regulation of lipoprotein lipase activity	0.02	<0.20
GO:0060330	regulation of response to interferon-gamma	0.00783	<0.20
GO:0009617	response to bacterium	0.03	<0.20
GO:0009607	response to biotic stimulus	0.02	<0.20
GO:0051707	response to other organism	0.02	<0.20
ENSG00000172058	SERF1A PPI subnetwork	0.01	<0.20
ENSG00000205572	SERF1B PPI subnetwork	0.01	<0.20
ENSG00000148082	SHC3 PPI subnetwork	0.02	<0.20
ENSG00000185634	SHC4 PPI subnetwork	0.00816	<0.20
ENSG00000124193	SRSF6 PPI subnetwork	0.02	<0.20
GO:0044403	symbiosis, encompassing mutualism through parasitism	0.03	<0.20
MP:0001260	increased body weight	0.01	<0.20
ENSG00000081479	LRP2 PPI subnetwork	0.02	<0.20
MP:0003567	abnormal fetal cardiomyocyte proliferation	0.01	<0.20
MP:0003662	abnormal long bone epiphyseal plate proliferative zone	0.02	<0.20
GO:0016323	basolateral plasma membrane	0.0063	<0.20
GO:0001568	blood vessel development	0.01	<0.20
GO:0048514	blood vessel morphogenesis	0.03	<0.20
GO:0042562	hormone binding	0.03	<0.20
MP:0008502	increased IgG3 level	0.00855	<0.20
ENSG00000075413	MARK3 PPI subnetwork	0.0052	<0.20
GO:0051287	NAD binding	0.00692	<0.20
GO:0048545	response to steroid hormone stimulus	0.01	<0.20
ENSG00000109072	SEBOX PPI subnetwork	0.01	<0.20
ENSG00000106366	SERPINE1 PPI subnetwork	0.03	<0.20
MP:0001179	thick pulmonary interalveolar septum	0.02	<0.20
GO:0001944	vasculature development	0.02	<0.20

MP:0000188	abnormal circulating glucose level	0.02	<0.20
MP:0000377	abnormal hair follicle morphology	0.01	<0.20
MP:0000267	abnormal heart development	0.00971	<0.20
MP:0000511	abnormal intestinal mucosa morphology	0.01	<0.20
MP:0002135	abnormal kidney morphology	0.02	<0.20
MP:0003659	abnormal lymph circulation	0.00541	<0.20
MP:0002344	abnormal lymph node B cell domain morphology	0.03	<0.20
MP:0002401	abnormal lymphopoiesis	0.01	<0.20
MP:0004779	abnormal production of surfactant	0.03	<0.20
MP:0005031	abnormal trophoblast layer morphology	0.0056	<0.20
MP:0004076	abnormal vitelline vascular remodeling	0.00365	<0.20
ENSG00000123268	ATF1 PPI subnetwork	0.01	<0.20
ENSG00000110955	ATP5B PPI subnetwork	0.0061	<0.20
GO:0060090	binding, bridging	0.00861	<0.20
ENSG00000179776	CDH5 PPI subnetwork	0.02	<0.20
ENSG00000184432	COPB2 PPI subnetwork	0.00368	<0.20
MP:0001258	decreased body length	0.03	<0.20
MP:0005517	decreased liver regeneration	0.00372	<0.20
MP:0008208	decreased pro-B cell number	0.00427	<0.20
MP:0003071	decreased vascular permeability	0.01	<0.20
MP:0003853	dry skin	0.01	<0.20
ENSG00000126767	ELK1 PPI subnetwork	0.02	<0.20
ENSG00000211653	ENSG00000211653 PPI subnetwork	0.02	<0.20
ENSG00000211660	ENSG00000211660 PPI subnetwork	0.02	<0.20
ENSG00000211973	ENSG00000211973 PPI subnetwork	0.01	<0.20
ENSG00000211979	ENSG00000211979 PPI subnetwork	0.01	<0.20
MP:0004180	failure of initiation of embryo turning	0.01	<0.20
MP:0001926	female infertility	0.00618	<0.20
ENSG00000138685	FGF2 PPI subnetwork	0.00358	<0.20
GO:0005925	focal adhesion	0.02	<0.20
MP:0005244	hemopericardium	0.02	<0.20
MP:0003331	hepatocellular carcinoma	0.01	<0.20
ENSG00000114315	HES1 PPI subnetwork	0.02	<0.20
MP:0004762	increased anti-double stranded DNA antibody level	0.02	<0.20
MP:0006042	increased apoptosis	0.00669	<0.20
MP:0005014	increased B cell number	0.02	<0.20
ENSG00000162434	JAK1 PPI subnetwork	0.00503	<0.20
ENSG00000105639	JAK3 PPI subnetwork	0.01	<0.20
KEGG_PENTOSE_PHOSPHATE_	KEGG_PENTOSE_PHOSPHATE_PATHWAY	0.01	<0.20
MP:0011423	kidney cortex atrophy	0.00888	<0.20
ENSG00000174697	LEP PPI subnetwork	0.0077	<0.20
ENSG00000014641	MDH1 PPI subnetwork	0.00917	<0.20
MP:0011427	mesangial cell hyperplasia	0.02	<0.20
GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors	0.03	<0.20
MP:0011109	partial lethality throughout fetal growth and development	0.00545	<0.20
GO:0001871	pattern binding	0.03	<0.20
GO:0001890	placenta development	0.00472	<0.20

GO:0030247	polysaccharide binding	0.03	<0.20
ENSG00000132825	PPP1R3D PPI subnetwork	0.00374	<0.20
GO:0030674	protein binding, bridging	0.01	<0.20
GO:0032403	protein complex binding	0.00661	<0.20
REACTOME_MEMBRANE_TRA	REACTOME_MEMBRANE_TRAFFICKING	0.01	<0.20
REACTOME_MYD88_CASCADE	REACTOME_MYD88_CASCADE_INITIATED_ON_PLASMA_MEM	0.00827	<0.20
REACTOME_P130CAS_LINKAG	REACTOME_P130CAS_LINKAGE_TO_MAPK_SIGNALING_FOR_	0.00661	<0.20
REACTOME_SIGNALING_BY_V	REACTOME_SIGNALING_BY_VEGF	0.00802	<0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_10_TLR10_CASCADE	0.00827	<0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_5_TLR5_CASCADE	0.00827	<0.20
REACTOME_VEGF_LIGAND:RE	REACTOME_VEGF_LIGAND:RECEPTOR_INTERACTIONS	0.00802	<0.20
GO:2000145	regulation of cell motility	0.02	<0.20
GO:0051270	regulation of cellular component movement	0.00679	<0.20
GO:0060191	regulation of lipase activity	0.02	<0.20
GO:0071900	regulation of protein serine/threonine kinase activity	0.01	<0.20
GO:0010035	response to inorganic substance	0.01	<0.20
ENSG00000119729	RHOQ PPI subnetwork	0.02	<0.20
MP:0001870	salivary gland inflammation	0.01	<0.20
ENSG00000095637	SORBS1 PPI subnetwork	0.00923	<0.20
ENSG00000142539	SPIB PPI subnetwork	0.00409	<0.20
MP:0004057	thin myocardium compact layer	0.01	<0.20
ENSG00000178952	TUFM PPI subnetwork	0.02	<0.20
MP:0001263	weight loss	0.00365	<0.20
ENSG00000117528	ABCD3 PPI subnetwork	0.01	<0.20
MP:0001726	abnormal allantois morphology	0.01	<0.20
MP:0008533	abnormal anterior visceral endoderm morphology	0.02	<0.20
MP:0001614	abnormal blood vessel morphology	0.00836	<0.20
MP:0001259	abnormal body weight	0.02	<0.20
MP:0000662	abnormal branching of the mammary ductal tree	0.01	<0.20
MP:0003658	abnormal capillary morphology	0.01	<0.20
MP:0003091	abnormal cell migration	0.00578	<0.20
MP:0008713	abnormal cytokine level	0.02	<0.20
MP:0004787	abnormal dorsal aorta morphology	0.01	<0.20
MP:0002408	abnormal double-positive T cell morphology	0.01	<0.20
MP:0003396	abnormal embryonic hematopoiesis	0.00745	<0.20
MP:0001239	abnormal epidermis stratum granulosum morphology	0.02	<0.20
MP:0003656	abnormal erythrocyte physiology	0.02	<0.20
MP:0001790	abnormal immune system physiology	0.00552	<0.20
MP:0001845	abnormal inflammatory response	0.01	<0.20
MP:0000281	abnormal interventricular septum morphology	0.02	<0.20
MP:0003628	abnormal leukocyte adhesion	0.00478	<0.20
MP:0003156	abnormal leukocyte migration	0.00368	<0.20
MP:0003055	abnormal long bone epiphyseal plate morphology	0.01	<0.20
MP:0000165	abnormal long bone hypertrophic chondrocyte zone	0.01	<0.20
MP:0005058	abnormal lysosome morphology	0.02	<0.20
MP:0002417	abnormal megakaryocyte morphology	0.0065	<0.20
MP:0005657	abnormal neural plate morphology	0.00625	<0.20

MP:0005464	abnormal platelet physiology	0.02	<0.20
MP:0003638	abnormal response/metabolism to endogenous compounds	0.02	<0.20
MP:0003227	abnormal vascular branching morphogenesis	0.00481	<0.20
MP:0006055	abnormal vascular endothelial cell morphology	0.00777	<0.20
MP:0005592	abnormal vascular smooth muscle morphology	0.01	<0.20
MP:0001721	absent visceral yolk sac blood islands	0.00388	<0.20
ENSG00000159251	ACTC1 PPI subnetwork	0.03	<0.20
GO:0002253	activation of immune response	0.02	<0.20
ENSG00000136518	ACTL6A PPI subnetwork	0.0045	<0.20
ENSG00000185736	ADARB2 PPI subnetwork	0.00404	<0.20
ENSG00000144218	AFF3 PPI subnetwork	0.02	<0.20
ENSG00000105221	AKT2 PPI subnetwork	0.01	<0.20
ENSG00000117020	AKT3 PPI subnetwork	0.02	<0.20
ENSG00000136383	ALPK3 PPI subnetwork	0.02	<0.20
ENSG00000163283	ALPP PPI subnetwork	0.02	<0.20
MP:0000343	altered response to myocardial infarction	0.00891	<0.20
GO:0003823	antigen binding	0.00677	<0.20
ENSG00000197043	ANXA6 PPI subnetwork	0.0051	<0.20
ENSG00000143761	ARF1 PPI subnetwork	0.00598	<0.20
ENSG00000101199	ARFGAP1 PPI subnetwork	0.02	<0.20
ENSG00000107863	ARHGAP21 PPI subnetwork	0.02	<0.20
ENSG00000150347	ARID5B PPI subnetwork	0.02	<0.20
ENSG00000111229	ARPC3 PPI subnetwork	0.02	<0.20
ENSG00000141480	ARRB2 PPI subnetwork	0.02	<0.20
ENSG00000151693	ASAP2 PPI subnetwork	0.00502	<0.20
ENSG00000129691	ASH2L PPI subnetwork	0.02	<0.20
ENSG00000156273	BACH1 PPI subnetwork	0.02	<0.20
ENSG00000103507	BCKDK PPI subnetwork	0.02	<0.20
ENSG00000029363	BCLAF1 PPI subnetwork	0.00692	<0.20
ENSG00000186716	BCR PPI subnetwork	0.00351	<0.20
ENSG00000102010	BMX PPI subnetwork	0.00613	<0.20
ENSG00000012048	BRCA1 PPI subnetwork	0.00467	<0.20
GO:0050873	brown fat cell differentiation	0.02	<0.20
ENSG00000010671	BTK PPI subnetwork	0.02	<0.20
ENSG00000182326	C1S PPI subnetwork	0.02	<0.20
ENSG00000077549	CAPZB PPI subnetwork	0.02	<0.20
MP:0003141	cardiac fibrosis	0.02	<0.20
ENSG00000106144	CASP2 PPI subnetwork	0.02	<0.20
ENSG00000164305	CASP3 PPI subnetwork	0.00379	<0.20
ENSG00000105974	CAV1 PPI subnetwork	0.01	<0.20
ENSG00000110395	CBL PPI subnetwork	0.00822	<0.20
ENSG00000114423	CBLB PPI subnetwork	0.02	<0.20
ENSG00000108691	CCL2 PPI subnetwork	0.02	<0.20
ENSG00000006075	CCL3 PPI subnetwork	0.02	<0.20
ENSG00000010278	CD9 PPI subnetwork	0.00528	<0.20
ENSG00000102225	CDK16 PPI subnetwork	0.00472	<0.20
ENSG00000135446	CDK4 PPI subnetwork	0.01	<0.20

GO:0005924	cell-substrate adherens junction	0.02	<0.20
ENSG00000166582	CENPV PPI subnetwork	0.02	<0.20
ENSG00000143702	CEP170 PPI subnetwork	0.02	<0.20
ENSG00000111642	CHD4 PPI subnetwork	0.00556	<0.20
GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	0.02	<0.20
GO:0000785	chromatin	0.02	<0.20
ENSG00000213341	CHUK PPI subnetwork	0.01	<0.20
ENSG00000123975	CKS2 PPI subnetwork	0.01	<0.20
ENSG00000013441	CLK1 PPI subnetwork	0.02	<0.20
ENSG00000179335	CLK3 PPI subnetwork	0.03	<0.20
ENSG00000164692	COL1A2 PPI subnetwork	0.00568	<0.20
MP:0002816	colitis	0.01	<0.20
MP:0011092	complete embryonic lethality	0.01	<0.20
MP:0011097	complete embryonic lethality before turning of embryo	0.02	<0.20
ENSG00000095794	CREM PPI subnetwork	0.02	<0.20
ENSG00000160741	CRTC2 PPI subnetwork	0.01	<0.20
ENSG00000070770	CSNK2A2 PPI subnetwork	0.00829	<0.20
GO:0001816	cytokine production	0.00837	<0.20
ENSG00000113758	DBN1 PPI subnetwork	0.02	<0.20
ENSG00000079785	DDX1 PPI subnetwork	0.02	<0.20
MP:0003503	decreased activity of thyroid	0.01	<0.20
MP:0005602	decreased angiogenesis	0.01	<0.20
MP:0005017	decreased B cell number	0.02	<0.20
MP:0000333	decreased bone marrow cell number	0.00357	<0.20
MP:0004016	decreased bone mass	0.01	<0.20
MP:0000352	decreased cell proliferation	0.01	<0.20
MP:0008813	decreased common myeloid progenitor cell number	0.01	<0.20
MP:0008973	decreased erythroid progenitor cell number	0.02	<0.20
MP:0004502	decreased incidence of chemically-induced tumors	0.00443	<0.20
MP:0000223	decreased monocyte cell number	0.03	<0.20
MP:0008874	decreased physiological sensitivity to xenobiotic	0.02	<0.20
MP:0008209	decreased pre-B cell number	0.01	<0.20
MP:0009400	decreased skeletal muscle fiber size	0.00461	<0.20
MP:0005597	decreased susceptibility to type I hypersensitivity reaction	0.00475	<0.20
MP:0005616	decreased susceptibility to type IV hypersensitivity reaction	0.01	<0.20
MP:0002843	decreased systemic arterial blood pressure	0.00436	<0.20
MP:0009133	decreased white fat cell size	0.00979	<0.20
MP:0001194	dermatitis	0.00977	<0.20
MP:0002753	dilated heart left ventricle	0.00607	<0.20
ENSG00000069345	DNAJA2 PPI subnetwork	0.00731	<0.20
ENSG00000107404	DVL1 PPI subnetwork	0.02	<0.20
ENSG00000105204	DYRK1B PPI subnetwork	0.00685	<0.20
ENSG00000156508	EEF1A1 PPI subnetwork	0.00828	<0.20
ENSG00000146648	EGFR PPI subnetwork	0.00371	<0.20
ENSG00000092847	EIF2C1 PPI subnetwork	0.02	<0.20
ENSG00000134759	ELP2 PPI subnetwork	0.02	<0.20
ENSG00000154380	ENAH PPI subnetwork	0.01	<0.20

GO:0005768	endosome	0.00693	<0.20
MP:0000702	enlarged lymph nodes	0.02	<0.20
MP:0000291	enlarged pericardium	0.02	<0.20
ENSG00000173366	ENSG00000173366 PPI subnetwork	0.01	<0.20
ENSG00000206274	ENSG00000206274 PPI subnetwork	0.01	<0.20
ENSG00000206407	ENSG00000206407 PPI subnetwork	0.01	<0.20
ENSG00000212860	ENSG00000212860 PPI subnetwork	0.01	<0.20
ENSG00000215292	ENSG00000215292 PPI subnetwork	0.01	<0.20
ENSG00000140009	ESR2 PPI subnetwork	0.00952	<0.20
GO:0009897	external side of plasma membrane	0.02	<0.20
ENSG00000184083	FAM120C PPI subnetwork	0.00836	<0.20
ENSG00000169710	FASN PPI subnetwork	0.0056	<0.20
ENSG00000143226	FCGR2A PPI subnetwork	0.02	<0.20
ENSG00000072694	FCGR2B PPI subnetwork	0.03	<0.20
ENSG00000203747	FCGR3A PPI subnetwork	0.02	<0.20
ENSG00000182511	FES PPI subnetwork	0.00377	<0.20
ENSG00000115641	FHL2 PPI subnetwork	0.00473	<0.20
ENSG00000102755	FLT1 PPI subnetwork	0.00357	<0.20
ENSG00000109458	GAB1 PPI subnetwork	0.00999	<0.20
ENSG00000112964	GHR PPI subnetwork	0.02	<0.20
MP:0011506	glomerular crescent	0.00585	<0.20
GO:0005355	glucose transmembrane transporter activity	0.02	<0.20
GO:0006096	glycolysis	0.03	<0.20
ENSG00000181656	GPR88 PPI subnetwork	0.00967	<0.20
MP:0002500	granulomatous inflammation	0.01	<0.20
ENSG00000154016	GRAP PPI subnetwork	0.00475	<0.20
GO:0019838	growth factor binding	0.02	<0.20
ENSG00000082701	GSK3B PPI subnetwork	0.02	<0.20
ENSG00000172534	HCFC1 PPI subnetwork	0.02	<0.20
ENSG00000101336	HCK PPI subnetwork	0.00748	<0.20
ENSG00000116478	HDAC1 PPI subnetwork	0.02	<0.20
ENSG00000196591	HDAC2 PPI subnetwork	0.01	<0.20
ENSG00000171720	HDAC3 PPI subnetwork	0.02	<0.20
ENSG00000061273	HDAC7 PPI subnetwork	0.01	<0.20
MP:0001853	heart inflammation	0.01	<0.20
GO:0048534	hemopoietic or lymphoid organ development	0.00485	<0.20
GO:0000792	heterochromatin	0.01	<0.20
ENSG00000168298	HIST1H1E PPI subnetwork	0.02	<0.20
GO:0035097	histone methyltransferase complex	0.02	<0.20
ENSG00000064961	HMG20B PPI subnetwork	0.00908	<0.20
ENSG00000135486	HNRNPA1 PPI subnetwork	0.01	<0.20
ENSG00000122566	HNRNPA2B1 PPI subnetwork	0.01	<0.20
ENSG00000197451	HNRNPAB PPI subnetwork	0.02	<0.20
ENSG00000138668	HNRNPD PPI subnetwork	0.00568	<0.20
ENSG00000165119	HNRNPK PPI subnetwork	0.00688	<0.20
ENSG00000153187	HNRNPU PPI subnetwork	0.00597	<0.20
ENSG00000204389	HSPA1A PPI subnetwork	0.01	<0.20

ENSG00000215328	HSPA1A PPI subnetwork	0.0065	<0.20
ENSG00000204388	HSPA1B PPI subnetwork	0.01	<0.20
ENSG00000212866	HSPA1B PPI subnetwork	0.01	<0.20
ENSG00000206383	HSPA1L PPI subnetwork	0.01	<0.20
ENSG00000170606	HSPA4 PPI subnetwork	0.02	<0.20
ENSG00000109971	HSPA8 PPI subnetwork	0.01	<0.20
ENSG00000144381	HSPD1 PPI subnetwork	0.02	<0.20
ENSG00000164270	HTR4 PPI subnetwork	0.00728	<0.20
ENSG00000086758	HUWE1 PPI subnetwork	0.02	<0.20
ENSG00000090339	ICAM1 PPI subnetwork	0.00589	<0.20
ENSG00000101365	IDH3B PPI subnetwork	0.02	<0.20
ENSG00000169306	IL1RAPL1 PPI subnetwork	0.01	<0.20
MP:0002467	impaired neutrophil phagocytosis	0.01	<0.20
MP:0005565	increased blood urea nitrogen level	0.02	<0.20
MP:0005599	increased cardiac muscle contractility	0.02	<0.20
MP:0008577	increased circulating interferon-gamma level	0.01	<0.20
MP:0002781	increased circulating testosterone level	0.0096	<0.20
MP:0003911	increased drinking behavior	0.01	<0.20
MP:0002493	increased IgG level	0.02	<0.20
MP:0003058	increased insulin secretion	0.01	<0.20
MP:0008807	increased liver iron level	0.02	<0.20
MP:0008181	increased marginal zone B cell number	0.01	<0.20
MP:0000220	increased monocyte cell number	0.03	<0.20
MP:0000219	increased neutrophil cell number	0.00603	<0.20
MP:0009814	increased prostaglandin level	0.0075	<0.20
MP:0010067	increased red blood cell distribution width	0.00906	<0.20
MP:0005399	increased susceptibility to fungal infection	0.02	<0.20
MP:0005015	increased T cell number	0.02	<0.20
ENSG00000115274	INO80B PPI subnetwork	0.01	<0.20
GO:0008286	insulin receptor signaling pathway	0.00528	<0.20
ENSG00000161638	ITGA5 PPI subnetwork	0.00939	<0.20
ENSG00000091409	ITGA6 PPI subnetwork	0.01	<0.20
ENSG00000135424	ITGA7 PPI subnetwork	0.02	<0.20
ENSG00000150093	ITGB1 PPI subnetwork	0.00932	<0.20
ENSG00000135916	ITM2C PPI subnetwork	0.02	<0.20
ENSG00000073614	KDM5A PPI subnetwork	0.00616	<0.20
ENSG00000128052	KDR PPI subnetwork	0.00432	<0.20
KEGG_ADHERENS_JUNCTION	KEGG_ADHERENS_JUNCTION	0.01	<0.20
KEGG_GLYCOLYSIS_GLUCONE	KEGG_GLYCOLYSIS_GLUCONEOGENESIS	0.01	<0.20
GO:0019210	kinase inhibitor activity	0.01	<0.20
ENSG00000105610	KLF1 PPI subnetwork	0.01	<0.20
ENSG00000102753	KPNA3 PPI subnetwork	0.02	<0.20
ENSG00000100079	LGALS2 PPI subnetwork	0.02	<0.20
ENSG00000163956	LRPAP1 PPI subnetwork	0.00904	<0.20
GO:0022884	macromolecule transmembrane transporter activity	0.03	<0.20
GO:0004709	MAP kinase kinase kinase activity	0.02	<0.20
ENSG00000186868	MAPT PPI subnetwork	0.01	<0.20

ENSG00000072518	MARK2 PPI subnetwork	0.02	<0.20
ENSG00000007264	MATK PPI subnetwork	0.00475	<0.20
ENSG00000171444	MCC PPI subnetwork	0.01	<0.20
ENSG00000065833	ME1 PPI subnetwork	0.00922	<0.20
GO:0042470	melanosome	0.01	<0.20
GO:0034708	methyltransferase complex	0.02	<0.20
MP:0002810	microcytic anemia	0.02	<0.20
ENSG00000087245	MMP2 PPI subnetwork	0.02	<0.20
ENSG00000155363	MOV10 PPI subnetwork	0.02	<0.20
ENSG00000166930	MS4A5 PPI subnetwork	0.00729	<0.20
ENSG00000164078	MST1R PPI subnetwork	0.00626	<0.20
ENSG00000101057	MYBL2 PPI subnetwork	0.01	<0.20
ENSG00000084676	NCOA1 PPI subnetwork	0.00667	<0.20
ENSG00000138293	NCOA4 PPI subnetwork	0.00638	<0.20
ENSG00000049759	NEDD4L PPI subnetwork	0.02	<0.20
GO:0030308	negative regulation of cell growth	0.02	<0.20
GO:0032269	negative regulation of cellular protein metabolic process	0.00605	<0.20
GO:0051048	negative regulation of secretion	0.00817	<0.20
ENSG00000119408	NEK6 PPI subnetwork	0.01	<0.20
ENSG00000116044	NFE2L2 PPI subnetwork	0.02	<0.20
ENSG00000109320	NFKB1 PPI subnetwork	0.00769	<0.20
ENSG00000001167	NFYA PPI subnetwork	0.02	<0.20
ENSG00000136352	NKX2-1 PPI subnetwork	0.02	<0.20
ENSG00000166197	NOLC1 PPI subnetwork	0.00448	<0.20
ENSG00000164867	NOS3 PPI subnetwork	0.02	<0.20
ENSG00000215440	NPEPL1 PPI subnetwork	0.01	<0.20
GO:0051169	nuclear transport	0.02	<0.20
GO:0006913	nucleocytoplasmic transport	0.02	<0.20
ENSG00000070882	OSBPL3 PPI subnetwork	0.01	<0.20
GO:0030728	ovulation	0.02	<0.20
ENSG00000171759	PAH PPI subnetwork	0.02	<0.20
ENSG00000049246	PER3 PPI subnetwork	0.03	<0.20
ENSG00000134686	PHC2 PPI subnetwork	0.00938	<0.20
GO:0019902	phosphatase binding	0.03	<0.20
GO:0048770	pigment granule	0.01	<0.20
ENSG00000051382	PIK3CB PPI subnetwork	0.02	<0.20
ENSG00000105851	PIK3CG PPI subnetwork	0.02	<0.20
ENSG00000196455	PIK3R4 PPI subnetwork	0.00365	<0.20
ENSG00000141506	PIK3R5 PPI subnetwork	0.02	<0.20
ENSG00000057294	PKP2 PPI subnetwork	0.02	<0.20
ENSG00000184381	PLA2G6 PPI subnetwork	0.02	<0.20
GO:0002576	platelet degranulation	0.02	<0.20
ENSG00000102024	PLS3 PPI subnetwork	0.02	<0.20
ENSG00000140464	PML PPI subnetwork	0.01	<0.20
ENSG00000100941	PNN PPI subnetwork	0.02	<0.20
MP:0002643	poikilocytosis	0.01	<0.20
MP:0001633	poor circulation	0.00844	<0.20

GO:0002684	positive regulation of immune system process	0.02	<0.20
GO:0051247	positive regulation of protein metabolic process	0.01	<0.20
GO:0045940	positive regulation of steroid metabolic process	0.03	<0.20
MP:0001732	postnatal growth retardation	0.02	<0.20
GO:0010608	posttranscriptional regulation of gene expression	0.00652	<0.20
ENSG00000204569	PPP1R10 PPI subnetwork	0.01	<0.20
ENSG00000206489	PPP1R10 PPI subnetwork	0.01	<0.20
ENSG00000154415	PPP1R3A PPI subnetwork	0.02	<0.20
ENSG00000132356	PRKAA1 PPI subnetwork	0.00429	<0.20
ENSG00000160310	PRMT2 PPI subnetwork	0.01	<0.20
GO:0006606	protein import into nucleus	0.00505	<0.20
GO:0004860	protein kinase inhibitor activity	0.02	<0.20
GO:0034504	protein localization to nucleus	0.00828	<0.20
GO:0008320	protein transmembrane transporter activity	0.03	<0.20
ENSG00000196504	PRPF40A PPI subnetwork	0.01	<0.20
ENSG00000169398	PTK2 PPI subnetwork	0.01	<0.20
ENSG00000120899	PTK2B PPI subnetwork	0.00415	<0.20
ENSG00000101213	PTK6 PPI subnetwork	0.02	<0.20
ENSG00000196396	PTPN1 PPI subnetwork	0.02	<0.20
ENSG00000070159	PTPN3 PPI subnetwork	0.02	<0.20
ENSG00000089159	PXN PPI subnetwork	0.02	<0.20
ENSG00000132155	RAF1 PPI subnetwork	0.02	<0.20
ENSG00000131759	RARA PPI subnetwork	0.00737	<0.20
ENSG00000145715	RASA1 PPI subnetwork	0.02	<0.20
ENSG00000146587	RBAK PPI subnetwork	0.01	<0.20
ENSG00000089902	RCOR1 PPI subnetwork	0.02	<0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1	0.00627	<0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_CHAPERONES_BY_IRE1ALPHA	0.00969	<0.20
REACTOME_APOPTOTIC_EXEC	REACTOME_APOPTOTIC_EXECUTION__PHASE	0.02	<0.20
REACTOME_CLATHRIN_DERIV	REACTOME_CLATHRIN_DERIVED_VESICLE_BUDDING	0.00614	<0.20
REACTOME_GLYCOGEN_BREA	REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	0.00593	<0.20
REACTOME_GOLGI_ASSOCIAT	REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	0.00887	<0.20
REACTOME_GRB2SOS_PROVII	REACTOME_GRB2SOS_PROVIDES_LINKAGE_TO_MAPK_SIGN/	0.01	<0.20
REACTOME_HORMONE:SENSI	REACTOME_HORMONE:SENSITIVE_LIPASE_HSL:MEDIATED_T	0.00472	<0.20
REACTOME_INTERLEUKIN:7_S	REACTOME_INTERLEUKIN:7_SIGNALING	0.01	<0.20
REACTOME_MYD88_DEPENDI	REACTOME_MYD88_DEPENDENT_CASCADE_INITIATED_ON_	0.01	<0.20
REACTOME_MYD88MAL_CAS	REACTOME_MYD88MAL_CASCADE_INITIATED_ON_PLASMA_	0.00403	<0.20
REACTOME_NFKB_AND_MAP	REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIA	0.01	<0.20
REACTOME_NGF_SIGNALLING	REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASM	0.00602	<0.20
REACTOME_PI3K_EVENTS_IN_	REACTOME_PI3K_EVENTS_IN_ERBB2_SIGNALING	0.00993	<0.20
REACTOME_PI3K_EVENTS_IN_	REACTOME_PI3K_EVENTS_IN_ERBB4_SIGNALING	0.02	<0.20
REACTOME_PI3KAKT_ACTIVA	REACTOME_PI3KAKT_ACTIVATION	0.01	<0.20
REACTOME_PROSTANOID_MI	REACTOME_PROSTANOID_METABOLISM	0.02	<0.20
REACTOME_SIGNAL_REGULA	REACTOME_SIGNAL_REGULATORY_PROTEIN_SIRP_FAMILY_I	0.0064	<0.20
REACTOME_SIGNALING_BY_E	REACTOME_SIGNALING_BY_EGFR_IN_CANCER	0.02	<0.20
REACTOME_SIGNALING_BY_I	REACTOME_SIGNALING_BY_INTERLEUKINS	0.00749	<0.20
REACTOME_SIGNALLING_BY_	REACTOME_SIGNALLING_BY_NGF	0.02	<0.20

REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_2_TLR2_CASCADE	0.00403	<0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_78_TLR78_CASCADE	0.01	<0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_9_TLR9_CASCADE	0.00875	<0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_TLR1TLR2_CASCADE	0.00403	<0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_TLR6TLR2_CASCADE	0.00403	<0.20
REACTOME_TRAF6_MEDIATEI	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_	0.01	<0.20
REACTOME_TRANS:GOLGI_NE	REACTOME_TRANS:GOLGI_NETWORK_VESICLE_BUDDING	0.00614	<0.20
REACTOME_UNFOLDED_PRO1	REACTOME_UNFOLDED_PROTEIN_RESPONSE	0.00665	<0.20
GO:0031329	regulation of cellular catabolic process	0.00953	<0.20
GO:0001817	regulation of cytokine production	0.02	<0.20
GO:0030100	regulation of endocytosis	0.00593	<0.20
GO:0045646	regulation of erythrocyte differentiation	0.02	<0.20
GO:0046320	regulation of fatty acid oxidation	0.02	<0.20
GO:0040008	regulation of growth	0.00832	<0.20
GO:0050727	regulation of inflammatory response	0.02	<0.20
GO:0033157	regulation of intracellular protein transport	0.00438	<0.20
GO:0010883	regulation of lipid storage	0.00701	<0.20
GO:0040014	regulation of multicellular organism growth	0.02	<0.20
GO:0032880	regulation of protein localization	0.02	<0.20
GO:0032101	regulation of response to external stimulus	0.00764	<0.20
GO:0032680	regulation of tumor necrosis factor production	0.02	<0.20
GO:0034097	response to cytokine stimulus	0.02	<0.20
GO:0010038	response to metal ion	0.00727	<0.20
ENSG00000165731	RET PPI subnetwork	0.02	<0.20
GO:0016918	retinal binding	0.02	<0.20
ENSG00000205937	RNPS1 PPI subnetwork	0.02	<0.20
GO:0030867	rough endoplasmic reticulum membrane	0.01	<0.20
ENSG00000108443	RPS6KB1 PPI subnetwork	0.00906	<0.20
ENSG00000124782	RREB1 PPI subnetwork	0.00825	<0.20
GO:0001726	ruffle	0.02	<0.20
ENSG00000159216	RUNX1 PPI subnetwork	0.03	<0.20
GO:0070461	SAGA-type complex	0.02	<0.20
MP:0001192	scaly skin	0.01	<0.20
ENSG00000136021	SCYL2 PPI subnetwork	0.02	<0.20
ENSG00000138802	SEC24B PPI subnetwork	0.02	<0.20
ENSG00000104897	SF3A2 PPI subnetwork	0.01	<0.20
ENSG00000189091	SF3B3 PPI subnetwork	0.03	<0.20
ENSG00000160999	SH2B2 PPI subnetwork	0.00808	<0.20
ENSG00000198478	SH3BGRL2 PPI subnetwork	0.00438	<0.20
ENSG00000107338	SHB PPI subnetwork	0.03	<0.20
ENSG00000129214	SHBG PPI subnetwork	0.02	<0.20
ENSG00000169375	SIN3A PPI subnetwork	0.02	<0.20
MP:0001212	skin lesions	0.01	<0.20
ENSG00000145604	SKP2 PPI subnetwork	0.02	<0.20
ENSG00000140284	SLC27A2 PPI subnetwork	0.02	<0.20
ENSG00000139514	SLC7A1 PPI subnetwork	0.02	<0.20
ENSG00000170365	SMAD1 PPI subnetwork	0.00934	<0.20

ENSG00000113658	SMAD5 PPI subnetwork	0.02	<0.20
ENSG00000099956	SMARCB1 PPI subnetwork	0.02	<0.20
ENSG00000184557	SOCS3 PPI subnetwork	0.03	<0.20
ENSG00000184985	SORCS2 PPI subnetwork	0.02	<0.20
ENSG00000134243	SORT1 PPI subnetwork	0.01	<0.20
ENSG00000163806	SPDYA PPI subnetwork	0.03	<0.20
ENSG00000066336	SPI1 PPI subnetwork	0.02	<0.20
ENSG00000118785	SPP1 PPI subnetwork	0.02	<0.20
ENSG00000125508	SRMS PPI subnetwork	0.03	<0.20
ENSG00000138378	STAT4 PPI subnetwork	0.01	<0.20
ENSG00000166888	STAT6 PPI subnetwork	0.00394	<0.20
ENSG00000060140	STYK1 PPI subnetwork	0.03	<0.20
ENSG00000197321	SVIL PPI subnetwork	0.02	<0.20
ENSG00000165025	SYK PPI subnetwork	0.00677	<0.20
ENSG00000171148	TADA3 PPI subnetwork	0.02	<0.20
ENSG00000178913	TAF7 PPI subnetwork	0.01	<0.20
ENSG00000070814	TCOF1 PPI subnetwork	0.02	<0.20
ENSG00000070759	TESK2 PPI subnetwork	0.01	<0.20
ENSG00000163513	TGFBR2 PPI subnetwork	0.0091	<0.20
MP:0002953	thick ventricular wall	0.0083	<0.20
MP:0000280	thin ventricular wall	0.01	<0.20
ENSG00000126351	THRA PPI subnetwork	0.00664	<0.20
GO:0030140	trans-Golgi network transport vesicle	0.00572	<0.20
GO:0003713	transcription coactivator activity	0.02	<0.20
ENSG00000130726	TRIM28 PPI subnetwork	0.00667	<0.20
ENSG00000167552	TUBA1A PPI subnetwork	0.02	<0.20
ENSG00000123416	TUBA1B PPI subnetwork	0.01	<0.20
GO:0032640	tumor necrosis factor production	0.02	<0.20
GO:0071706	tumor necrosis factor superfamily cytokine production	0.02	<0.20
ENSG00000074966	TXK PPI subnetwork	0.01	<0.20
ENSG00000138592	USP8 PPI subnetwork	0.01	<0.20
ENSG00000065268	WDR18 PPI subnetwork	0.00659	<0.20
ENSG00000065978	YBX1 PPI subnetwork	0.02	<0.20
ENSG00000166913	YWHAB PPI subnetwork	0.02	<0.20
ENSG00000108953	YWHAE PPI subnetwork	0.01	<0.20
ENSG00000170027	YWHAG PPI subnetwork	0.00688	<0.20
ENSG00000108175	ZMIZ1 PPI subnetwork	0.02	<0.20
ENSG00000121741	ZMYM2 PPI subnetwork	0.00481	<0.20
ENSG00000147130	ZMYM3 PPI subnetwork	0.00588	<0.20
ENSG00000015171	ZMYND11 PPI subnetwork	0.00411	<0.20
ENSG00000103343	ZNF174 PPI subnetwork	0.00392	<0.20
ENSG00000130803	ZNF317 PPI subnetwork	0.01	<0.20
ENSG00000160094	ZNF362 PPI subnetwork	0.00516	<0.20
ENSG00000148143	ZNF462 PPI subnetwork	0.00822	<0.20
ENSG00000166716	ZNF592 PPI subnetwork	0.02	<0.20
ENSG00000143373	ZNF687 PPI subnetwork	0.02	<0.20
ENSG00000169957	ZNF768 PPI subnetwork	0.00614	<0.20

ENSG00000158691	ZSCAN12 PPI subnetwork	0.00913	<0.20
ENSG00000110244	APOA4 PPI subnetwork	0.04	>=0.20
GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptid	0.08	>=0.20
GO:0016811	hydrolase activity, acting on carbon-nitrogen (but not peptid	0.19	>=0.20
MP:0004772	abnormal bile secretion	0.03	>=0.20
GO:0009310	amine catabolic process	0.14	>=0.20
GO:0070988	demethylation	0.13	>=0.20
GO:0042439	ethanolamine-containing compound metabolic process	0.03	>=0.20
GO:0030299	intestinal cholesterol absorption	0.04	>=0.20
KEGG_LINOLEIC_ACID_METAE	KEGG_LINOLEIC_ACID_METABOLISM	0.12	>=0.20
KEGG_RETINOL_METABOLISM	KEGG_RETINOL_METABOLISM	0.06	>=0.20
ENSG00000167751	KLK2 PPI subnetwork	0.03	>=0.20
ENSG00000167768	KRT1 PPI subnetwork	0.04	>=0.20
GO:0015718	monocarboxylic acid transport	0.08	>=0.20
GO:0006730	one-carbon metabolic process	0.05	>=0.20
GO:0019637	organophosphate metabolic process	0.05	>=0.20
ENSG00000141378	PTRH2 PPI subnetwork	0.16	>=0.20
REACTOME_ABCA_TRANSPOR	REACTOME_ABCA_TRANSPORTERS_IN_LIPID_HOMEOSTASIS	0.06	>=0.20
REACTOME_BILE_ACID_AND_	REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	0.03	>=0.20
REACTOME_BIOLOGICAL_OXI	REACTOME_BIOLOGICAL_OXIDATIONS	0.04	>=0.20
REACTOME_CYTOCHROME_P4	REACTOME_CYTOCHROME_P450_:_ARRANGED_BY_SUBSTRA	0.03	>=0.20
REACTOME_RECYCLING_OF_E	REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	0.03	>=0.20
GO:0031099	regeneration	0.05	>=0.20
GO:0016229	steroid dehydrogenase activity	0.11	>=0.20
ENSG00000145192	AHSG PPI subnetwork	0.05	>=0.20
GO:0008209	androgen metabolic process	0.09	>=0.20
GO:0070330	aromatase activity	0.3	>=0.20
GO:0019439	aromatic compound catabolic process	0.32	>=0.20
GO:0008206	bile acid metabolic process	0.11	>=0.20
GO:0043603	cellular amide metabolic process	0.05	>=0.20
GO:0009063	cellular amino acid catabolic process	0.17	>=0.20
GO:0006520	cellular amino acid metabolic process	0.06	>=0.20
GO:0006725	cellular aromatic compound metabolic process	0.11	>=0.20
GO:0006576	cellular biogenic amine metabolic process	0.23	>=0.20
GO:0006575	cellular modified amino acid metabolic process	0.14	>=0.20
MP:0006043	decreased apoptosis	0.04	>=0.20
MP:0003983	decreased cholesterol level	0.12	>=0.20
MP:0005166	decreased susceptibility to injury	0.11	>=0.20
GO:0004175	endopeptidase activity	0.04	>=0.20
GO:0009064	glutamine family amino acid metabolic process	0.64	>=0.20
MP:0000512	intestinal ulcer	0.04	>=0.20
GO:0016863	intramolecular oxidoreductase activity, transposing C=C bon	0.07	>=0.20
ENSG00000134070	IRAK2 PPI subnetwork	0.08	>=0.20
KEGG_ABC_TRANSPORTERS	KEGG_ABC_TRANSPORTERS	0.29	>=0.20
KEGG_ALPHA_LINOLENIC_ACI	KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	0.12	>=0.20
KEGG_CYSTEINE_AND_METHI	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	0.12	>=0.20
KEGG_DRUG_METABOLISM_C	KEGG_DRUG_METABOLISM_OTHER_ENZYMES	0.15	>=0.20

KEGG_PANTOTHENATE_AND_	KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	0.04	>=0.20
KEGG_PRIMARY_BILE_ACID_B	KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	0.06	>=0.20
KEGG_STEROID_HORMONE_E	KEGG_STEROID_HORMONE_BIOSYNTHESIS	0.07	>=0.20
ENSG00000160285	LSS PPI subnetwork	0.04	>=0.20
GO:0004497	monooxygenase activity	0.05	>=0.20
GO:0071941	nitrogen cycle metabolic process	0.07	>=0.20
GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	0.1	>=0.20
GO:0016709	oxidoreductase activity, acting on paired donors, with incorp	0.12	>=0.20
ENSG00000156453	PCDH1 PPI subnetwork	0.04	>=0.20
GO:0006644	phospholipid metabolic process	0.1	>=0.20
ENSG00000170927	PKHD1 PPI subnetwork	0.06	>=0.20
GO:0034377	plasma lipoprotein particle assembly	0.03	>=0.20
GO:0046930	pore complex	0.16	>=0.20
GO:0065005	protein-lipid complex assembly	0.03	>=0.20
GO:0030170	pyridoxal phosphate binding	0.05	>=0.20
REACTOME_ABC:FAMILY_PRC	REACTOME_ABC:FAMILY_PROTEINS_MEDIATED_TRANSPORT	0.11	>=0.20
REACTOME_HEXOSE_TRANSP	REACTOME_HEXOSE_TRANSPORT	0.06	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_POLYAMINES	0.32	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKIN	0.33	>=0.20
REACTOME_SULFUR_AMINO_	REACTOME_SULFUR_AMINO_ACID_METABOLISM	0.11	>=0.20
REACTOME_SYNTHESIS_OF_B	REACTOME_SYNTHESIS_OF_BILE_ACIDS_AND_BILE_SALTS	0.05	>=0.20
REACTOME_TRYPTOPHAN_CA	REACTOME_TRYPTOPHAN_CATABOLISM	0.07	>=0.20
REACTOME_XENOBIOTICS	REACTOME_XENOBIOTICS	0.17	>=0.20
GO:0042304	regulation of fatty acid biosynthetic process	0.07	>=0.20
ENSG00000149131	SERPING1 PPI subnetwork	0.22	>=0.20
GO:0033764	steroid dehydrogenase activity, acting on the CH-OH group o	0.18	>=0.20
GO:0008395	steroid hydroxylase activity	0.17	>=0.20
GO:0008483	transaminase activity	0.26	>=0.20
GO:0070279	vitamin B6 binding	0.05	>=0.20
GO:0006766	vitamin metabolic process	0.03	>=0.20
GO:0009309	amine biosynthetic process	0.59	>=0.20
GO:0006702	androgen biosynthetic process	0.21	>=0.20
GO:0009074	aromatic amino acid family catabolic process	0.36	>=0.20
GO:0006699	bile acid biosynthetic process	0.37	>=0.20
GO:0072378	blood coagulation, fibrin clot formation	0.15	>=0.20
GO:0016408	C-acyltransferase activity	0.31	>=0.20
ENSG00000103502	CDIPT PPI subnetwork	0.15	>=0.20
GO:0008652	cellular amino acid biosynthetic process	0.45	>=0.20
GO:0071466	cellular response to xenobiotic stimulus	0.19	>=0.20
GO:0015936	coenzyme A metabolic process	0.1	>=0.20
GO:0051184	cofactor transporter activity	0.08	>=0.20
ENSG00000067596	DHX8 PPI subnetwork	0.28	>=0.20
ENSG00000077348	EXOSC5 PPI subnetwork	0.39	>=0.20
ENSG00000066926	FECH PPI subnetwork	0.08	>=0.20
ENSG00000086205	FOLH1 PPI subnetwork	0.31	>=0.20
ENSG00000131459	GFPT2 PPI subnetwork	0.08	>=0.20
GO:0015929	hexosaminidase activity	0.06	>=0.20

GO:0006720	isoprenoid metabolic process	0.25	>=0.20
KEGG_OTHER_GLYCAN_DEGR	KEGG_OTHER_GLYCAN_DEGRADATION	0.05	>=0.20
ENSG00000185621	LMLN PPI subnetwork	0.06	>=0.20
ENSG00000106355	LSM5 PPI subnetwork	0.24	>=0.20
ENSG00000151224	MAT1A PPI subnetwork	0.19	>=0.20
GO:0008168	methyltransferase activity	0.37	>=0.20
GO:0033865	nucleoside bisphosphate metabolic process	0.23	>=0.20
ENSG00000133027	PEMT PPI subnetwork	0.18	>=0.20
GO:0017187	peptidyl-glutamic acid carboxylation	0.15	>=0.20
GO:0018200	peptidyl-glutamic acid modification	0.26	>=0.20
ENSG00000164751	PEX2 PPI subnetwork	0.09	>=0.20
GO:0008654	phospholipid biosynthetic process	0.42	>=0.20
GO:0043687	post-translational protein modification	0.65	>=0.20
GO:0018214	protein carboxylation	0.15	>=0.20
ENSG00000165630	PRPF18 PPI subnetwork	0.12	>=0.20
GO:0046128	purine ribonucleoside metabolic process	0.16	>=0.20
REACTOME_ENDOGENOUS_S	REACTOME_ENDOGENOUS_STEROLS	0.06	>=0.20
REACTOME_VITAMIN_B5_PAI	REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM	0.05	>=0.20
GO:0009410	response to xenobiotic stimulus	0.19	>=0.20
ENSG00000125352	RNF113A PPI subnetwork	0.19	>=0.20
ENSG00000197249	SERPINA1 PPI subnetwork	0.35	>=0.20
ENSG00000169371	SNUPN PPI subnetwork	0.51	>=0.20
ENSG00000126768	TIMM17B PPI subnetwork	0.08	>=0.20
GO:0016769	transferase activity, transferring nitrogenous groups	0.26	>=0.20
GO:0016741	transferase activity, transferring one-carbon groups	0.33	>=0.20
GO:0016763	transferase activity, transferring pentosyl groups	0.33	>=0.20
GO:0006805	xenobiotic metabolic process	0.21	>=0.20
MP:0006271	abnormal involution of the mammary gland	0.06	>=0.20
GO:0016634	oxidoreductase activity, acting on the CH-CH group of donors	0.09	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND	0.04	>=0.20
GO:0043176	amine binding	0.13	>=0.20
GO:0006956	complement activation	0.04	>=0.20
GO:0015908	fatty acid transport	0.11	>=0.20
GO:0042445	hormone metabolic process	0.16	>=0.20
GO:0016860	intramolecular oxidoreductase activity	0.08	>=0.20
GO:0031418	L-ascorbic acid binding	0.04	>=0.20
GO:0032369	negative regulation of lipid transport	0.04	>=0.20
ENSG00000034693	PEX3 PPI subnetwork	0.1	>=0.20
GO:0004620	phospholipase activity	0.03	>=0.20
ENSG00000151576	QTRTD1 PPI subnetwork	0.05	>=0.20
MP:0001282	short vibrissae	0.11	>=0.20
MP:0003702	abnormal chromosome morphology	0.04	>=0.20
MP:0001146	abnormal testis morphology	0.07	>=0.20
GO:0016407	acetyltransferase activity	0.08	>=0.20
GO:0016597	amino acid binding	0.03	>=0.20
ENSG00000130208	APOC1 PPI subnetwork	0.15	>=0.20
ENSG00000105726	ATP13A1 PPI subnetwork	0.14	>=0.20

ENSG00000039537	C6 PPI subnetwork	0.03	>=0.20
ENSG00000171735	CAMTA1 PPI subnetwork	0.05	>=0.20
ENSG00000112186	CAP2 PPI subnetwork	0.12	>=0.20
GO:0016840	carbon-nitrogen lyase activity	0.06	>=0.20
GO:0004091	carboxylesterase activity	0.07	>=0.20
ENSG00000125810	CD93 PPI subnetwork	0.03	>=0.20
GO:0034754	cellular hormone metabolic process	0.06	>=0.20
ENSG00000137975	CLCA2 PPI subnetwork	0.06	>=0.20
GO:0006957	complement activation, alternative pathway	0.08	>=0.20
GO:0006958	complement activation, classical pathway	0.09	>=0.20
ENSG00000213923	CSNK1E PPI subnetwork	0.06	>=0.20
ENSG00000174177	CTU2 PPI subnetwork	0.09	>=0.20
ENSG00000105671	DDX49 PPI subnetwork	0.33	>=0.20
ENSG00000158796	DEDD PPI subnetwork	0.26	>=0.20
ENSG00000196540	ENSG00000196540 PPI subnetwork	0.06	>=0.20
ENSG00000212645	ENSG00000212645 PPI subnetwork	0.1	>=0.20
ENSG00000178607	ERN1 PPI subnetwork	0.05	>=0.20
ENSG00000103089	FA2H PPI subnetwork	0.17	>=0.20
ENSG00000179715	FAM113B PPI subnetwork	0.06	>=0.20
ENSG00000104835	FBXO17 PPI subnetwork	0.07	>=0.20
GO:0046527	glucosyltransferase activity	0.09	>=0.20
GO:0006544	glycine metabolic process	0.33	>=0.20
GO:0008158	hedgehog receptor activity	0.35	>=0.20
ENSG00000182054	IDH2 PPI subnetwork	0.18	>=0.20
GO:0050892	intestinal absorption	0.05	>=0.20
GO:0031300	intrinsic to organelle membrane	0.07	>=0.20
ENSG00000185507	IRF7 PPI subnetwork	0.06	>=0.20
KEGG_ALANINE_ASPARTATE_	KEGG_ALANINE_ASPARTATE_AND_GLUTAMATE_METABOLIS	0.34	>=0.20
KEGG_BUTANOATE_METABOI	KEGG_BUTANOATE_METABOLISM	0.08	>=0.20
KEGG_DRUG_METABOLISM_C	KEGG_DRUG_METABOLISM_CYTOCHROME_P450	0.11	>=0.20
KEGG_MATURITY_ONSET_DIA	KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	0.08	>=0.20
KEGG_METABOLISM_OF_XEN	KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P	0.17	>=0.20
ENSG00000132361	KIAA0664 PPI subnetwork	0.03	>=0.20
GO:0044241	lipid digestion	0.09	>=0.20
ENSG00000198336	MYL4 PPI subnetwork	0.06	>=0.20
ENSG00000140795	MYLK3 PPI subnetwork	0.09	>=0.20
GO:0016712	oxidoreductase activity, acting on paired donors, with incorp	0.22	>=0.20
ENSG00000083093	PALB2 PPI subnetwork	0.06	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_BETA:CELL_DEVELOPMENT	0.06	>=0.20
GO:0014070	response to organic cyclic compound	0.03	>=0.20
ENSG00000122484	RPAP2 PPI subnetwork	0.18	>=0.20
GO:0009071	serine family amino acid catabolic process	0.32	>=0.20
GO:0009069	serine family amino acid metabolic process	0.28	>=0.20
ENSG00000136169	SETDB2 PPI subnetwork	0.05	>=0.20
ENSG00000197818	SLC9A8 PPI subnetwork	0.09	>=0.20
ENSG00000104549	SQLE PPI subnetwork	0.05	>=0.20
GO:0006721	terpenoid metabolic process	0.46	>=0.20

GO:0006767	water-soluble vitamin metabolic process	0.06	>=0.20
MP:0010377	abnormal gut flora balance	0.64	>=0.20
MP:0009548	abnormal platelet aggregation	0.06	>=0.20
ENSG00000129354	AP1M2 PPI subnetwork	0.07	>=0.20
GO:0009072	aromatic amino acid family metabolic process	0.36	>=0.20
ENSG00000017260	ATP2C1 PPI subnetwork	0.27	>=0.20
GO:0015721	bile acid and bile salt transport	0.45	>=0.20
GO:0007597	blood coagulation, intrinsic pathway	0.1	>=0.20
ENSG00000084774	CAD PPI subnetwork	0.03	>=0.20
GO:0008643	carbohydrate transport	0.08	>=0.20
GO:0016830	carbon-carbon lyase activity	0.13	>=0.20
GO:0046942	carboxylic acid transport	0.35	>=0.20
ENSG00000003400	CASP10 PPI subnetwork	0.12	>=0.20
ENSG00000169217	CD2BP2 PPI subnetwork	0.04	>=0.20
GO:0042402	cellular biogenic amine catabolic process	0.51	>=0.20
GO:0071222	cellular response to lipopolysaccharide	0.04	>=0.20
GO:0071219	cellular response to molecule of bacterial origin	0.03	>=0.20
GO:0006695	cholesterol biosynthetic process	0.05	>=0.20
ENSG00000141076	CIRH1A PPI subnetwork	0.53	>=0.20
ENSG00000104938	CLEC4M PPI subnetwork	0.24	>=0.20
GO:0016289	CoA hydrolase activity	0.17	>=0.20
GO:0009108	coenzyme biosynthetic process	0.03	>=0.20
GO:0051188	cofactor biosynthetic process	0.08	>=0.20
ENSG00000111605	CPSF6 PPI subnetwork	0.2	>=0.20
ENSG00000101343	CRNKL1 PPI subnetwork	0.06	>=0.20
ENSG00000163510	CWC22 PPI subnetwork	0.19	>=0.20
GO:0004869	cysteine-type endopeptidase inhibitor activity	0.08	>=0.20
GO:0019835	cytolysis	0.28	>=0.20
ENSG00000067048	DDX3Y PPI subnetwork	0.25	>=0.20
MP:0008565	decreased interferon-beta secretion	0.13	>=0.20
GO:0009595	detection of biotic stimulus	0.11	>=0.20
ENSG00000109606	DHX15 PPI subnetwork	0.33	>=0.20
ENSG00000150990	DHX37 PPI subnetwork	0.77	>=0.20
ENSG00000086189	DIMT1 PPI subnetwork	0.5	>=0.20
ENSG00000083520	DIS3 PPI subnetwork	0.59	>=0.20
ENSG00000148719	DNAJB12 PPI subnetwork	0.24	>=0.20
ENSG00000204348	DOM3Z PPI subnetwork	0.28	>=0.20
ENSG00000206346	DOM3Z PPI subnetwork	0.28	>=0.20
GO:0017144	drug metabolic process	0.81	>=0.20
ENSG00000119718	EIF2B2 PPI subnetwork	0.15	>=0.20
ENSG00000170522	ELOVL6 PPI subnetwork	0.19	>=0.20
GO:0004519	endonuclease activity	0.61	>=0.20
GO:0004521	endoribonuclease activity	0.68	>=0.20
ENSG00000100181	ENSG00000100181 PPI subnetwork	0.06	>=0.20
ENSG00000144158	ENSG00000144158 PPI subnetwork	0.2	>=0.20
ENSG00000160220	ENSG00000160220 PPI subnetwork	0.66	>=0.20
ENSG00000182367	ENSG00000182367 PPI subnetwork	0.44	>=0.20

ENSG00000186676	ENSG00000186676 PPI subnetwork	0.06	>=0.20
ENSG00000187899	ENSG00000187899 PPI subnetwork	0.69	>=0.20
ENSG00000206266	ENSG00000206266 PPI subnetwork	0.28	>=0.20
ENSG00000213764	ENSG00000213764 PPI subnetwork	0.04	>=0.20
ENSG00000134398	ERN2 PPI subnetwork	0.52	>=0.20
ENSG00000086619	ERO1LB PPI subnetwork	0.68	>=0.20
ENSG00000171824	EXOSC10 PPI subnetwork	0.49	>=0.20
ENSG00000178896	EXOSC4 PPI subnetwork	0.91	>=0.20
ENSG00000180185	FAHD1 PPI subnetwork	0.24	>=0.20
GO:0015645	fatty acid ligase activity	0.1	>=0.20
GO:0042730	fibrinolysis	0.04	>=0.20
MP:0000418	focal hair loss	0.44	>=0.20
MP:0000784	forebrain hypoplasia	0.08	>=0.20
ENSG00000089154	GCN1L1 PPI subnetwork	0.04	>=0.20
GO:0030203	glycosaminoglycan metabolic process	0.08	>=0.20
ENSG00000132196	HSD17B7 PPI subnetwork	0.03	>=0.20
GO:0002455	humoral immune response mediated by circulating immunog	0.13	>=0.20
ENSG00000115594	IL1R1 PPI subnetwork	0.03	>=0.20
ENSG00000115590	IL1R2 PPI subnetwork	0.07	>=0.20
GO:0002252	immune effector process	0.05	>=0.20
MP:0008412	increased cellular sensitivity to oxidative stress	0.12	>=0.20
MP:0008873	increased physiological sensitivity to xenobiotic	0.03	>=0.20
GO:0046218	indolalkylamine catabolic process	0.52	>=0.20
GO:0042436	indole-containing compound catabolic process	0.52	>=0.20
GO:0032592	integral to mitochondrial membrane	0.11	>=0.20
GO:0016866	intramolecular transferase activity	0.22	>=0.20
GO:0031227	intrinsic to endoplasmic reticulum membrane	0.39	>=0.20
GO:0008299	isoprenoid biosynthetic process	0.54	>=0.20
KEGG_NICOTINATE_AND_NIC	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	0.05	>=0.20
KEGG_PORPHYRIN_AND_CHL	KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	0.12	>=0.20
KEGG_TERPENOID_BACKBONI	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	0.24	>=0.20
ENSG00000145332	KLHL8 PPI subnetwork	0.04	>=0.20
ENSG00000149357	LAMTOR1 PPI subnetwork	0.27	>=0.20
GO:0055102	lipase inhibitor activity	0.17	>=0.20
GO:0031663	lipopolysaccharide-mediated signaling pathway	0.21	>=0.20
ENSG00000164167	LSM6 PPI subnetwork	0.3	>=0.20
ENSG00000052802	MSMO1 PPI subnetwork	0.04	>=0.20
ENSG00000182636	NDN PPI subnetwork	0.7	>=0.20
ENSG00000100138	NHP2L1 PPI subnetwork	0.09	>=0.20
ENSG00000141101	NOB1 PPI subnetwork	0.67	>=0.20
GO:0004518	nuclease activity	0.85	>=0.20
GO:0009116	nucleoside metabolic process	0.22	>=0.20
GO:0016779	nucleotidyltransferase activity	0.4	>=0.20
ENSG00000132182	NUP210 PPI subnetwork	0.55	>=0.20
ENSG00000108559	NUP88 PPI subnetwork	0.11	>=0.20
ENSG00000198104	OR2T6 PPI subnetwork	0.05	>=0.20
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donor	0.19	>=0.20

ENSG00000175575	PAAF1 PPI subnetwork	0.19	>=0.20
GO:0015939	pantothenate metabolic process	0.38	>=0.20
ENSG00000184588	PDE4B PPI subnetwork	0.14	>=0.20
ENSG00000161395	PGAP3 PPI subnetwork	0.49	>=0.20
GO:0006656	phosphatidylcholine biosynthetic process	0.22	>=0.20
GO:0009395	phospholipid catabolic process	0.32	>=0.20
ENSG00000142892	PIGK PPI subnetwork	0.16	>=0.20
ENSG00000171566	PLRG1 PPI subnetwork	0.13	>=0.20
ENSG00000105258	POLR2I PPI subnetwork	0.06	>=0.20
GO:0006595	polyamine metabolic process	0.99	>=0.20
GO:0006778	porphyrin-containing compound metabolic process	0.32	>=0.20
GO:0010907	positive regulation of glucose metabolic process	0.12	>=0.20
GO:0010952	positive regulation of peptidase activity	0.4	>=0.20
ENSG00000167815	PRDX2 PPI subnetwork	0.28	>=0.20
GO:0051260	protein homooligomerization	0.07	>=0.20
GO:0051289	protein homotetramerization	0.12	>=0.20
ENSG00000110107	PRPF19 PPI subnetwork	0.39	>=0.20
GO:0009982	pseudouridine synthase activity	0.5	>=0.20
ENSG00000041357	PSMA4 PPI subnetwork	0.41	>=0.20
ENSG00000100902	PSMA6 PPI subnetwork	0.49	>=0.20
ENSG00000161057	PSMC2 PPI subnetwork	0.08	>=0.20
ENSG00000087191	PSMC5 PPI subnetwork	0.07	>=0.20
ENSG00000159352	PSMD4 PPI subnetwork	0.04	>=0.20
ENSG00000103035	PSMD7 PPI subnetwork	0.19	>=0.20
GO:0042559	pteridine-containing compound biosynthetic process	0.31	>=0.20
GO:0042558	pteridine-containing compound metabolic process	0.38	>=0.20
ENSG00000184489	PTP4A3 PPI subnetwork	0.04	>=0.20
GO:0042278	purine nucleoside metabolic process	0.17	>=0.20
GO:0072524	pyridine-containing compound metabolic process	0.09	>=0.20
GO:0019362	pyridine nucleotide metabolic process	0.09	>=0.20
ENSG00000172780	RAB43 PPI subnetwork	0.36	>=0.20
ENSG00000113456	RAD1 PPI subnetwork	0.32	>=0.20
ENSG00000134597	RBMX2 PPI subnetwork	0.29	>=0.20
ENSG00000120158	RCL1 PPI subnetwork	0.7	>=0.20
REACTOME_AMINO_ACID_SY	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSI	0.2	>=0.20
REACTOME_CLEAVAGE_OF_G	REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE	0.15	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_PROTEINS	0.24	>=0.20
REACTOME_MRNA_PROCESSI	REACTOME_MRNA_PROCESSING	0.09	>=0.20
REACTOME_PHASE_II_CONJU	REACTOME_PHASE_II_CONJUGATION	0.32	>=0.20
REACTOME_POST:ELONGATIC	REACTOME_POST:ELONGATION_PROCESSING_OF_THE_TRAI	0.15	>=0.20
REACTOME_POST:TRANSLATI	REACTOME_POST:TRANSLATIONAL_PROTEIN_MODIFICATIOI	0.3	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_	0.1	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMIN	0.15	>=0.20
GO:0050818	regulation of coagulation	0.05	>=0.20
GO:0030162	regulation of proteolysis	0.07	>=0.20
GO:0032354	response to follicle-stimulating hormone stimulus	0.16	>=0.20
GO:0004540	ribonuclease activity	0.73	>=0.20

GO:0009119	ribonucleoside metabolic process	0.26	>=0.20
ENSG00000167526	RPL13 PPI subnetwork	0.13	>=0.20
ENSG00000205246	RPSAP58 PPI subnetwork	0.48	>=0.20
ENSG00000085721	RRN3 PPI subnetwork	0.78	>=0.20
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	0.08	>=0.20
ENSG00000099194	SCD PPI subnetwork	0.04	>=0.20
GO:0019748	secondary metabolic process	0.55	>=0.20
GO:0046459	short-chain fatty acid metabolic process	0.79	>=0.20
ENSG00000125835	SNRPB PPI subnetwork	0.07	>=0.20
ENSG00000167088	SNRPD1 PPI subnetwork	0.05	>=0.20
GO:0016126	sterol biosynthetic process	0.08	>=0.20
GO:0000097	sulfur amino acid biosynthetic process	0.46	>=0.20
ENSG00000113407	TARS PPI subnetwork	0.11	>=0.20
ENSG00000099797	TECR PPI subnetwork	0.05	>=0.20
ENSG00000100726	TELO2 PPI subnetwork	0.35	>=0.20
GO:0033013	tetrapyrrole metabolic process	0.32	>=0.20
ENSG00000100109	TFIP11 PPI subnetwork	0.16	>=0.20
MP:0001200	thick skin	0.03	>=0.20
ENSG00000116001	TIA1 PPI subnetwork	0.14	>=0.20
ENSG00000157873	TNFRSF14 PPI subnetwork	0.11	>=0.20
GO:0046915	transition metal ion transmembrane transporter activity	0.21	>=0.20
ENSG00000196459	TRAPPC2 PPI subnetwork	0.04	>=0.20
ENSG00000071539	TRIP13 PPI subnetwork	0.14	>=0.20
GO:0008033	tRNA processing	0.9	>=0.20
GO:0006569	tryptophan catabolic process	0.52	>=0.20
GO:0006568	tryptophan metabolic process	0.6	>=0.20
GO:0045351	type I interferon biosynthetic process	0.79	>=0.20
ENSG00000011260	UTP18 PPI subnetwork	0.31	>=0.20
ENSG00000100284	TOM1 PPI subnetwork	0.07	>=0.20
ENSG00000174718	C12orf35 PPI subnetwork	0.1	>=0.20
ENSG00000135047	CTSL1 PPI subnetwork	0.03	>=0.20
ENSG00000215320	ENSG00000215320 PPI subnetwork	0.04	>=0.20
GO:0006635	fatty acid beta-oxidation	0.09	>=0.20
ENSG00000124610	HIST1H1A PPI subnetwork	0.09	>=0.20
ENSG00000135100	HNF1A PPI subnetwork	0.03	>=0.20
ENSG00000125538	IL1B PPI subnetwork	0.07	>=0.20
KEGG_ARACHIDONIC_ACID_M	KEGG_ARACHIDONIC_ACID_METABOLISM	0.06	>=0.20
KEGG_VALINE_LEUCINE_AND_	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	0.05	>=0.20
MP:0001289	persistence of hyaloid vascular system	0.03	>=0.20
REACTOME_TRANSPORT_TO_	REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUEN	0.27	>=0.20
GO:0016782	transferase activity, transferring sulfur-containing groups	0.38	>=0.20
MP:0009660	abnormal induced retinal neovascularization	0.14	>=0.20
MP:0005342	abnormal intestinal lipid absorption	0.06	>=0.20
MP:0005065	abnormal neutrophil morphology	0.04	>=0.20
MP:0004756	abnormal proximal convoluted tubule morphology	0.07	>=0.20
MP:0001120	abnormal uterus morphology	0.47	>=0.20
GO:0043178	alcohol binding	0.38	>=0.20

ENSG00000072958	AP1M1 PPI subnetwork	0.03	>=0.20
ENSG00000124198	ARFGEF2 PPI subnetwork	0.38	>=0.20
GO:0008207	C21-steroid hormone metabolic process	0.22	>=0.20
GO:0034435	cholesterol esterification	0.11	>=0.20
GO:0030132	clathrin coat of coated pit	0.05	>=0.20
ENSG00000101439	CST3 PPI subnetwork	0.14	>=0.20
MP:0001274	curly vibrissae	0.18	>=0.20
MP:0008484	decreased spleen germinal center size	0.07	>=0.20
ENSG00000108272	DHRS11 PPI subnetwork	0.06	>=0.20
ENSG00000128829	EIF2AK4 PPI subnetwork	0.03	>=0.20
GO:0019840	isoprenoid binding	0.07	>=0.20
KEGG_GLYOXYLATE_AND_DIC	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	0.13	>=0.20
KEGG_HISTIDINE_METABOLIS	KEGG_HISTIDINE_METABOLISM	0.14	>=0.20
KEGG_PROPANOATE_METAB(	KEGG_PROPANOATE_METABOLISM	0.04	>=0.20
GO:0015923	mannosidase activity	0.21	>=0.20
GO:0015924	mannosyl-oligosaccharide mannosidase activity	0.24	>=0.20
ENSG00000196549	MME PPI subnetwork	0.03	>=0.20
GO:0005326	neurotransmitter transporter activity	0.16	>=0.20
ENSG00000116962	NID1 PPI subnetwork	0.46	>=0.20
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	0.03	>=0.20
GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group	0.17	>=0.20
GO:0016641	oxidoreductase activity, acting on the CH-NH2 group of dono	0.03	>=0.20
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donor	0.03	>=0.20
GO:0016500	protein-hormone receptor activity	0.18	>=0.20
ENSG00000103479	RBL2 PPI subnetwork	0.05	>=0.20
REACTOME_ASPARAGINE_N:L	REACTOME_ASPARAGINE_N:LINKED_GLYCOSYLATION	0.28	>=0.20
REACTOME_FACILITATIVE_NA	REACTOME_FACILITATIVE_NA:INDEPENDENT_GLUCOSE_TRA	0.07	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_INSULIN:LIKE_GROWTH_FACT	0.04	>=0.20
MP:0011346	renal tubule atrophy	0.09	>=0.20
GO:0005501	retinoid binding	0.11	>=0.20
ENSG00000156482	RPL30 PPI subnetwork	0.09	>=0.20
ENSG00000172594	SMPDL3A PPI subnetwork	0.07	>=0.20
GO:0034433	steroid esterification	0.11	>=0.20
GO:0034434	sterol esterification	0.11	>=0.20
GO:0008146	sulfotransferase activity	0.66	>=0.20
GO:0006790	sulfur compound metabolic process	0.23	>=0.20
ENSG00000162298	SYVN1 PPI subnetwork	0.26	>=0.20
ENSG00000105197	TIMM50 PPI subnetwork	0.08	>=0.20
ENSG00000105289	TJP3 PPI subnetwork	0.03	>=0.20
GO:0042311	vasodilation	0.09	>=0.20
MP:0001211	wrinkled skin	0.13	>=0.20
ENSG00000186660	ZFP91 PPI subnetwork	0.05	>=0.20
ENSG00000108270	AATF PPI subnetwork	0.91	>=0.20
MP:0003111	abnormal cell nucleus morphology	0.11	>=0.20
MP:0002855	abnormal cochlear ganglion morphology	0.69	>=0.20
MP:0005410	abnormal fertilization	0.12	>=0.20
MP:0004966	abnormal inner cell mass proliferation	0.22	>=0.20

MP:0002446	abnormal macrophage morphology	0.07	>=0.20
MP:0001125	abnormal oocyte morphology	0.07	>=0.20
MP:0002060	abnormal skin morphology	0.27	>=0.20
MP:0002674	abnormal sperm motility	0.5	>=0.20
ENSG00000146109	ABT1 PPI subnetwork	0.76	>=0.20
ENSG00000101473	ACOT8 PPI subnetwork	0.03	>=0.20
GO:0006919	activation of cysteine-type endopeptidase activity involved ir	0.6	>=0.20
GO:0007250	activation of NF-kappaB-inducing kinase activity	0.67	>=0.20
GO:0008633	activation of pro-apoptotic gene products	0.81	>=0.20
GO:0006637	acyl-CoA metabolic process	0.08	>=0.20
GO:0002250	adaptive immune response	0.57	>=0.20
GO:0002460	adaptive immune response based on somatic recombination	0.53	>=0.20
GO:0019400	alditol metabolic process	0.21	>=0.20
ENSG00000088035	ALG6 PPI subnetwork	0.13	>=0.20
ENSG00000183684	ALYREF PPI subnetwork	0.07	>=0.20
MP:0003311	aminoaciduria	0.17	>=0.20
GO:0006026	aminoglycan catabolic process	0.71	>=0.20
GO:0006022	aminoglycan metabolic process	0.26	>=0.20
ENSG00000182287	AP1S2 PPI subnetwork	0.2	>=0.20
ENSG00000168374	ARF4 PPI subnetwork	0.05	>=0.20
ENSG00000120805	ARL1 PPI subnetwork	0.21	>=0.20
ENSG00000170632	ARMC10 PPI subnetwork	0.08	>=0.20
GO:0009067	aspartate family amino acid biosynthetic process	0.8	>=0.20
GO:0009066	aspartate family amino acid metabolic process	0.54	>=0.20
ENSG00000149311	ATM PPI subnetwork	0.58	>=0.20
GO:0016887	ATPase activity	0.36	>=0.20
GO:0019724	B cell mediated immunity	0.46	>=0.20
ENSG00000123685	BATF3 PPI subnetwork	0.03	>=0.20
ENSG00000140379	BCL2A1 PPI subnetwork	0.7	>=0.20
ENSG00000110330	BIRC2 PPI subnetwork	0.07	>=0.20
ENSG00000023445	BIRC3 PPI subnetwork	0.31	>=0.20
ENSG00000165733	BMS1 PPI subnetwork	0.69	>=0.20
ENSG00000104221	BRF2 PPI subnetwork	0.11	>=0.20
ENSG00000113460	BRIX1 PPI subnetwork	0.55	>=0.20
ENSG00000160469	BRSK1 PPI subnetwork	0.91	>=0.20
ENSG00000137656	BUD13 PPI subnetwork	0.5	>=0.20
ENSG00000106245	BUD31 PPI subnetwork	0.2	>=0.20
ENSG00000112578	BYSL PPI subnetwork	0.55	>=0.20
ENSG00000196943	C14orf21 PPI subnetwork	0.73	>=0.20
ENSG00000131043	C20orf4 PPI subnetwork	0.16	>=0.20
ENSG00000100346	CACNA1I PPI subnetwork	0.04	>=0.20
ENSG00000179218	CALR PPI subnetwork	0.18	>=0.20
ENSG00000131236	CAP1 PPI subnetwork	0.15	>=0.20
GO:0015144	carbohydrate transmembrane transporter activity	0.07	>=0.20
GO:0016884	carbon-nitrogen ligase activity, with glutamine as amido-N-d	0.88	>=0.20
GO:0016831	carboxy-lyase activity	0.88	>=0.20
GO:0046943	carboxylic acid transmembrane transporter activity	0.21	>=0.20

ENSG00000137752	CASP1 PPI subnetwork	0.04	>=0.20
ENSG00000105141	CASP14 PPI subnetwork	0.05	>=0.20
GO:0071013	catalytic step 2 spliceosome	0.22	>=0.20
ENSG00000060339	CCAR1 PPI subnetwork	0.05	>=0.20
ENSG00000105248	CCDC94 PPI subnetwork	0.42	>=0.20
ENSG00000134480	CCNH PPI subnetwork	0.24	>=0.20
ENSG00000085063	CD59 PPI subnetwork	0.05	>=0.20
ENSG00000168438	CDC40 PPI subnetwork	0.09	>=0.20
ENSG00000154162	CDH12 PPI subnetwork	0.14	>=0.20
ENSG00000115816	CEBPZ PPI subnetwork	0.76	>=0.20
GO:0071843	cellular component biogenesis at cellular level	0.95	>=0.20
GO:0006879	cellular iron ion homeostasis	0.41	>=0.20
GO:0043094	cellular metabolic compound salvage	0.26	>=0.20
GO:0071371	cellular response to gonadotropin stimulus	0.1	>=0.20
GO:0071383	cellular response to steroid hormone stimulus	0.17	>=0.20
ENSG00000113282	CLINT1 PPI subnetwork	0.14	>=0.20
ENSG00000092853	CLSPN PPI subnetwork	0.79	>=0.20
ENSG00000188986	COBRA1 PPI subnetwork	0.1	>=0.20
ENSG00000135775	COG2 PPI subnetwork	0.48	>=0.20
ENSG00000187498	COL4A1 PPI subnetwork	0.05	>=0.20
ENSG00000134871	COL4A2 PPI subnetwork	0.13	>=0.20
MP:0011096	complete embryonic lethality before somite formation	0.05	>=0.20
ENSG00000165934	CPSF2 PPI subnetwork	0.04	>=0.20
ENSG00000119203	CPSF3 PPI subnetwork	0.03	>=0.20
ENSG00000149532	CPSF7 PPI subnetwork	0.05	>=0.20
ENSG00000141551	CSNK1D PPI subnetwork	0.25	>=0.20
ENSG00000101138	CSTF1 PPI subnetwork	0.06	>=0.20
ENSG00000108296	CWC25 PPI subnetwork	0.04	>=0.20
GO:0004197	cysteine-type endopeptidase activity	0.34	>=0.20
GO:0008234	cysteine-type peptidase activity	0.39	>=0.20
GO:0042107	cytokine metabolic process	0.06	>=0.20
ENSG00000164934	DCAF13 PPI subnetwork	0.87	>=0.20
ENSG00000172795	DCP2 PPI subnetwork	0.66	>=0.20
ENSG00000178105	DDX10 PPI subnetwork	0.61	>=0.20
ENSG00000088205	DDX18 PPI subnetwork	0.54	>=0.20
ENSG00000174243	DDX23 PPI subnetwork	0.12	>=0.20
ENSG00000125485	DDX31 PPI subnetwork	0.42	>=0.20
ENSG00000141141	DDX52 PPI subnetwork	0.55	>=0.20
GO:0019239	deaminase activity	0.25	>=0.20
MP:0008563	decreased interferon-alpha secretion	0.04	>=0.20
MP:0009767	decreased sensitivity to xenobiotic induced morbidity/morta	0.1	>=0.20
MP:0004042	decreased susceptibility to kidney reperfusion injury	0.13	>=0.20
GO:0050829	defense response to Gram-negative bacterium	0.75	>=0.20
GO:0050830	defense response to Gram-positive bacterium	0.53	>=0.20
ENSG00000072849	DERL2 PPI subnetwork	0.16	>=0.20
ENSG00000140829	DHX38 PPI subnetwork	0.04	>=0.20
MP:0005036	diarrhea	0.25	>=0.20

GO:0043648	dicarboxylic acid metabolic process	0.25	>=0.20
GO:0022600	digestive system process	0.05	>=0.20
GO:0016101	diterpenoid metabolic process	0.56	>=0.20
ENSG00000130826	DKC1 PPI subnetwork	0.54	>=0.20
GO:0006304	DNA modification	0.85	>=0.20
ENSG00000086061	DNAJA1 PPI subnetwork	0.13	>=0.20
ENSG00000126698	DNAJC8 PPI subnetwork	0.06	>=0.20
GO:0042737	drug catabolic process	0.75	>=0.20
ENSG00000134109	EDEM1 PPI subnetwork	0.1	>=0.20
ENSG00000111361	EIF2B1 PPI subnetwork	0.53	>=0.20
ENSG00000070785	EIF2B3 PPI subnetwork	0.21	>=0.20
ENSG00000115211	EIF2B4 PPI subnetwork	0.61	>=0.20
ENSG00000134001	EIF2S1 PPI subnetwork	0.24	>=0.20
ENSG00000161960	EIF4A1 PPI subnetwork	0.17	>=0.20
ENSG00000114867	EIF4G1 PPI subnetwork	0.31	>=0.20
ENSG00000075151	EIF4G3 PPI subnetwork	0.18	>=0.20
ENSG00000118402	ELOVL4 PPI subnetwork	0.16	>=0.20
GO:0016893	endonuclease activity, active with either ribo- or deoxyribonu	0.89	>=0.20
MP:0003068	enlarged kidney	0.04	>=0.20
ENSG00000108515	ENO3 PPI subnetwork	0.09	>=0.20
ENSG00000032514	ENSG00000032514 PPI subnetwork	0.56	>=0.20
ENSG00000111987	ENSG00000111987 PPI subnetwork	0.1	>=0.20
ENSG00000126749	ENSG00000126749 PPI subnetwork	0.95	>=0.20
ENSG00000182953	ENSG00000182953 PPI subnetwork	0.86	>=0.20
ENSG00000183405	ENSG00000183405 PPI subnetwork	0.93	>=0.20
ENSG00000185057	ENSG00000185057 PPI subnetwork	0.67	>=0.20
ENSG00000206267	ENSG00000206267 PPI subnetwork	0.89	>=0.20
ENSG00000212981	ENSG00000212981 PPI subnetwork	0.52	>=0.20
ENSG00000214485	ENSG00000214485 PPI subnetwork	0.76	>=0.20
ENSG00000197586	ENTPD6 PPI subnetwork	0.41	>=0.20
ENSG00000136628	EPRS PPI subnetwork	0.15	>=0.20
GO:0030134	ER to Golgi transport vesicle	0.51	>=0.20
GO:0012507	ER to Golgi transport vesicle membrane	0.52	>=0.20
GO:0006888	ER to Golgi vesicle-mediated transport	0.34	>=0.20
ENSG00000104884	ERCC2 PPI subnetwork	0.58	>=0.20
ENSG00000163161	ERCC3 PPI subnetwork	0.38	>=0.20
ENSG00000125991	ERGIC3 PPI subnetwork	0.15	>=0.20
ENSG00000197930	ERO1L PPI subnetwork	0.23	>=0.20
ENSG00000089048	ESF1 PPI subnetwork	0.84	>=0.20
GO:0072663	establishment of protein localization to peroxisome	0.66	>=0.20
ENSG00000120705	ETF1 PPI subnetwork	0.51	>=0.20
ENSG00000105379	ETFB PPI subnetwork	0.14	>=0.20
ENSG00000171311	EXOSC1 PPI subnetwork	0.81	>=0.20
ENSG00000107371	EXOSC3 PPI subnetwork	0.65	>=0.20
GO:0006633	fatty acid biosynthetic process	0.09	>=0.20
ENSG00000150337	FCGR1A PPI subnetwork	0.04	>=0.20
ENSG00000134363	FST PPI subnetwork	0.26	>=0.20

ENSG00000068438	FTSJ1 PPI subnetwork	0.06	>=0.20
ENSG00000109534	GAR1 PPI subnetwork	0.95	>=0.20
ENSG00000092208	GEMIN2 PPI subnetwork	0.08	>=0.20
ENSG00000105373	GLTSCR2 PPI subnetwork	0.87	>=0.20
GO:0006536	glutamate metabolic process	0.83	>=0.20
GO:0009084	glutamine family amino acid biosynthetic process	0.45	>=0.20
GO:0006541	glutamine metabolic process	0.95	>=0.20
GO:0046474	glycerophospholipid biosynthetic process	0.7	>=0.20
GO:0006650	glycerophospholipid metabolic process	0.43	>=0.20
ENSG00000163938	GNL3 PPI subnetwork	0.37	>=0.20
ENSG00000108587	GOSR1 PPI subnetwork	0.34	>=0.20
ENSG00000105220	GPI PPI subnetwork	0.03	>=0.20
ENSG00000103342	GSPT1 PPI subnetwork	0.67	>=0.20
ENSG00000188342	GTF2F2 PPI subnetwork	0.09	>=0.20
ENSG00000128708	HAT1 PPI subnetwork	0.36	>=0.20
ENSG00000180353	HCLS1 PPI subnetwork	0.09	>=0.20
ENSG00000115677	HDLBP PPI subnetwork	0.09	>=0.20
ENSG00000119285	HEATR1 PPI subnetwork	0.59	>=0.20
GO:0004386	helicase activity	0.32	>=0.20
GO:0042054	histone methyltransferase activity	0.16	>=0.20
ENSG00000177733	HNRNPA0 PPI subnetwork	0.05	>=0.20
GO:0030897	HOPS complex	0.08	>=0.20
GO:0006959	humoral immune response	0.19	>=0.20
ENSG00000136273	HUS1 PPI subnetwork	0.88	>=0.20
ENSG00000138413	IDH1 PPI subnetwork	0.41	>=0.20
ENSG00000070061	IKBKAP PPI subnetwork	0.18	>=0.20
ENSG00000136634	IL10 PPI subnetwork	0.04	>=0.20
GO:0019865	immunoglobulin binding	0.06	>=0.20
GO:0016064	immunoglobulin mediated immune response	0.42	>=0.20
ENSG00000177971	IMP3 PPI subnetwork	0.81	>=0.20
ENSG00000136718	IMP4 PPI subnetwork	0.86	>=0.20
MP:0000928	incomplete cephalic closure	0.3	>=0.20
MP:0008641	increased circulating interleukin-1 beta level	0.05	>=0.20
MP:0002404	increased intestinal adenoma incidence	0.14	>=0.20
MP:0009336	increased splenocyte proliferation	0.78	>=0.20
MP:0005027	increased susceptibility to parasitic infection	0.08	>=0.20
MP:0002418	increased susceptibility to viral infection	0.29	>=0.20
GO:0006586	indolalkylamine metabolic process	0.86	>=0.20
GO:0042430	indole-containing compound metabolic process	0.86	>=0.20
GO:0032637	interleukin-8 production	0.19	>=0.20
MP:0002957	intestinal adenocarcinoma	0.11	>=0.20
GO:0016862	intramolecular oxidoreductase activity, interconverting keto-	0.08	>=0.20
ENSG00000196497	IPO4 PPI subnetwork	0.08	>=0.20
ENSG00000198001	IRAK4 PPI subnetwork	0.25	>=0.20
GO:0051536	iron-sulfur cluster binding	0.92	>=0.20
GO:0055072	iron ion homeostasis	0.28	>=0.20
ENSG00000182359	KBTBD3 PPI subnetwork	0.07	>=0.20

ENSG00000105438	KDELR1 PPI subnetwork	0.3	>=0.20
KEGG_BASE_EXCISION_REPAI	KEGG_BASE_EXCISION_REPAIR	0.76	>=0.20
KEGG_BIOSYNTHESIS_OF_UN	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	0.05	>=0.20
KEGG_GLYCOSAMINOGLYCAN	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SU	0.99	>=0.20
KEGG_N_GLYCAN_BIOSYNTHE	KEGG_N_GLYCAN_BIOSYNTHESIS	0.62	>=0.20
KEGG_NON_HOMOLOGOUS_	KEGG_NON_HOMOLOGOUS_END_JOINING	0.47	>=0.20
KEGG_ONE_CARBON_POOL_B	KEGG_ONE_CARBON_POOL_BY_FOLATE	0.37	>=0.20
KEGG_PHENYLALANINE_MET	KEGG_PHENYLALANINE_METABOLISM	0.06	>=0.20
MP:0002893	ketoaciduria	0.05	>=0.20
ENSG00000136813	KIAA0368 PPI subnetwork	0.17	>=0.20
ENSG00000137177	KIF13A PPI subnetwork	0.57	>=0.20
ENSG00000111615	KRR1 PPI subnetwork	0.76	>=0.20
GO:0007595	lactation	0.12	>=0.20
ENSG00000174720	LARP7 PPI subnetwork	0.61	>=0.20
GO:0005770	late endosome	0.17	>=0.20
GO:0002443	leukocyte mediated immunity	0.56	>=0.20
MP:0001152	Leydig cell hyperplasia	0.08	>=0.20
GO:0003706	ligand-regulated transcription factor activity	0.18	>=0.20
GO:0042158	lipoprotein biosynthetic process	0.86	>=0.20
ENSG00000175536	LIPT2 PPI subnetwork	0.68	>=0.20
GO:0034374	low-density lipoprotein particle remodeling	0.15	>=0.20
ENSG00000172850	LSM2 PPI subnetwork	0.1	>=0.20
ENSG00000204392	LSM2 PPI subnetwork	0.1	>=0.20
ENSG00000170860	LSM3 PPI subnetwork	0.79	>=0.20
ENSG00000130520	LSM4 PPI subnetwork	0.34	>=0.20
ENSG00000007392	LUC7L PPI subnetwork	0.22	>=0.20
MP:0008102	lymph node hyperplasia	0.18	>=0.20
GO:0002449	lymphocyte mediated immunity	0.62	>=0.20
GO:0005765	lysosomal membrane	0.07	>=0.20
GO:0000030	mannosyltransferase activity	0.88	>=0.20
ENSG00000112159	MDN1 PPI subnetwork	0.49	>=0.20
ENSG00000141434	MEP1B PPI subnetwork	0.09	>=0.20
GO:0051540	metal cluster binding	0.92	>=0.20
GO:0032259	methylation	0.31	>=0.20
ENSG00000185432	METTL7A PPI subnetwork	0.49	>=0.20
GO:0031903	microbody membrane	0.05	>=0.20
ENSG00000020426	MNAT1 PPI subnetwork	0.14	>=0.20
ENSG00000061987	MON2 PPI subnetwork	0.57	>=0.20
GO:0008028	monocarboxylic acid transmembrane transporter activity	0.07	>=0.20
ENSG00000103152	MPG PPI subnetwork	0.09	>=0.20
ENSG00000124383	MPHOSPH10 PPI subnetwork	0.72	>=0.20
GO:0051028	mRNA transport	0.63	>=0.20
ENSG00000172172	MRPL13 PPI subnetwork	0.32	>=0.20
ENSG00000158042	MRPL17 PPI subnetwork	0.85	>=0.20
ENSG00000112651	MRPL2 PPI subnetwork	0.86	>=0.20
ENSG00000108826	MRPL27 PPI subnetwork	0.49	>=0.20
ENSG00000131368	MRPS25 PPI subnetwork	0.27	>=0.20

ENSG00000072952	MRVI1 PPI subnetwork	0.1	>=0.20
ENSG00000147649	MTDH PPI subnetwork	0.28	>=0.20
ENSG00000167508	MVD PPI subnetwork	0.69	>=0.20
GO:0016410	N-acyltransferase activity	0.48	>=0.20
ENSG00000172766	NAA16 PPI subnetwork	0.17	>=0.20
ENSG00000173418	NAA20 PPI subnetwork	0.12	>=0.20
GO:0006739	NADP metabolic process	0.15	>=0.20
ENSG00000135372	NAT10 PPI subnetwork	0.7	>=0.20
ENSG00000114503	NCBP2 PPI subnetwork	0.04	>=0.20
GO:0034660	ncRNA metabolic process	0.9	>=0.20
GO:0034470	ncRNA processing	0.9	>=0.20
GO:0030195	negative regulation of blood coagulation	0.05	>=0.20
GO:0050819	negative regulation of coagulation	0.11	>=0.20
GO:0045814	negative regulation of gene expression, epigenetic	0.66	>=0.20
ENSG00000165525	NEMF PPI subnetwork	0.35	>=0.20
ENSG00000129460	NGDN PPI subnetwork	0.86	>=0.20
ENSG00000145912	NHP2 PPI subnetwork	0.55	>=0.20
GO:0046496	nicotinamide nucleotide metabolic process	0.1	>=0.20
GO:0046209	nitric oxide metabolic process	0.05	>=0.20
ENSG00000173145	NOC3L PPI subnetwork	0.68	>=0.20
ENSG00000115761	NOL10 PPI subnetwork	0.67	>=0.20
ENSG00000140939	NOL3 PPI subnetwork	0.21	>=0.20
ENSG00000165271	NOL6 PPI subnetwork	0.57	>=0.20
ENSG00000087269	NOP14 PPI subnetwork	0.79	>=0.20
ENSG00000101361	NOP56 PPI subnetwork	0.28	>=0.20
ENSG00000055044	NOP58 PPI subnetwork	0.51	>=0.20
ENSG00000147383	NSDHL PPI subnetwork	0.16	>=0.20
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-medi	0.83	>=0.20
GO:0005635	nuclear envelope	0.36	>=0.20
GO:0031965	nuclear membrane	0.62	>=0.20
GO:0005643	nuclear pore	0.67	>=0.20
GO:0015931	nucleobase-containing compound transport	0.38	>=0.20
GO:0044452	nucleolar part	0.88	>=0.20
ENSG00000173566	NUDT18 PPI subnetwork	0.13	>=0.20
GO:0031080	Nup107-160 complex	0.61	>=0.20
ENSG00000124789	NUP153 PPI subnetwork	0.47	>=0.20
ENSG00000113569	NUP155 PPI subnetwork	0.88	>=0.20
ENSG00000163002	NUP35 PPI subnetwork	0.49	>=0.20
ENSG00000138750	NUP54 PPI subnetwork	0.09	>=0.20
ENSG00000213024	NUP62 PPI subnetwork	0.44	>=0.20
ENSG00000102900	NUP93 PPI subnetwork	0.34	>=0.20
ENSG00000139496	NUPL1 PPI subnetwork	0.5	>=0.20
ENSG00000136243	NUPL2 PPI subnetwork	0.63	>=0.20
ENSG00000138430	OLA1 PPI subnetwork	0.21	>=0.20
GO:0015849	organic acid transport	0.38	>=0.20
GO:0006733	oxidoreduction coenzyme metabolic process	0.1	>=0.20
ENSG00000185624	P4HB PPI subnetwork	0.14	>=0.20

ENSG00000100836	PABPN1 PPI subnetwork	0.05	>=0.20
ENSG00000111845	PAK1IP1 PPI subnetwork	0.62	>=0.20
MP:0004969	pale kidney	0.18	>=0.20
ENSG00000121274	PAPD5 PPI subnetwork	0.97	>=0.20
MP:0011106	partial embryonic lethality before somite formation	0.32	>=0.20
ENSG00000177425	PAWR PPI subnetwork	0.13	>=0.20
ENSG00000132646	PCNA PPI subnetwork	0.27	>=0.20
ENSG00000148843	PDCD11 PPI subnetwork	0.61	>=0.20
ENSG00000167004	PDIA3 PPI subnetwork	0.13	>=0.20
GO:0018208	peptidyl-proline modification	0.33	>=0.20
GO:0005778	peroxisomal membrane	0.05	>=0.20
GO:0043574	peroxisomal transport	0.38	>=0.20
ENSG00000124587	PEX6 PPI subnetwork	0.15	>=0.20
ENSG00000112357	PEX7 PPI subnetwork	0.18	>=0.20
ENSG00000142657	PGD PPI subnetwork	0.07	>=0.20
ENSG00000100410	PHF5A PPI subnetwork	0.05	>=0.20
ENSG00000140451	PIF1 PPI subnetwork	0.35	>=0.20
GO:0042440	pigment metabolic process	0.81	>=0.20
ENSG00000104368	PLAT PPI subnetwork	0.07	>=0.20
ENSG00000047315	POLR2B PPI subnetwork	0.05	>=0.20
ENSG00000102978	POLR2C PPI subnetwork	0.05	>=0.20
ENSG00000144231	POLR2D PPI subnetwork	0.04	>=0.20
ENSG00000099817	POLR2E PPI subnetwork	0.11	>=0.20
ENSG00000100142	POLR2F PPI subnetwork	0.17	>=0.20
ENSG00000168002	POLR2G PPI subnetwork	0.08	>=0.20
ENSG00000163882	POLR2H PPI subnetwork	0.18	>=0.20
ENSG00000005075	POLR2J PPI subnetwork	0.11	>=0.20
ENSG00000147669	POLR2K PPI subnetwork	0.23	>=0.20
ENSG00000177700	POLR2L PPI subnetwork	0.2	>=0.20
GO:0019751	polyol metabolic process	0.27	>=0.20
GO:0000272	polysaccharide catabolic process	0.11	>=0.20
GO:0030194	positive regulation of blood coagulation	0.11	>=0.20
GO:0050820	positive regulation of coagulation	0.1	>=0.20
GO:2001056	positive regulation of cysteine-type endopeptidase activity	0.65	>=0.20
GO:0043280	positive regulation of cysteine-type endopeptidase activity in	0.65	>=0.20
GO:0010950	positive regulation of endopeptidase activity	0.56	>=0.20
GO:0045723	positive regulation of fatty acid biosynthetic process	0.17	>=0.20
GO:0046889	positive regulation of lipid biosynthetic process	0.04	>=0.20
GO:0010575	positive regulation vascular endothelial growth factor produc	0.33	>=0.20
GO:0009791	post-embryonic development	0.65	>=0.20
ENSG00000131238	PPT1 PPI subnetwork	0.07	>=0.20
GO:0045120	pronucleus	0.09	>=0.20
GO:0022624	proteasome accessory complex	0.81	>=0.20
GO:0072662	protein localization to peroxisome	0.66	>=0.20
GO:0051604	protein maturation	0.41	>=0.20
GO:0019903	protein phosphatase binding	0.04	>=0.20
GO:0016485	protein processing	0.52	>=0.20

GO:0009306	protein secretion	0.24	>=0.20
GO:0006625	protein targeting to peroxisome	0.66	>=0.20
GO:0051262	protein tetramerization	0.13	>=0.20
ENSG00000117360	PRPF3 PPI subnetwork	0.1	>=0.20
ENSG00000136875	PRPF4 PPI subnetwork	0.12	>=0.20
ENSG00000101161	PRPF6 PPI subnetwork	0.03	>=0.20
ENSG00000164985	PSIP1 PPI subnetwork	0.45	>=0.20
ENSG00000143106	PSMA5 PPI subnetwork	0.61	>=0.20
ENSG00000101182	PSMA7 PPI subnetwork	0.58	>=0.20
ENSG00000159377	PSMB4 PPI subnetwork	0.52	>=0.20
ENSG00000142507	PSMB6 PPI subnetwork	0.58	>=0.20
ENSG00000165916	PSMC3 PPI subnetwork	0.04	>=0.20
ENSG00000013275	PSMC4 PPI subnetwork	0.18	>=0.20
ENSG00000173692	PSMD1 PPI subnetwork	0.17	>=0.20
ENSG00000197170	PSMD12 PPI subnetwork	0.25	>=0.20
ENSG00000185627	PSMD13 PPI subnetwork	0.15	>=0.20
ENSG00000115233	PSMD14 PPI subnetwork	0.15	>=0.20
ENSG00000175166	PSMD2 PPI subnetwork	0.14	>=0.20
ENSG00000108344	PSMD3 PPI subnetwork	0.37	>=0.20
ENSG00000099341	PSMD8 PPI subnetwork	0.25	>=0.20
ENSG00000091127	PUS7 PPI subnetwork	0.59	>=0.20
ENSG00000136045	PWP1 PPI subnetwork	0.17	>=0.20
GO:0072525	pyridine-containing compound biosynthetic process	0.69	>=0.20
GO:0019363	pyridine nucleotide biosynthetic process	0.69	>=0.20
ENSG00000105404	RABAC1 PPI subnetwork	0.04	>=0.20
ENSG00000152942	RAD17 PPI subnetwork	0.55	>=0.20
ENSG00000101146	RAE1 PPI subnetwork	0.85	>=0.20
ENSG00000106344	RBM28 PPI subnetwork	0.62	>=0.20
ENSG00000188739	RBM34 PPI subnetwork	0.66	>=0.20
ENSG00000003756	RBM5 PPI subnetwork	0.03	>=0.20
ENSG00000131795	RBM8A PPI subnetwork	0.08	>=0.20
ENSG00000147274	RBMX PPI subnetwork	0.11	>=0.20
REACTOME_APOPTOSIS	REACTOME_APOPTOSIS	0.37	>=0.20
REACTOME_ASSEMBLY_OF_TI	REACTOME_ASSEMBLY_OF_THE_PRE:REPLICATIVE_COMPLEX	0.62	>=0.20
REACTOME_ASSOCIATION_OF	REACTOME_ASSOCIATION_OF_LICENSING_FACTORS_WITH_T	0.58	>=0.20
REACTOME_ASSOCIATION_OF	REACTOME_ASSOCIATION_OF_TRICCCT_WITH_TARGET_PRO	0.15	>=0.20
REACTOME_BASE_EXCISION_I	REACTOME_BASE_EXCISION_REPAIR	0.82	>=0.20
REACTOME_BIOSYNTHESIS_O	REACTOME_BIOSYNTHESIS_OF_THE_N:GLYCAN_PRECURSOR	0.54	>=0.20
REACTOME_CHOLESTEROL_BI	REACTOME_CHOLESTEROL_BIOSYNTHESIS	0.06	>=0.20
REACTOME_DNA_REPAIR	REACTOME_DNA_REPAIR	0.95	>=0.20
REACTOME_EXPORT_OF_VIRA	REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FRC	0.59	>=0.20
REACTOME_HIV_INFECTION	REACTOME_HIV_INFECTION	0.31	>=0.20
REACTOME_HIV_LIFE_CYCLE	REACTOME_HIV_LIFE_CYCLE	0.24	>=0.20
REACTOME_INTERACTIONS_C	REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR	0.57	>=0.20
REACTOME_INTRINSIC_PATH\	REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	0.25	>=0.20
REACTOME_LATE_PHASE_OF_	REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	0.34	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_RNA	0.64	>=0.20

REACTOME_MITOCHONDRIAL	REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION	0.64	>=0.20
REACTOME_MRNA_3:END_PR	REACTOME_MRNA_3:END_PROCESSING	0.08	>=0.20
REACTOME_MRNA_DECAY_B'	REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE	0.86	>=0.20
REACTOME_MRNA_SPLICING	REACTOME_MRNA_SPLICING	0.03	>=0.20
REACTOME_MRNA_SPLICING_	REACTOME_MRNA_SPLICING_:_MAJOR_PATHWAY	0.03	>=0.20
REACTOME_MRNA_SPLICING_	REACTOME_MRNA_SPLICING_:_MINOR_PATHWAY	0.32	>=0.20
REACTOME_N:GLYCAN_TRIMI	REACTOME_N:GLYCAN_TRIMMING_IN_THE_ER_AND_CALNE	0.27	>=0.20
REACTOME_NEPNS2_INTERAC	REACTOME_NEPNS2_INTERACTS_WITH_THE_CELLULAR_EXP	0.56	>=0.20
REACTOME_NUCLEAR_IMPOR	REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN	0.5	>=0.20
REACTOME_P53:INDEPENDEN	REACTOME_P53:INDEPENDENT_DNA_DAMAGE_RESPONSE	0.69	>=0.20
REACTOME_P53:INDEPENDEN	REACTOME_P53:INDEPENDENT_G1S_DNA_DAMAGE_CHECKI	0.69	>=0.20
REACTOME_POST:ELONGATIC	REACTOME_POST:ELONGATION_PROCESSING_OF_INTRON:C	0.08	>=0.20
REACTOME_POST:ELONGATIC	REACTOME_POST:ELONGATION_PROCESSING_OF_INTRONLE	0.62	>=0.20
REACTOME_PROCESSING_OF_	REACTOME_PROCESSING_OF_CAPPED_INTRON:CONTAINING	0.11	>=0.20
REACTOME_PROCESSING_OF_	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE:MR	0.62	>=0.20
REACTOME_REMOVAL_OF_DI	REACTOME_REMOVAL_OF_DNA_PATCH_CONTAINING_ABAS	0.85	>=0.20
REACTOME_RESOLUTION_OF_	REACTOME_RESOLUTION_OF_ABASIC_SITES_AP_SITES	0.82	>=0.20
REACTOME_RESOLUTION_OF_	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE	0.85	>=0.20
REACTOME_REV:MEDIATED_N	REACTOME_REV:MEDIATED_NUCLEAR_EXPORT_OF_HIV:1_R	0.6	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	0.12	>=0.20
REACTOME_SPHINGOLIPID_M	REACTOME_SPHINGOLIPID_METABOLISM	0.19	>=0.20
REACTOME_SYNTHESIS_OF_V	REACTOME_SYNTHESIS_OF_VERY_LONG:CHAIN_FATTY_ACYL	0.12	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FRO	0.33	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FRO	0.53	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FR	0.65	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYT	0.32	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_T	0.62	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_THE_SLBP_INDEPENDENT_MAT	0.67	>=0.20
REACTOME_UBIQUITIN_MEDI	REACTOME_UBIQUITIN_MEDIATED_DEGRADATION_OF_PHO	0.69	>=0.20
MP:0000493	rectal prolapse	0.12	>=0.20
GO:0043281	regulation of cysteine-type endopeptidase activity involved in	0.2	>=0.20
GO:0010827	regulation of glucose transport	0.4	>=0.20
GO:0045088	regulation of innate immune response	0.08	>=0.20
ENSG00000157916	RER1 PPI subnetwork	0.51	>=0.20
GO:0034698	response to gonadotropin stimulus	0.16	>=0.20
GO:0010212	response to ionizing radiation	0.81	>=0.20
GO:0042594	response to starvation	0.18	>=0.20
GO:0009636	response to toxin	0.57	>=0.20
GO:0009411	response to UV	0.98	>=0.20
GO:0033273	response to vitamin	0.1	>=0.20
GO:0004745	retinol dehydrogenase activity	0.47	>=0.20
ENSG00000058729	RIOK2 PPI subnetwork	0.8	>=0.20
GO:0009451	RNA modification	0.89	>=0.20
ENSG00000070423	RNF126 PPI subnetwork	0.18	>=0.20
ENSG00000023191	RNH1 PPI subnetwork	0.04	>=0.20
ENSG00000147403	RPL10 PPI subnetwork	0.62	>=0.20
ENSG00000105640	RPL18A PPI subnetwork	0.7	>=0.20

ENSG00000131469	RPL27 PPI subnetwork	0.59	>=0.20
ENSG00000100316	RPL3 PPI subnetwork	0.13	>=0.20
ENSG00000174444	RPL4 PPI subnetwork	0.41	>=0.20
ENSG00000122406	RPL5 PPI subnetwork	0.64	>=0.20
ENSG00000177600	RPLP2 PPI subnetwork	0.42	>=0.20
ENSG00000142534	RPS11 PPI subnetwork	0.52	>=0.20
ENSG00000110700	RPS13 PPI subnetwork	0.48	>=0.20
ENSG00000134419	RPS15A PPI subnetwork	0.48	>=0.20
ENSG00000138326	RPS24 PPI subnetwork	0.63	>=0.20
ENSG00000145425	RPS3A PPI subnetwork	0.17	>=0.20
ENSG00000083845	RPS5 PPI subnetwork	0.75	>=0.20
ENSG00000052749	RRP12 PPI subnetwork	0.85	>=0.20
ENSG00000160208	RRP1B PPI subnetwork	0.74	>=0.20
ENSG00000114767	RRP9 PPI subnetwork	0.94	>=0.20
ENSG00000031698	SARS PPI subnetwork	0.21	>=0.20
ENSG00000175467	SART1 PPI subnetwork	0.22	>=0.20
GO:0005044	scavenger receptor activity	0.07	>=0.20
ENSG00000078808	SDF4 PPI subnetwork	0.3	>=0.20
ENSG00000071537	SEL1L PPI subnetwork	0.08	>=0.20
GO:0009070	serine family amino acid biosynthetic process	0.52	>=0.20
ENSG00000166401	SERPINB8 PPI subnetwork	0.61	>=0.20
ENSG00000087365	SF3B2 PPI subnetwork	0.06	>=0.20
ENSG00000169976	SF3B5 PPI subnetwork	0.04	>=0.20
ENSG00000204351	SKIV2L PPI subnetwork	0.89	>=0.20
ENSG00000206353	SKIV2L PPI subnetwork	0.89	>=0.20
ENSG00000155380	SLC16A1 PPI subnetwork	0.36	>=0.20
ENSG00000075415	SLC25A3 PPI subnetwork	0.17	>=0.20
ENSG00000176273	SLC35G1 PPI subnetwork	0.05	>=0.20
ENSG00000164609	SLU7 PPI subnetwork	0.43	>=0.20
GO:0030532	small nuclear ribonucleoprotein complex	0.76	>=0.20
ENSG00000072501	SMC1A PPI subnetwork	0.1	>=0.20
ENSG00000119953	SMNDC1 PPI subnetwork	0.35	>=0.20
ENSG00000104852	SNRNP70 PPI subnetwork	0.05	>=0.20
ENSG00000131876	SNRPA1 PPI subnetwork	0.04	>=0.20
ENSG00000125870	SNRPB2 PPI subnetwork	0.09	>=0.20
ENSG00000125743	SNRPD2 PPI subnetwork	0.05	>=0.20
ENSG00000100028	SNRPD3 PPI subnetwork	0.13	>=0.20
ENSG00000182004	SNRPE PPI subnetwork	0.16	>=0.20
ENSG00000139343	SNRPF PPI subnetwork	0.09	>=0.20
ENSG00000143977	SNRPG PPI subnetwork	0.09	>=0.20
ENSG00000128739	SNRPN PPI subnetwork	0.55	>=0.20
ENSG00000214265	SNURF PPI subnetwork	0.54	>=0.20
ENSG00000152582	SPEF2 PPI subnetwork	0.13	>=0.20
ENSG00000133104	SPG20 PPI subnetwork	0.13	>=0.20
GO:0005681	spliceosomal complex	0.42	>=0.20
ENSG00000198911	SREBF2 PPI subnetwork	0.06	>=0.20
GO:0032933	SREBP-mediated signaling pathway	0.48	>=0.20

ENSG00000133226	SRRM1 PPI subnetwork	0.04	>=0.20
ENSG00000161547	SRSF2 PPI subnetwork	0.04	>=0.20
ENSG00000112081	SRSF3 PPI subnetwork	0.03	>=0.20
ENSG00000116350	SRSF4 PPI subnetwork	0.04	>=0.20
ENSG00000100650	SRSF5 PPI subnetwork	0.05	>=0.20
ENSG00000115875	SRSF7 PPI subnetwork	0.06	>=0.20
ENSG00000111786	SRSF9 PPI subnetwork	0.1	>=0.20
ENSG00000173465	SSSCA1 PPI subnetwork	0.34	>=0.20
GO:0043401	steroid hormone mediated signaling pathway	0.2	>=0.20
ENSG00000163541	SUCLG1 PPI subnetwork	0.08	>=0.20
GO:0000096	sulfur amino acid metabolic process	0.46	>=0.20
ENSG00000183751	TBL3 PPI subnetwork	0.58	>=0.20
MP:0003205	testicular atrophy	0.05	>=0.20
ENSG00000163810	TGM4 PPI subnetwork	0.11	>=0.20
GO:0035383	thioester metabolic process	0.08	>=0.20
GO:0016790	thiolester hydrolase activity	0.42	>=0.20
ENSG00000138297	TIMM23 PPI subnetwork	0.23	>=0.20
ENSG00000150455	TIRAP PPI subnetwork	0.13	>=0.20
ENSG00000140332	TLE3 PPI subnetwork	0.37	>=0.20
ENSG00000164342	TLR3 PPI subnetwork	0.16	>=0.20
ENSG00000136869	TLR4 PPI subnetwork	0.03	>=0.20
ENSG00000086598	TMED2 PPI subnetwork	0.06	>=0.20
ENSG00000117500	TMED5 PPI subnetwork	0.04	>=0.20
GO:0034142	toll-like receptor 4 signaling pathway	0.33	>=0.20
GO:0008063	Toll signaling pathway	0.21	>=0.20
ENSG00000131323	TRAF3 PPI subnetwork	0.56	>=0.20
ENSG00000175104	TRAF6 PPI subnetwork	0.05	>=0.20
GO:0006353	transcription termination, DNA-dependent	0.75	>=0.20
GO:0016765	transferase activity, transferring alkyl or aryl (other than met	0.14	>=0.20
ENSG00000054116	TRAPPC3 PPI subnetwork	0.11	>=0.20
GO:0004549	tRNA-specific ribonuclease activity	0.6	>=0.20
GO:0000049	tRNA binding	0.42	>=0.20
GO:0006399	tRNA metabolic process	0.86	>=0.20
GO:0006400	tRNA modification	0.89	>=0.20
ENSG00000167721	TSR1 PPI subnetwork	0.51	>=0.20
ENSG00000137285	TUBB2B PPI subnetwork	0.13	>=0.20
ENSG00000173876	TUBB8 PPI subnetwork	0.18	>=0.20
ENSG00000141759	TXNL4A PPI subnetwork	0.06	>=0.20
ENSG00000130985	UBA1 PPI subnetwork	0.05	>=0.20
ENSG00000134882	UBAC2 PPI subnetwork	0.22	>=0.20
ENSG00000184787	UBE2G2 PPI subnetwork	0.07	>=0.20
ENSG00000151148	UBE3B PPI subnetwork	0.47	>=0.20
ENSG00000130939	UBE4B PPI subnetwork	0.06	>=0.20
ENSG00000125351	UPF3B PPI subnetwork	0.13	>=0.20
ENSG00000183520	UTP11L PPI subnetwork	0.8	>=0.20
ENSG00000164338	UTP15 PPI subnetwork	0.76	>=0.20
ENSG00000120800	UTP20 PPI subnetwork	0.91	>=0.20

ENSG00000132467	UTP3 PPI subnetwork	0.89	>=0.20
GO:0044437	vacuolar part	0.04	>=0.20
GO:0051180	vitamin transport	0.27	>=0.20
ENSG00000071462	WBSCR22 PPI subnetwork	0.84	>=0.20
ENSG00000065183	WDR3 PPI subnetwork	0.61	>=0.20
ENSG00000134987	WDR36 PPI subnetwork	0.7	>=0.20
ENSG00000204221	WDR46 PPI subnetwork	0.81	>=0.20
ENSG00000206284	WDR46 PPI subnetwork	0.81	>=0.20
GO:0022829	wide pore channel activity	0.24	>=0.20
GO:0042813	Wnt-activated receptor activity	0.09	>=0.20
ENSG00000076924	XAB2 PPI subnetwork	0.44	>=0.20
ENSG00000101966	XIAP PPI subnetwork	0.33	>=0.20
ENSG00000136936	XPA PPI subnetwork	0.98	>=0.20
ENSG00000154767	XPC PPI subnetwork	0.84	>=0.20
ENSG00000184575	XPOT PPI subnetwork	0.06	>=0.20
ENSG00000079246	XRCC5 PPI subnetwork	0.08	>=0.20
ENSG00000100722	ZC3H14 PPI subnetwork	0.13	>=0.20
ENSG00000065548	ZC3H15 PPI subnetwork	0.92	>=0.20
GO:0005385	zinc ion transmembrane transporter activity	0.43	>=0.20
ENSG00000146007	ZMAT2 PPI subnetwork	0.37	>=0.20
ENSG00000084073	ZMPSTE24 PPI subnetwork	0.74	>=0.20
GO:0001892	embryonic placenta development	0.16	>=0.20
MP:0011086	partial postnatal lethality	0.03	>=0.20
MP:0002092	abnormal eye morphology	0.11	>=0.20
MP:0005294	abnormal heart ventricle morphology	0.03	>=0.20
MP:0001176	abnormal lung development	0.25	>=0.20
MP:0001134	absent corpus luteum	0.1	>=0.20
GO:0003995	acyl-CoA dehydrogenase activity	0.03	>=0.20
ENSG00000163347	CLDN1 PPI subnetwork	0.36	>=0.20
MP:0002780	decreased circulating testosterone level	0.11	>=0.20
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	0.21	>=0.20
GO:0016577	histone demethylation	0.05	>=0.20
GO:0060711	labyrinthine layer development	0.19	>=0.20
GO:0017046	peptide hormone binding	0.19	>=0.20
ENSG00000173889	PHC3 PPI subnetwork	0.06	>=0.20
GO:0008214	protein dealkylation	0.06	>=0.20
GO:0006482	protein demethylation	0.06	>=0.20
MP:0002191	abnormal artery morphology	0.09	>=0.20
MP:0002432	abnormal CD4-positive T cell morphology	0.03	>=0.20
MP:0000780	abnormal corpus callosum morphology	0.4	>=0.20
MP:0000427	abnormal hair cycle	0.24	>=0.20
MP:0000383	abnormal hair follicle orientation	0.14	>=0.20
MP:0010763	abnormal hematopoietic stem cell physiology	0.35	>=0.20
MP:0005329	abnormal myocardium layer morphology	0.16	>=0.20
MP:0003720	abnormal neural tube closure	0.2	>=0.20
MP:0000696	abnormal Peyer's patch morphology	0.09	>=0.20
MP:0002230	abnormal primitive streak formation	0.04	>=0.20

MP:0002792	abnormal retinal vasculature morphology	0.03	>=0.20
MP:0005508	abnormal skeleton morphology	0.07	>=0.20
MP:0003149	abnormal tectorial membrane morphology	0.04	>=0.20
MP:0002098	abnormal vibrissa morphology	0.21	>=0.20
GO:0007568	aging	0.04	>=0.20
GO:0001525	angiogenesis	0.03	>=0.20
ENSG00000161203	AP2M1 PPI subnetwork	0.04	>=0.20
ENSG00000142192	APP PPI subnetwork	0.15	>=0.20
ENSG00000049618	ARID1B PPI subnetwork	0.06	>=0.20
ENSG00000171681	ATF7IP PPI subnetwork	0.04	>=0.20
ENSG00000103126	AXIN1 PPI subnetwork	0.03	>=0.20
GO:0001540	beta-amyloid binding	0.46	>=0.20
MP:0004187	cardia bifida	0.12	>=0.20
ENSG00000142273	CBLC PPI subnetwork	0.04	>=0.20
ENSG00000100888	CHD8 PPI subnetwork	0.03	>=0.20
GO:0004693	cyclin-dependent protein kinase activity	0.03	>=0.20
GO:0004861	cyclin-dependent protein kinase inhibitor activity	0.03	>=0.20
GO:0016538	cyclin-dependent protein kinase regulator activity	0.15	>=0.20
GO:0044433	cytoplasmic vesicle part	0.06	>=0.20
ENSG00000165732	DDX21 PPI subnetwork	0.16	>=0.20
ENSG00000108654	DDX5 PPI subnetwork	0.04	>=0.20
MP:0005181	decreased circulating estradiol level	0.06	>=0.20
MP:0005478	decreased circulating thyroxine level	0.26	>=0.20
MP:0004200	decreased fetal size	0.08	>=0.20
MP:0004905	decreased uterus weight	0.47	>=0.20
MP:0003409	decreased width of hypertrophic chondrocyte zone	0.03	>=0.20
ENSG00000091140	DLD PPI subnetwork	0.25	>=0.20
MP:0000440	domed cranium	0.18	>=0.20
ENSG00000135144	DTX1 PPI subnetwork	0.13	>=0.20
ENSG00000161202	DVL3 PPI subnetwork	0.08	>=0.20
ENSG00000090776	EFNB1 PPI subnetwork	0.19	>=0.20
GO:0043542	endothelial cell migration	0.14	>=0.20
MP:0000642	enlarged adrenal glands	0.03	>=0.20
ENSG00000141456	ENSG00000141456 PPI subnetwork	0.04	>=0.20
ENSG00000186852	ENSG00000186852 PPI subnetwork	0.06	>=0.20
ENSG00000212908	ENSG00000212908 PPI subnetwork	0.14	>=0.20
ENSG00000116106	EPHA4 PPI subnetwork	0.56	>=0.20
ENSG00000133216	EPHB2 PPI subnetwork	0.05	>=0.20
ENSG00000082805	ERC1 PPI subnetwork	0.03	>=0.20
MP:0011353	expanded mesangial matrix	0.04	>=0.20
GO:0007565	female pregnancy	0.05	>=0.20
MP:0005264	glomerulosclerosis	0.08	>=0.20
GO:0005539	glycosaminoglycan binding	0.03	>=0.20
GO:0008201	heparin binding	0.09	>=0.20
ENSG00000100644	HIF1A PPI subnetwork	0.07	>=0.20
ENSG00000189403	HMGB1 PPI subnetwork	0.08	>=0.20
ENSG00000168811	IL12A PPI subnetwork	0.15	>=0.20

ENSG00000113302	IL12B PPI subnetwork	0.11	>=0.20
ENSG00000169194	IL13 PPI subnetwork	0.06	>=0.20
ENSG00000169429	IL8 PPI subnetwork	0.05	>=0.20
MP:0004796	increased anti-histone antibody level	0.25	>=0.20
MP:0006094	increased fat cell size	0.04	>=0.20
MP:0008186	increased pro-B cell number	0.04	>=0.20
MP:0005658	increased susceptibility to diet-induced obesity	0.11	>=0.20
MP:0010872	increased trabecular bone mass	0.08	>=0.20
MP:0010810	increased type II pneumocyte number	0.11	>=0.20
MP:0002962	increased urine protein level	0.04	>=0.20
GO:0008629	induction of apoptosis by intracellular signals	0.2	>=0.20
KEGG_NOTCH_SIGNALING_PA	KEGG_NOTCH_SIGNALING_PATHWAY	0.15	>=0.20
KEGG_PROSTATE_CANCER	KEGG_PROSTATE_CANCER	0.04	>=0.20
KEGG_SPHINGOLIPID_METAB	KEGG_SPHINGOLIPID_METABOLISM	0.37	>=0.20
KEGG_VEGF_SIGNALING_PATI	KEGG_VEGF_SIGNALING_PATHWAY	0.05	>=0.20
ENSG00000102554	KLF5 PPI subnetwork	0.1	>=0.20
ENSG00000213416	KRTAP4-12 PPI subnetwork	0.14	>=0.20
GO:0015909	long-chain fatty acid transport	0.2	>=0.20
ENSG00000107643	MAPK8 PPI subnetwork	0.04	>=0.20
GO:0005740	mitochondrial envelope	0.03	>=0.20
GO:0005849	mRNA cleavage factor complex	0.06	>=0.20
ENSG00000132780	NASP PPI subnetwork	0.04	>=0.20
GO:0030336	negative regulation of cell migration	0.1	>=0.20
GO:2000146	negative regulation of cell motility	0.13	>=0.20
GO:0051271	negative regulation of cellular component movement	0.07	>=0.20
ENSG00000170515	PA2G4 PPI subnetwork	0.03	>=0.20
GO:0030166	proteoglycan biosynthetic process	0.24	>=0.20
ENSG00000122679	RAMP3 PPI subnetwork	0.04	>=0.20
REACTOME_AMYLOIDS	REACTOME_AMYLOIDS	0.23	>=0.20
REACTOME_MITOCHONDRIAL	REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA:OXIDATIOI	0.12	>=0.20
GO:0030334	regulation of cell migration	0.03	>=0.20
GO:0010817	regulation of hormone levels	0.07	>=0.20
GO:0051591	response to cAMP	0.11	>=0.20
ENSG00000172602	RND1 PPI subnetwork	0.18	>=0.20
GO:0005791	rough endoplasmic reticulum	0.04	>=0.20
GO:0030141	secretory granule	0.05	>=0.20
MP:0000592	short tail	0.2	>=0.20
MP:0001786	skin edema	0.07	>=0.20
MP:0002774	small prostate gland	0.54	>=0.20
MP:0000416	sparse hair	0.14	>=0.20
ENSG00000100380	ST13 PPI subnetwork	0.04	>=0.20
GO:0051119	sugar transmembrane transporter activity	0.07	>=0.20
GO:0044272	sulfur compound biosynthetic process	0.13	>=0.20
GO:0050321	tau-protein kinase activity	0.03	>=0.20
MP:0001245	thick dermal layer	0.06	>=0.20
ENSG00000156299	TIAM1 PPI subnetwork	0.04	>=0.20
ENSG00000115705	TPO PPI subnetwork	0.1	>=0.20

MP:0001201	translucent skin	0.06	>=0.20
ENSG00000140740	UQCRC2 PPI subnetwork	0.03	>=0.20
GO:0030120	vesicle coat	0.07	>=0.20
ENSG00000134308	YWHAQ PPI subnetwork	0.04	>=0.20
GO:0051084	'de novo' posttranslational protein folding	0.94	>=0.20
GO:0006458	'de novo' protein folding	0.94	>=0.20
GO:0005545	1-phosphatidylinositol binding	0.18	>=0.20
GO:0006103	2-oxoglutarate metabolic process	0.82	>=0.20
GO:0051537	2 iron, 2 sulfur cluster binding	0.86	>=0.20
GO:0000175	3'-5'-exoribonuclease activity	0.96	>=0.20
GO:0008408	3'-5' exonuclease activity	1	>=0.20
GO:0004115	3',5'-cyclic-AMP phosphodiesterase activity	0.27	>=0.20
GO:0047555	3',5'-cyclic-GMP phosphodiesterase activity	0.95	>=0.20
GO:0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	0.55	>=0.20
GO:0051539	4 iron, 4 sulfur cluster binding	0.97	>=0.20
GO:0031672	A band	0.71	>=0.20
ENSG00000094914	AAAS PPI subnetwork	0.64	>=0.20
ENSG00000115977	AAK1 PPI subnetwork	0.31	>=0.20
ENSG00000090861	AARS PPI subnetwork	0.05	>=0.20
ENSG00000165029	ABCA1 PPI subnetwork	0.12	>=0.20
ENSG00000131269	ABCB7 PPI subnetwork	0.09	>=0.20
ENSG00000069431	ABCC9 PPI subnetwork	0.25	>=0.20
ENSG00000164163	ABCE1 PPI subnetwork	0.54	>=0.20
ENSG00000033050	ABCF2 PPI subnetwork	0.19	>=0.20
MP:0010465	aberrant origin of the right subclavian artery	0.82	>=0.20
ENSG00000136754	ABI1 PPI subnetwork	0.12	>=0.20
ENSG00000097007	ABL1 PPI subnetwork	0.1	>=0.20
ENSG00000099204	ABLIM1 PPI subnetwork	0.28	>=0.20
ENSG00000173210	ABLIM3 PPI subnetwork	0.44	>=0.20
MP:0008898	abnormal acrosome morphology	0.6	>=0.20
MP:0005402	abnormal action potential	0.98	>=0.20
MP:0004163	abnormal adenohypophysis morphology	0.98	>=0.20
MP:0003235	abnormal alisphenoid bone morphology	0.99	>=0.20
MP:0004189	abnormal alveolar process morphology	0.45	>=0.20
MP:0002650	abnormal ameloblast morphology	0.85	>=0.20
MP:0002885	abnormal AMPA-mediated synaptic currents	0.98	>=0.20
MP:0000260	abnormal angiogenesis	0.03	>=0.20
MP:0004784	abnormal anterior cardinal vein morphology	0.36	>=0.20
MP:0005193	abnormal anterior eye segment morphology	1	>=0.20
MP:0002452	abnormal antigen presenting cell physiology	0.55	>=0.20
MP:0009862	abnormal aorta elastic tissue morphology	0.81	>=0.20
MP:0000272	abnormal aorta morphology	0.97	>=0.20
MP:0009866	abnormal aorta wall morphology	0.13	>=0.20
MP:0004113	abnormal aortic arch morphology	0.96	>=0.20
MP:0002747	abnormal aortic valve morphology	0.93	>=0.20
MP:0001676	abnormal apical ectodermal ridge morphology	0.79	>=0.20
MP:0001648	abnormal apoptosis	0.31	>=0.20

MP:0000297	abnormal atrioventricular cushion morphology	0.42	>=0.20
MP:0000572	abnormal autopod morphology	0.7	>=0.20
MP:0001684	abnormal axial mesoderm	0.48	>=0.20
MP:0002114	abnormal axial skeleton morphology	0.35	>=0.20
MP:0002961	abnormal axon guidance	1	>=0.20
MP:0005404	abnormal axon morphology	0.91	>=0.20
MP:0003651	abnormal axon outgrowth	0.8	>=0.20
MP:0004768	abnormal axonal transport	0.93	>=0.20
MP:0008217	abnormal B cell activation	0.27	>=0.20
MP:0002144	abnormal B cell differentiation	0.05	>=0.20
MP:0004939	abnormal B cell morphology	0.63	>=0.20
MP:0002459	abnormal B cell physiology	0.12	>=0.20
MP:0005153	abnormal B cell proliferation	0.21	>=0.20
MP:0006007	abnormal basal ganglion morphology	0.92	>=0.20
MP:0004272	abnormal basement membrane morphology	0.51	>=0.20
MP:0010029	abnormal basicranium morphology	0.95	>=0.20
MP:0000079	abnormal basioccipital bone morphology	0.93	>=0.20
MP:0000106	abnormal basisphenoid bone morphology	1	>=0.20
MP:0004924	abnormal behavior	0.91	>=0.20
MP:0009745	abnormal behavioral response to xenobiotic	1	>=0.20
MP:0002929	abnormal bile duct development	0.18	>=0.20
MP:0002928	abnormal bile duct morphology	0.6	>=0.20
MP:0005167	abnormal blood-brain barrier function	0.41	>=0.20
MP:0002128	abnormal blood circulation	0.09	>=0.20
MP:0000233	abnormal blood flow velocity	0.26	>=0.20
MP:0001777	abnormal body temperature homeostasis	0.05	>=0.20
MP:0000065	abnormal bone marrow cavity morphology	0.34	>=0.20
MP:0002398	abnormal bone marrow cell morphology/development	0.37	>=0.20
MP:0008271	abnormal bone ossification	0.16	>=0.20
MP:0002998	abnormal bone remodeling	0.14	>=0.20
MP:0002199	abnormal brain commissure morphology	0.98	>=0.20
MP:0000913	abnormal brain development	0.77	>=0.20
MP:0004101	abnormal brain interneuron morphology	0.99	>=0.20
MP:0002152	abnormal brain morphology	0.48	>=0.20
MP:0000822	abnormal brain ventricle morphology	0.71	>=0.20
MP:0004994	abnormal brain wave pattern	1	>=0.20
MP:0008026	abnormal brain white matter morphology	0.55	>=0.20
MP:0004738	abnormal brainstem auditory evoked potential	0.76	>=0.20
MP:0002672	abnormal branchial arch artery morphology	0.52	>=0.20
MP:0002884	abnormal branchial arch morphology	0.37	>=0.20
MP:0011024	abnormal branching involved in lung morphogenesis	0.86	>=0.20
MP:0001951	abnormal breathing pattern	1	>=0.20
MP:0004231	abnormal calcium ion homeostasis	0.67	>=0.20
MP:0002972	abnormal cardiac muscle contractility	0.49	>=0.20
MP:0004084	abnormal cardiac muscle relaxation	0.33	>=0.20
MP:0004783	abnormal cardinal vein morphology	0.43	>=0.20
MP:0001544	abnormal cardiovascular system physiology	0.15	>=0.20

MP:0000554	abnormal carpal bone morphology	1	>=0.20
MP:0000164	abnormal cartilage development	0.83	>=0.20
MP:0000163	abnormal cartilage morphology	0.55	>=0.20
MP:0002759	abnormal caudal vertebrae morphology	0.26	>=0.20
MP:0008076	abnormal CD4-positive T cell differentiation	0.84	>=0.20
MP:0005463	abnormal CD4-positive T cell physiology	0.55	>=0.20
MP:0008080	abnormal CD8-positive T cell differentiation	0.93	>=0.20
MP:0005010	abnormal CD8-positive T cell morphology	1	>=0.20
MP:0004392	abnormal CD8-positive T cell physiology	0.56	>=0.20
MP:0003077	abnormal cell cycle	0.19	>=0.20
MP:0004045	abnormal cell cycle checkpoint function	0.64	>=0.20
MP:0000857	abnormal cerebellar foliation	0.95	>=0.20
MP:0004098	abnormal cerebellar granule cell morphology	0.78	>=0.20
MP:0000886	abnormal cerebellar granule layer	0.9	>=0.20
MP:0000889	abnormal cerebellar molecular layer	0.99	>=0.20
MP:0000875	abnormal cerebellar Purkinje cell layer	0.29	>=0.20
MP:0000854	abnormal cerebellum development	0.99	>=0.20
MP:0000872	abnormal cerebellum external granule cell layer morphology	0.95	>=0.20
MP:0000849	abnormal cerebellum morphology	0.89	>=0.20
MP:0000864	abnormal cerebellum vermis morphology	0.98	>=0.20
MP:0000788	abnormal cerebral cortex morphology	0.4	>=0.20
MP:0008540	abnormal cerebrum morphology	0.83	>=0.20
MP:0004607	abnormal cervical atlas morphology	0.97	>=0.20
MP:0004608	abnormal cervical axis morphology	0.99	>=0.20
MP:0003048	abnormal cervical vertebrae morphology	0.79	>=0.20
MP:0003484	abnormal channel response	1	>=0.20
MP:0000166	abnormal chondrocyte morphology	0.24	>=0.20
MP:0002836	abnormal chorion morphology	0.05	>=0.20
MP:0000820	abnormal choroid plexus morphology	0.74	>=0.20
MP:0004816	abnormal class switch recombination	0.37	>=0.20
MP:0005298	abnormal clavicle morphology	0.97	>=0.20
MP:0000952	abnormal CNS glial cell morphology	0.54	>=0.20
MP:0002206	abnormal CNS synaptic transmission	1	>=0.20
MP:0000367	abnormal coat/ hair morphology	0.07	>=0.20
MP:0002075	abnormal coat/hair pigmentation	0.38	>=0.20
MP:0000031	abnormal cochlea morphology	0.96	>=0.20
MP:0004521	abnormal cochlear hair cell stereociliary bundle morphology	0.79	>=0.20
MP:0004632	abnormal cochlear OHC efferent innervation pattern	0.99	>=0.20
MP:0004399	abnormal cochlear outer hair cell morphology	0.98	>=0.20
MP:0003308	abnormal cochlear sensory epithelium morphology	0.68	>=0.20
MP:0000495	abnormal colon morphology	0.04	>=0.20
MP:0006410	abnormal common myeloid progenitor cell morphology	0.11	>=0.20
MP:0003797	abnormal compact bone morphology	0.07	>=0.20
MP:0004022	abnormal cone electrophysiology	0.98	>=0.20
MP:0001469	abnormal contextual conditioning behavior	1	>=0.20
MP:0001312	abnormal cornea morphology	0.99	>=0.20
MP:0006000	abnormal corneal epithelium morphology	0.98	>=0.20

MP:0010551	abnormal coronary vessel morphology	0.06	>=0.20
MP:0002878	abnormal corticospinal tract morphology	1	>=0.20
MP:0001081	abnormal cranial ganglia morphology	0.94	>=0.20
MP:0002835	abnormal cranial suture morphology	0.57	>=0.20
MP:0002116	abnormal craniofacial bone morphology	0.89	>=0.20
MP:0003935	abnormal craniofacial development	0.79	>=0.20
MP:0000428	abnormal craniofacial morphology	0.98	>=0.20
MP:0000438	abnormal cranium morphology	0.99	>=0.20
MP:0002258	abnormal cricoid cartilage morphology	0.46	>=0.20
MP:0004249	abnormal crista ampullaris morphology	0.9	>=0.20
MP:0004409	abnormal crista ampullaris neuroepithelium morphology	0.93	>=0.20
MP:0001454	abnormal cued conditioning behavior	1	>=0.20
MP:0008438	abnormal cutaneous collagen fibril morphology	0.3	>=0.20
MP:0003009	abnormal cytokine secretion	0.06	>=0.20
MP:0005078	abnormal cytotoxic T cell physiology	0.99	>=0.20
MP:0008143	abnormal dendrite morphology	0.26	>=0.20
MP:0002455	abnormal dendritic cell antigen presentation	0.08	>=0.20
MP:0008115	abnormal dendritic cell differentiation	0.17	>=0.20
MP:0005461	abnormal dendritic cell morphology	0.62	>=0.20
MP:0002376	abnormal dendritic cell physiology	0.14	>=0.20
MP:0009936	abnormal dendritic spine morphology	0.95	>=0.20
MP:0000812	abnormal dentate gyrus morphology	0.6	>=0.20
MP:0002818	abnormal dentin morphology	0.61	>=0.20
MP:0003360	abnormal depression-related behavior	0.44	>=0.20
MP:0001243	abnormal dermal layer morphology	0.08	>=0.20
MP:0002084	abnormal developmental patterning	0.93	>=0.20
MP:0002279	abnormal diaphragm morphology	0.06	>=0.20
MP:0000830	abnormal diencephalon morphology	0.94	>=0.20
MP:0000462	abnormal digestive system morphology	0.33	>=0.20
MP:0001663	abnormal digestive system physiology	0.45	>=0.20
MP:0006280	abnormal digit development	0.81	>=0.20
MP:0002110	abnormal digit morphology	0.83	>=0.20
MP:0004190	abnormal direction of embryo turning	0.62	>=0.20
MP:0004252	abnormal direction of heart looping	0.93	>=0.20
MP:0004736	abnormal distortion product otoacoustic emission	0.83	>=0.20
MP:0008058	abnormal DNA repair	0.69	>=0.20
MP:0001905	abnormal dopamine level	0.92	>=0.20
MP:0000961	abnormal dorsal root ganglion morphology	0.72	>=0.20
MP:0002407	abnormal double-negative T cell morphology	0.75	>=0.20
MP:0001422	abnormal drinking behavior	0.71	>=0.20
MP:0003271	abnormal duodenum morphology	0.93	>=0.20
MP:0003938	abnormal ear development	0.75	>=0.20
MP:0002102	abnormal ear morphology	1	>=0.20
MP:0001431	abnormal eating behavior	0.93	>=0.20
MP:0001675	abnormal ectoderm development	0.3	>=0.20
MP:0001672	abnormal embryogenesis/ development	0.16	>=0.20
MP:0003890	abnormal embryonic-extraembryonic boundary morphology	0.35	>=0.20

MP:0004131	abnormal embryonic cilium morphology	0.94	>=0.20
MP:0003886	abnormal embryonic epiblast morphology	0.65	>=0.20
MP:0002088	abnormal embryonic growth/weight/body size	0.11	>=0.20
MP:0004261	abnormal embryonic neuroepithelium morphology	0.07	>=0.20
MP:0002085	abnormal embryonic tissue morphology	0.36	>=0.20
MP:0002572	abnormal emotion/affect behavior	0.84	>=0.20
MP:0002576	abnormal enamel morphology	1	>=0.20
MP:0003974	abnormal endocardium morphology	0.03	>=0.20
MP:0008272	abnormal endochondral bone ossification	0.67	>=0.20
MP:0006011	abnormal endolymphatic duct morphology	0.89	>=0.20
MP:0002914	abnormal endplate potential	1	>=0.20
MP:0001045	abnormal enteric ganglia morphology	0.9	>=0.20
MP:0001044	abnormal enteric nervous system morphology	1	>=0.20
MP:0001046	abnormal enteric neuron morphology	0.72	>=0.20
MP:0008883	abnormal enterocyte proliferation	0.2	>=0.20
MP:0002465	abnormal eosinophil physiology	0.06	>=0.20
MP:0001216	abnormal epidermal layer morphology	0.08	>=0.20
MP:0001231	abnormal epidermis stratum basale morphology	0.06	>=0.20
MP:0001240	abnormal epidermis stratum corneum morphology	0.37	>=0.20
MP:0001236	abnormal epidermis stratum spinosum morphology	0.39	>=0.20
MP:0004933	abnormal epididymis epithelium morphology	0.03	>=0.20
MP:0002631	abnormal epididymis morphology	0.05	>=0.20
MP:0006395	abnormal epiphyseal plate morphology	0.79	>=0.20
MP:0000467	abnormal esophagus morphology	0.61	>=0.20
MP:0002910	abnormal excitatory postsynaptic currents	1	>=0.20
MP:0002912	abnormal excitatory postsynaptic potential	1	>=0.20
MP:0002332	abnormal exercise endurance	0.54	>=0.20
MP:0005205	abnormal eye anterior chamber morphology	1	>=0.20
MP:0001286	abnormal eye development	0.9	>=0.20
MP:0001299	abnormal eye distance/ position	0.99	>=0.20
MP:0005551	abnormal eye electrophysiology	0.81	>=0.20
MP:0005253	abnormal eye physiology	0.98	>=0.20
MP:0001324	abnormal eye pigmentation	0.44	>=0.20
MP:0001340	abnormal eyelid morphology	0.25	>=0.20
MP:0003743	abnormal facial morphology	0.66	>=0.20
MP:0001071	abnormal facial nerve morphology	0.75	>=0.20
MP:0005168	abnormal female meiosis	0.79	>=0.20
MP:0000559	abnormal femur morphology	0.46	>=0.20
MP:0002161	abnormal fertility/fecundity	0.98	>=0.20
MP:0008788	abnormal fetal cardiomyocyte morphology	0.39	>=0.20
MP:0002187	abnormal fibula morphology	0.95	>=0.20
MP:0000925	abnormal floor plate morphology	0.98	>=0.20
MP:0005449	abnormal food intake	0.07	>=0.20
MP:0009379	abnormal foot pigmentation	0.59	>=0.20
MP:0003232	abnormal forebrain development	0.8	>=0.20
MP:0000783	abnormal forebrain morphology	0.46	>=0.20
MP:0000474	abnormal foregut morphology	0.45	>=0.20

MP:0000550	abnormal forelimb morphology	0.94	>=0.20
MP:0006354	abnormal fourth branchial arch artery morphology	0.03	>=0.20
MP:0003194	abnormal frequency of paradoxical sleep	0.11	>=0.20
MP:0000107	abnormal frontal bone morphology	0.99	>=0.20
MP:0004008	abnormal GABA-mediated receptor currents	1	>=0.20
MP:0001406	abnormal gait	0.92	>=0.20
MP:0001929	abnormal gametogenesis	0.42	>=0.20
MP:0003892	abnormal gastric gland morphology	0.42	>=0.20
MP:0004139	abnormal gastric parietal cell morphology	0.5	>=0.20
MP:0001695	abnormal gastrulation	0.16	>=0.20
MP:0002163	abnormal gland morphology	0.96	>=0.20
MP:0003634	abnormal glial cell morphology	0.29	>=0.20
MP:0003690	abnormal glial cell physiology	0.24	>=0.20
MP:0011320	abnormal glomerular capillary morphology	0.77	>=0.20
MP:0001096	abnormal glossopharyngeal ganglion morphology	0.99	>=0.20
MP:0008111	abnormal granulocyte differentiation	0.32	>=0.20
MP:0003704	abnormal hair follicle development	0.04	>=0.20
MP:0003809	abnormal hair shaft morphology	0.37	>=0.20
MP:0011260	abnormal head mesenchyme morphology	0.16	>=0.20
MP:0000432	abnormal head morphology	0.83	>=0.20
MP:0001963	abnormal hearing physiology	0.98	>=0.20
MP:0003105	abnormal heart atrium morphology	0.5	>=0.20
MP:0003921	abnormal heart left ventricle morphology	0.03	>=0.20
MP:0000269	abnormal heart looping	0.96	>=0.20
MP:0006065	abnormal heart position or orientation	1	>=0.20
MP:0001629	abnormal heart rate	0.95	>=0.20
MP:0003920	abnormal heart right ventricle morphology	0.04	>=0.20
MP:0006113	abnormal heart septum morphology	1	>=0.20
MP:0000270	abnormal heart tube morphology	0.61	>=0.20
MP:0000285	abnormal heart valve morphology	0.36	>=0.20
MP:0002123	abnormal hematopoiesis	0.18	>=0.20
MP:0004808	abnormal hematopoietic stem cell morphology	0.12	>=0.20
MP:0006108	abnormal hindbrain development	0.76	>=0.20
MP:0000841	abnormal hindbrain morphology	0.94	>=0.20
MP:0000556	abnormal hindlimb morphology	0.73	>=0.20
MP:0008221	abnormal hippocampal commissure morphology	0.76	>=0.20
MP:0002761	abnormal hippocampal mossy fiber morphology	0.99	>=0.20
MP:0008267	abnormal hippocampus CA3 region morphology	0.99	>=0.20
MP:0000808	abnormal hippocampus development	0.93	>=0.20
MP:0000813	abnormal hippocampus layer morphology	0.66	>=0.20
MP:0000807	abnormal hippocampus morphology	0.13	>=0.20
MP:0008284	abnormal hippocampus pyramidal cell layer	0.98	>=0.20
MP:0009940	abnormal hippocampus pyramidal cell morphology	0.56	>=0.20
MP:0003953	abnormal hormone level	0.12	>=0.20
MP:0005296	abnormal humerus morphology	1	>=0.20
MP:0001800	abnormal humoral immune response	0.1	>=0.20
MP:0003056	abnormal hyoid bone morphology	0.96	>=0.20

MP:0000837	abnormal hypothalamus morphology	0.51	>=0.20
MP:0001819	abnormal immune cell physiology	0.13	>=0.20
MP:0000716	abnormal immune system cell morphology	0.04	>=0.20
MP:0000685	abnormal immune system morphology	0.25	>=0.20
MP:0002722	abnormal immune system organ morphology	0.07	>=0.20
MP:0002490	abnormal immunoglobulin level	0.58	>=0.20
MP:0003137	abnormal impulse conducting system conduction	0.85	>=0.20
MP:0005358	abnormal incisor morphology	0.9	>=0.20
MP:0005106	abnormal incus morphology	1	>=0.20
MP:0002945	abnormal inhibitory postsynaptic currents	1	>=0.20
MP:0002718	abnormal inner cell mass morphology	0.16	>=0.20
MP:0000026	abnormal inner ear morphology	0.86	>=0.20
MP:0004532	abnormal inner hair cell stereociliary bundle morphology	0.63	>=0.20
MP:0002184	abnormal innervation	0.95	>=0.20
MP:0003564	abnormal insulin secretion	0.05	>=0.20
MP:0006267	abnormal intercalated disc morphology	0.32	>=0.20
MP:0008750	abnormal interferon level	0.43	>=0.20
MP:0004173	abnormal intervertebral disk morphology	0.92	>=0.20
MP:0001666	abnormal intestinal absorption	0.17	>=0.20
MP:0003449	abnormal intestinal goblet cell morphology	0.05	>=0.20
MP:0000477	abnormal intestine morphology	0.23	>=0.20
MP:0001322	abnormal iris morphology	0.9	>=0.20
MP:0005102	abnormal iris pigmentation	0.09	>=0.20
MP:0000454	abnormal jaw morphology	1	>=0.20
MP:0002932	abnormal joint morphology	0.87	>=0.20
MP:0002656	abnormal keratinocyte differentiation	0.5	>=0.20
MP:0002655	abnormal keratinocyte morphology	0.13	>=0.20
MP:0003453	abnormal keratinocyte physiology	0.04	>=0.20
MP:0004754	abnormal kidney collecting duct morphology	0.87	>=0.20
MP:0000521	abnormal kidney cortex morphology	0.34	>=0.20
MP:0000527	abnormal kidney development	0.94	>=0.20
MP:0003014	abnormal kidney medulla morphology	0.36	>=0.20
MP:0002136	abnormal kidney physiology	0.03	>=0.20
MP:0005362	abnormal Langerhans cell physiology	0.14	>=0.20
MP:0000823	abnormal lateral ventricle morphology	0.99	>=0.20
MP:0001706	abnormal left-right axis patterning	0.83	>=0.20
MP:0005545	abnormal lens development	0.91	>=0.20
MP:0002840	abnormal lens fiber morphology	0.93	>=0.20
MP:0001303	abnormal lens morphology	0.9	>=0.20
MP:0001292	abnormal lens vesicle development	0.98	>=0.20
MP:0000217	abnormal leukocyte cell number	0.03	>=0.20
MP:0008246	abnormal leukocyte morphology	0.26	>=0.20
MP:0002442	abnormal leukocyte physiology	0.03	>=0.20
MP:0003627	abnormal leukocyte tethering or rolling	0.06	>=0.20
MP:0002786	abnormal Leydig cell morphology	0.84	>=0.20
MP:0002115	abnormal limb bone morphology	0.94	>=0.20
MP:0005650	abnormal limb bud morphology	0.91	>=0.20

MP:0006279	abnormal limb development	0.96	>=0.20
MP:0003313	abnormal locomotor activation	0.82	>=0.20
MP:0001392	abnormal locomotor behavior	0.94	>=0.20
MP:0003312	abnormal locomotor coordination	1	>=0.20
MP:0004214	abnormal long bone diaphysis morphology	0.28	>=0.20
MP:0000131	abnormal long bone epiphysis morphology	0.89	>=0.20
MP:0000133	abnormal long bone metaphysis morphology	0.04	>=0.20
MP:0003723	abnormal long bone morphology	0.52	>=0.20
MP:0001898	abnormal long term depression	1	>=0.20
MP:0002801	abnormal long term object recognition memory	0.81	>=0.20
MP:0002207	abnormal long term potentiation	0.9	>=0.20
MP:0003049	abnormal lumbar vertebrae morphology	0.9	>=0.20
MP:0001175	abnormal lung morphology	0.14	>=0.20
MP:0010825	abnormal lung saccule morphology	0.45	>=0.20
MP:0004007	abnormal lung vasculature morphology	0.56	>=0.20
MP:0008828	abnormal lymph node cell ratio	0.9	>=0.20
MP:0008522	abnormal lymph node germinal center morphology	0.3	>=0.20
MP:0002339	abnormal lymph node morphology	0.79	>=0.20
MP:0000717	abnormal lymphocyte cell number	0.16	>=0.20
MP:0002619	abnormal lymphocyte morphology	0.33	>=0.20
MP:0003945	abnormal lymphocyte physiology	0.21	>=0.20
MP:0003172	abnormal lysosome physiology	0.05	>=0.20
MP:0006362	abnormal male germ cell morphology	0.19	>=0.20
MP:0005169	abnormal male meiosis	0.96	>=0.20
MP:0001145	abnormal male reproductive system morphology	0.93	>=0.20
MP:0000029	abnormal malleus morphology	1	>=0.20
MP:0000628	abnormal mammary gland development	0.1	>=0.20
MP:0009504	abnormal mammary gland epithelium morphology	0.4	>=0.20
MP:0006269	abnormal mammary gland growth during pregnancy	0.86	>=0.20
MP:0000458	abnormal mandible morphology	0.99	>=0.20
MP:0000359	abnormal mast cell morphology	0.14	>=0.20
MP:0002423	abnormal mast cell physiology	0.2	>=0.20
MP:0001386	abnormal maternal nurturing	1	>=0.20
MP:0000455	abnormal maxilla morphology	1	>=0.20
MP:0005587	abnormal Meckel's cartilage morphology	1	>=0.20
MP:0000846	abnormal medulla oblongata morphology	0.99	>=0.20
MP:0002413	abnormal megakaryocyte progenitor cell morphology	0.05	>=0.20
MP:0005075	abnormal melanosome morphology	0.82	>=0.20
MP:0000035	abnormal membranous labyrinth morphology	0.41	>=0.20
MP:0006301	abnormal mesenchyme morphology	0.37	>=0.20
MP:0005232	abnormal mesenteric lymph node morphology	0.25	>=0.20
MP:0001680	abnormal mesoderm development	0.81	>=0.20
MP:0010984	abnormal metanephric mesenchyme morphology	0.97	>=0.20
MP:0004096	abnormal midbrain-hindbrain boundary development	1	>=0.20
MP:0003864	abnormal midbrain development	0.94	>=0.20
MP:0000897	abnormal midbrain morphology	0.84	>=0.20
MP:0000049	abnormal middle ear morphology	1	>=0.20

MP:0005105	abnormal middle ear ossicle morphology	1	>=0.20
MP:0004835	abnormal miniature endplate potential	1	>=0.20
MP:0004753	abnormal miniature excitatory postsynaptic currents	1	>=0.20
MP:0009435	abnormal miniature inhibitory postsynaptic currents	1	>=0.20
MP:0006036	abnormal mitochondrial physiology	0.67	>=0.20
MP:0004046	abnormal mitosis	0.44	>=0.20
MP:0009760	abnormal mitotic spindle morphology	0.68	>=0.20
MP:0000286	abnormal mitral valve morphology	0.39	>=0.20
MP:0003932	abnormal molar crown morphology	0.98	>=0.20
MP:0002689	abnormal molar morphology	1	>=0.20
MP:0002066	abnormal motor capabilities/coordination/movement	1	>=0.20
MP:0001516	abnormal motor coordination/ balance	0.61	>=0.20
MP:0002804	abnormal motor learning	1	>=0.20
MP:0000940	abnormal motor neuron innervation	0.99	>=0.20
MP:0000937	abnormal motor neuron morphology	0.94	>=0.20
MP:0005547	abnormal Muller cell morphology	0.94	>=0.20
MP:0005620	abnormal muscle contractility	0.59	>=0.20
MP:0000733	abnormal muscle development	0.18	>=0.20
MP:0004145	abnormal muscle electrophysiology	0.99	>=0.20
MP:0004087	abnormal muscle fiber morphology	0.41	>=0.20
MP:0001052	abnormal muscle innervation	0.97	>=0.20
MP:0002108	abnormal muscle morphology	0.05	>=0.20
MP:0002106	abnormal muscle physiology	0.41	>=0.20
MP:0000750	abnormal muscle regeneration	0.34	>=0.20
MP:0003871	abnormal myelin sheath morphology	0.46	>=0.20
MP:0000920	abnormal myelination	0.42	>=0.20
MP:0000278	abnormal myocardial fiber morphology	0.04	>=0.20
MP:0004215	abnormal myocardial fiber physiology	0.1	>=0.20
MP:0000729	abnormal myogenesis	0.72	>=0.20
MP:0000102	abnormal nasal bone morphology	0.99	>=0.20
MP:0004726	abnormal nasal capsule morphology	1	>=0.20
MP:0002237	abnormal nasal cavity morphology	1	>=0.20
MP:0002239	abnormal nasal septum morphology	1	>=0.20
MP:0005403	abnormal nerve conduction	0.99	>=0.20
MP:0003861	abnormal nervous system development	0.88	>=0.20
MP:0002272	abnormal nervous system electrophysiology	1	>=0.20
MP:0003632	abnormal nervous system morphology	0.62	>=0.20
MP:0003633	abnormal nervous system physiology	0.94	>=0.20
MP:0002950	abnormal neural crest cell migration	0.3	>=0.20
MP:0004837	abnormal neural fold formation	0.74	>=0.20
MP:0002151	abnormal neural tube morphology/development	0.55	>=0.20
MP:0008415	abnormal neurite morphology	1	>=0.20
MP:0000074	abnormal neurocranium morphology	0.81	>=0.20
MP:0001053	abnormal neuromuscular synapse morphology	1	>=0.20
MP:0009937	abnormal neuron differentiation	0.3	>=0.20
MP:0002882	abnormal neuron morphology	0.93	>=0.20
MP:0004811	abnormal neuron physiology	1	>=0.20

MP:0002948	abnormal neuron specification	0.86	>=0.20
MP:0006009	abnormal neuronal migration	0.87	>=0.20
MP:0005445	abnormal neurotransmitter secretion	1	>=0.20
MP:0010766	abnormal NK cell physiology	0.8	>=0.20
MP:0008042	abnormal NK T cell physiology	0.18	>=0.20
MP:0002736	abnormal nociception after inflammation	1	>=0.20
MP:0003964	abnormal noradrenaline level	0.75	>=0.20
MP:0002233	abnormal nose morphology	0.84	>=0.20
MP:0002825	abnormal notochord morphology	1	>=0.20
MP:0005269	abnormal occipital bone morphology	0.68	>=0.20
MP:0002864	abnormal ocular fundus morphology	0.79	>=0.20
MP:0000819	abnormal olfactory bulb morphology	1	>=0.20
MP:0008789	abnormal olfactory epithelium morphology	1	>=0.20
MP:0005236	abnormal olfactory nerve morphology	0.98	>=0.20
MP:0006092	abnormal olfactory neuron morphology	0.95	>=0.20
MP:0000953	abnormal oligodendrocyte morphology	0.96	>=0.20
MP:0003425	abnormal optic vesicle formation	0.07	>=0.20
MP:0000042	abnormal organ of Corti morphology	0.53	>=0.20
MP:0004522	abnormal orientation of cochlear hair cell stereociliary bundl	1	>=0.20
MP:0008395	abnormal osteoblast differentiation	0.13	>=0.20
MP:0004986	abnormal osteoblast morphology	0.48	>=0.20
MP:0005006	abnormal osteoblast physiology	0.19	>=0.20
MP:0008396	abnormal osteoclast differentiation	0.04	>=0.20
MP:0004982	abnormal osteoclast morphology	0.05	>=0.20
MP:0001541	abnormal osteoclast physiology	0.03	>=0.20
MP:0000039	abnormal otic capsule morphology	0.43	>=0.20
MP:0006030	abnormal otic vesicle development	0.81	>=0.20
MP:0002894	abnormal otolith morphology	0.9	>=0.20
MP:0002177	abnormal outer ear morphology	0.87	>=0.20
MP:0004527	abnormal outer hair cell stereociliary bundle morphology	0.11	>=0.20
MP:0006126	abnormal outflow tract development	0.51	>=0.20
MP:0001970	abnormal pain threshold	0.92	>=0.20
MP:0009887	abnormal palatal shelf fusion at midline	0.82	>=0.20
MP:0003755	abnormal palate morphology	0.99	>=0.20
MP:0003934	abnormal pancreas development	0.56	>=0.20
MP:0001944	abnormal pancreas morphology	0.81	>=0.20
MP:0002693	abnormal pancreas physiology	0.8	>=0.20
MP:0009146	abnormal pancreatic acinar cell morphology	0.19	>=0.20
MP:0005215	abnormal pancreatic islet morphology	0.62	>=0.20
MP:0000109	abnormal parietal bone morphology	0.71	>=0.20
MP:0005353	abnormal patella morphology	1	>=0.20
MP:0004509	abnormal pelvic girdle bone morphology	0.58	>=0.20
MP:0002389	abnormal Peyer's patch follicle morphology	0.81	>=0.20
MP:0002391	abnormal Peyer's patch germinal center morphology	0.9	>=0.20
MP:0005306	abnormal phalanx morphology	0.94	>=0.20
MP:0003730	abnormal photoreceptor inner segment morphology	1	>=0.20
MP:0003729	abnormal photoreceptor outer segment morphology	0.94	>=0.20

MP:0003817	abnormal pituitary diverticulum morphology	0.97	>=0.20
MP:0000633	abnormal pituitary gland morphology	0.99	>=0.20
MP:0003231	abnormal placenta vasculature	0.03	>=0.20
MP:0001526	abnormal placing response	0.92	>=0.20
MP:0004722	abnormal platelet dense granule number	0.4	>=0.20
MP:0002913	abnormal PNS synaptic transmission	0.98	>=0.20
MP:0005326	abnormal podocyte morphology	0.47	>=0.20
MP:0000848	abnormal pons morphology	0.46	>=0.20
MP:0004919	abnormal positive T cell selection	0.99	>=0.20
MP:0002980	abnormal postural reflex	1	>=0.20
MP:0001504	abnormal posture	0.99	>=0.20
MP:0004448	abnormal presphenoid bone morphology	0.93	>=0.20
MP:0002211	abnormal primary sex determination	0.94	>=0.20
MP:0004066	abnormal primitive node morphology	0.98	>=0.20
MP:0002231	abnormal primitive streak morphology	0.46	>=0.20
MP:0001158	abnormal prostate gland morphology	0.8	>=0.20
MP:0004452	abnormal pterygoid process morphology	1	>=0.20
MP:0002273	abnormal pulmonary alveolus epithelial cell morphology	0.12	>=0.20
MP:0002270	abnormal pulmonary alveolus morphology	0.05	>=0.20
MP:0010903	abnormal pulmonary alveolus wall morphology	0.93	>=0.20
MP:0003209	abnormal pulmonary elastic fiber morphology	0.75	>=0.20
MP:0001384	abnormal pup retrieval	0.93	>=0.20
MP:0008572	abnormal Purkinje cell dendrite morphology	1	>=0.20
MP:0000877	abnormal Purkinje cell morphology	1	>=0.20
MP:0003648	abnormal radial glial cell morphology	0.45	>=0.20
MP:0000552	abnormal radius morphology	0.83	>=0.20
MP:0001961	abnormal reflex	1	>=0.20
MP:0004946	abnormal regulatory T cell physiology	0.09	>=0.20
MP:0003954	abnormal Reichert's membrane morphology	0.5	>=0.20
MP:0011348	abnormal renal glomerulus basement membrane morpholog	0.42	>=0.20
MP:0010107	abnormal renal reabsorbtion	0.93	>=0.20
MP:0002703	abnormal renal tubule morphology	0.45	>=0.20
MP:0003936	abnormal reproductive system development	0.88	>=0.20
MP:0001919	abnormal reproductive system physiology	0.47	>=0.20
MP:0005164	abnormal response to injury	0.1	>=0.20
MP:0005671	abnormal response to transplant	0.71	>=0.20
MP:0001325	abnormal retina morphology	0.59	>=0.20
MP:0006072	abnormal retinal apoptosis	0.96	>=0.20
MP:0001006	abnormal retinal cone cell morphology	1	>=0.20
MP:0008056	abnormal retinal ganglion cell morphology	0.88	>=0.20
MP:0005241	abnormal retinal ganglion layer morphology	0.94	>=0.20
MP:0003733	abnormal retinal inner nuclear layer morphology	0.5	>=0.20
MP:0006303	abnormal retinal nerve fiber layer morphology	0.96	>=0.20
MP:0006069	abnormal retinal neuronal layer morphology	0.93	>=0.20
MP:0003731	abnormal retinal outer nuclear layer morphology	0.53	>=0.20
MP:0003732	abnormal retinal outer plexiform layer morphology	1	>=0.20
MP:0003728	abnormal retinal photoreceptor layer morphology	0.99	>=0.20

MP:0001004	abnormal retinal photoreceptor morphology	0.93	>=0.20
MP:0005103	abnormal retinal pigmentation	0.38	>=0.20
MP:0006074	abnormal retinal rod bipolar cell morphology	0.6	>=0.20
MP:0001005	abnormal retinal rod cell morphology	0.51	>=0.20
MP:0008456	abnormal retinal rod cell outer segment morphology	0.99	>=0.20
MP:0000933	abnormal rhombomere morphology	0.87	>=0.20
MP:0008148	abnormal rib-sternum attachment	0.99	>=0.20
MP:0002823	abnormal rib development	0.99	>=0.20
MP:0000150	abnormal rib morphology	0.89	>=0.20
MP:0004021	abnormal rod electrophysiology	0.99	>=0.20
MP:0005221	abnormal rostral-caudal axis patterning	0.3	>=0.20
MP:0003050	abnormal sacral vertebrae morphology	0.96	>=0.20
MP:0004090	abnormal sarcomere morphology	0.69	>=0.20
MP:0000149	abnormal scapula morphology	0.96	>=0.20
MP:0001106	abnormal Schwann cell morphology	0.45	>=0.20
MP:0002651	abnormal sciatic nerve morphology	0.11	>=0.20
MP:0006029	abnormal sclerotome morphology	0.06	>=0.20
MP:0009655	abnormal secondary palate development	0.92	>=0.20
MP:0002428	abnormal semicircular canal morphology	0.98	>=0.20
MP:0002746	abnormal semilunar valve morphology	0.89	>=0.20
MP:0002059	abnormal seminal vesicle morphology	0.57	>=0.20
MP:0002216	abnormal seminiferous tubule morphology	0.49	>=0.20
MP:0000968	abnormal sensory neuron innervation pattern	0.99	>=0.20
MP:0000967	abnormal sensory neuron projections	1	>=0.20
MP:0005322	abnormal serotonin level	0.87	>=0.20
MP:0002784	abnormal Sertoli cell morphology	0.94	>=0.20
MP:0002566	abnormal sexual interaction	0.68	>=0.20
MP:0003463	abnormal single cell response	1	>=0.20
MP:0006355	abnormal sixth branchial arch artery morphology	0.14	>=0.20
MP:0003084	abnormal skeletal muscle fiber morphology	0.56	>=0.20
MP:0009409	abnormal skeletal muscle fiber type ratio	0.41	>=0.20
MP:0000759	abnormal skeletal muscle morphology	0.59	>=0.20
MP:0002113	abnormal skeleton development	0.06	>=0.20
MP:0001533	abnormal skeleton physiology	0.14	>=0.20
MP:0001191	abnormal skin condition	0.05	>=0.20
MP:0002095	abnormal skin pigmentation	0.99	>=0.20
MP:0001501	abnormal sleep pattern	0.51	>=0.20
MP:0004841	abnormal small intestine crypts of Lieberkuhn morphology	0.35	>=0.20
MP:0000443	abnormal snout morphology	0.35	>=0.20
MP:0001360	abnormal social investigation	1	>=0.20
MP:0002752	abnormal somatic nervous system morphology	0.66	>=0.20
MP:0005423	abnormal somatic nervous system physiology	0.97	>=0.20
MP:0001688	abnormal somite development	0.34	>=0.20
MP:0005222	abnormal somite size	0.4	>=0.20
MP:0001463	abnormal spatial learning	1	>=0.20
MP:0009838	abnormal sperm axoneme morphology	0.82	>=0.20
MP:0008892	abnormal sperm flagellum morphology	0.91	>=0.20

MP:0009230	abnormal sperm head morphology	0.48	>=0.20
MP:0009232	abnormal sperm nucleus morphology	0.28	>=0.20
MP:0004543	abnormal sperm physiology	0.78	>=0.20
MP:0006380	abnormal spermatid morphology	0.29	>=0.20
MP:0006379	abnormal spermatocyte morphology	1	>=0.20
MP:0001156	abnormal spermatogenesis	0.64	>=0.20
MP:0001932	abnormal spermiogenesis	0.75	>=0.20
MP:0008840	abnormal spike wave discharge	1	>=0.20
MP:0004100	abnormal spinal cord interneuron morphology	0.98	>=0.20
MP:0000955	abnormal spinal cord morphology	0.98	>=0.20
MP:0008027	abnormal spinal cord white matter morphology	0.93	>=0.20
MP:0001077	abnormal spinal nerve morphology	0.88	>=0.20
MP:0004174	abnormal spine curvature	0.9	>=0.20
MP:0008470	abnormal spleen B cell follicle morphology	0.41	>=0.20
MP:0002359	abnormal spleen germinal center morphology	0.63	>=0.20
MP:0002362	abnormal spleen marginal zone morphology	0.07	>=0.20
MP:0002358	abnormal spleen periarteriolar lymphoid sheath morphology	0.41	>=0.20
MP:0002356	abnormal spleen red pulp morphology	0.06	>=0.20
MP:0008826	abnormal splenic cell ratio	0.13	>=0.20
MP:0004423	abnormal squamosal bone morphology	0.76	>=0.20
MP:0005107	abnormal stapes morphology	0.99	>=0.20
MP:0004322	abnormal sternebra morphology	0.92	>=0.20
MP:0000157	abnormal sternum morphology	0.62	>=0.20
MP:0008277	abnormal sternum ossification	0.66	>=0.20
MP:0000471	abnormal stomach epithelium morphology	0.78	>=0.20
MP:0000473	abnormal stomach glandular epithelium morphology	0.99	>=0.20
MP:0000470	abnormal stomach morphology	0.51	>=0.20
MP:0010792	abnormal stomach mucosa morphology	0.03	>=0.20
MP:0000048	abnormal stria vascularis morphology	0.22	>=0.20
MP:0004077	abnormal striatum morphology	0.47	>=0.20
MP:0008023	abnormal styloid process morphology	0.99	>=0.20
MP:0001436	abnormal suckling behavior	0.74	>=0.20
MP:0010769	abnormal survival	0.08	>=0.20
MP:0001008	abnormal sympathetic ganglion morphology	0.98	>=0.20
MP:0004859	abnormal synaptic plasticity	1	>=0.20
MP:0003635	abnormal synaptic transmission	1	>=0.20
MP:0004769	abnormal synaptic vesicle morphology	1	>=0.20
MP:0004792	abnormal synaptic vesicle number	1	>=0.20
MP:0004770	abnormal synaptic vesicle recycling	1	>=0.20
MP:0000230	abnormal systemic arterial blood pressure	0.04	>=0.20
MP:0008088	abnormal T-helper 1 cell differentiation	0.95	>=0.20
MP:0005465	abnormal T-helper 1 physiology	0.08	>=0.20
MP:0005466	abnormal T-helper 2 physiology	0.16	>=0.20
MP:0001828	abnormal T cell activation	0.13	>=0.20
MP:0002145	abnormal T cell differentiation	0.77	>=0.20
MP:0008037	abnormal T cell morphology	0.79	>=0.20
MP:0006387	abnormal T cell number	0.04	>=0.20

MP:0002444	abnormal T cell physiology	0.28	>=0.20
MP:0005094	abnormal T cell proliferation	0.83	>=0.20
MP:0003944	abnormal T cell subpopulation ratio	0.21	>=0.20
MP:0002111	abnormal tail morphology	0.24	>=0.20
MP:0005104	abnormal tarsal bone morphology	1	>=0.20
MP:0000934	abnormal telencephalon development	0.85	>=0.20
MP:0000787	abnormal telencephalon morphology	0.76	>=0.20
MP:0005503	abnormal tendon morphology	0.92	>=0.20
MP:0000832	abnormal thalamus morphology	0.87	>=0.20
MP:0004624	abnormal thoracic cage morphology	0.93	>=0.20
MP:0003047	abnormal thoracic vertebrae morphology	0.94	>=0.20
MP:0003850	abnormal thymocyte activation	0.35	>=0.20
MP:0008827	abnormal thymus cell ratio	0.97	>=0.20
MP:0002375	abnormal thymus medulla morphology	0.9	>=0.20
MP:0000703	abnormal thymus morphology	0.17	>=0.20
MP:0002260	abnormal thyroid cartilage morphology	0.93	>=0.20
MP:0004696	abnormal thyroid follicle morphology	0.19	>=0.20
MP:0000558	abnormal tibia morphology	0.93	>=0.20
MP:0000764	abnormal tongue epithelium morphology	0.28	>=0.20
MP:0000762	abnormal tongue morphology	0.96	>=0.20
MP:0004136	abnormal tongue muscle morphology	0.91	>=0.20
MP:0000116	abnormal tooth development	0.83	>=0.20
MP:0002100	abnormal tooth morphology	0.95	>=0.20
MP:0001968	abnormal touch/ nociception	1	>=0.20
MP:0000130	abnormal trabecular bone morphology	0.15	>=0.20
MP:0003120	abnormal tracheal cartilage morphology	0.84	>=0.20
MP:0001092	abnormal trigeminal ganglion morphology	0.95	>=0.20
MP:0001065	abnormal trigeminal nerve morphology	0.61	>=0.20
MP:0005028	abnormal trophectoderm morphology	0.18	>=0.20
MP:0010454	abnormal truncus arteriosus septation	0.66	>=0.20
MP:0000030	abnormal tympanic ring morphology	0.8	>=0.20
MP:0002275	abnormal type II pneumocyte morphology	0.26	>=0.20
MP:0005108	abnormal ulna morphology	0.59	>=0.20
MP:0003672	abnormal ureter development	1	>=0.20
MP:0000534	abnormal ureter morphology	1	>=0.20
MP:0006032	abnormal ureteric bud morphology	0.79	>=0.20
MP:0000538	abnormal urinary bladder morphology	0.78	>=0.20
MP:0010386	abnormal urinary bladder physiology	1	>=0.20
MP:0004014	abnormal uterine environment	0.04	>=0.20
MP:0006090	abnormal utricle morphology	1	>=0.20
MP:0003542	abnormal vascular endothelial cell development	0.03	>=0.20
MP:0000364	abnormal vascular regression	0.13	>=0.20
MP:0005595	abnormal vascular smooth muscle physiology	1	>=0.20
MP:0000250	abnormal vasoconstriction	0.62	>=0.20
MP:0003384	abnormal ventral body wall morphology	1	>=0.20
MP:0003993	abnormal ventral spinal root morphology	0.97	>=0.20
MP:0005225	abnormal vertebrae development	0.96	>=0.20

MP:0000137	abnormal vertebrae morphology	0.69	>=0.20
MP:0004599	abnormal vertebral arch morphology	0.99	>=0.20
MP:0000141	abnormal vertebral body morphology	0.22	>=0.20
MP:0004703	abnormal vertebral column morphology	0.39	>=0.20
MP:0002856	abnormal vestibular ganglion morphology	0.96	>=0.20
MP:0006089	abnormal vestibular saccule morphology	0.95	>=0.20
MP:0000034	abnormal vestibule morphology	0.89	>=0.20
MP:0003703	abnormal vestibulocochlear ganglion morphology	0.69	>=0.20
MP:0011186	abnormal visceral endoderm morphology	0.12	>=0.20
MP:0002090	abnormal vision	0.64	>=0.20
MP:0011228	abnormal vitamin D level	0.38	>=0.20
MP:0001529	abnormal vocalization	0.88	>=0.20
MP:0002243	abnormal vomeronasal organ morphology	0.99	>=0.20
MP:0000159	abnormal xiphoid process morphology	0.98	>=0.20
MP:0004091	abnormal Z lines	0.91	>=0.20
MP:0003216	absence seizures	0.97	>=0.20
MP:0003087	absent allantois	0.27	>=0.20
MP:0005030	absent amnion	0.45	>=0.20
MP:0000298	absent atrioventricular cushions	0.27	>=0.20
MP:0008071	absent B cells	0.05	>=0.20
MP:0004763	absent brainstem auditory evoked potential	0.55	>=0.20
MP:0005171	absent coat pigmentation	0.66	>=0.20
MP:0004405	absent cochlear hair cells	0.87	>=0.20
MP:0000239	absent common myeloid progenitor cells	0.1	>=0.20
MP:0002196	absent corpus callosum	0.91	>=0.20
MP:0004737	absent distortion product otoacoustic emissions	0.77	>=0.20
MP:0004132	absent embryonic cilia	0.9	>=0.20
MP:0009009	absent estrous cycle	0.18	>=0.20
MP:0000926	absent floor plate	0.55	>=0.20
MP:0009546	absent gastric milk in neonates	0.46	>=0.20
MP:0000125	absent incisors	0.9	>=0.20
MP:0000520	absent kidney	0.99	>=0.20
MP:0003161	absent lateral semicircular canal	0.99	>=0.20
MP:0004813	absent linear vestibular evoked potential	0.94	>=0.20
MP:0001899	absent long term depression	1	>=0.20
MP:0008024	absent lymph nodes	0.42	>=0.20
MP:0000087	absent mandible	0.99	>=0.20
MP:0008212	absent mature B cells	0.07	>=0.20
MP:0001132	absent mature ovarian follicles	0.72	>=0.20
MP:0000430	absent maxillary shelf	1	>=0.20
MP:0001683	absent mesoderm	0.24	>=0.20
MP:0003451	absent olfactory bulb	0.6	>=0.20
MP:0002777	absent ovarian follicles	0.97	>=0.20
MP:0002831	absent Peyer's patches	0.18	>=0.20
MP:0008585	absent photoreceptor outer segment	0.97	>=0.20
MP:0006358	absent pinna reflex	0.99	>=0.20
MP:0009331	absent primitive node	0.46	>=0.20

MP:0000036	absent semicircular canals	1	>=0.20
MP:0000690	absent spleen	0.9	>=0.20
MP:0008474	absent spleen germinal center	0.15	>=0.20
MP:0004204	absent stapes	0.95	>=0.20
MP:0006359	absent startle reflex	0.61	>=0.20
MP:0008070	absent T cells	0.96	>=0.20
MP:0001714	absent trophoblast giant cells	0.88	>=0.20
MP:0003722	absent ureter	0.91	>=0.20
MP:0001284	absent vibrissae	0.23	>=0.20
ENSG00000151498	ACAD8 PPI subnetwork	0.48	>=0.20
ENSG00000115361	ACADL PPI subnetwork	0.15	>=0.20
ENSG00000157766	ACAN PPI subnetwork	0.17	>=0.20
MP:0001874	acanthosis	0.04	>=0.20
ENSG00000102977	ACD PPI subnetwork	0.97	>=0.20
GO:0006085	acetyl-CoA biosynthetic process	0.49	>=0.20
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	0.65	>=0.20
GO:0046356	acetyl-CoA catabolic process	0.89	>=0.20
GO:0006084	acetyl-CoA metabolic process	0.27	>=0.20
GO:0004889	acetylcholine-activated cation-selective channel activity	0.95	>=0.20
GO:0005892	acetylcholine-gated channel complex	0.92	>=0.20
GO:0042166	acetylcholine binding	0.99	>=0.20
GO:0015464	acetylcholine receptor activity	0.99	>=0.20
GO:0008376	acetylgalactosaminyltransferase activity	1	>=0.20
GO:0008375	acetylglucosaminyltransferase activity	0.87	>=0.20
GO:0016881	acid-amino acid ligase activity	0.77	>=0.20
GO:0015172	acidic amino acid transmembrane transporter activity	1	>=0.20
GO:0015800	acidic amino acid transport	1	>=0.20
MP:0003031	acidosis	0.98	>=0.20
ENSG00000100813	ACIN1 PPI subnetwork	0.77	>=0.20
ENSG00000100412	ACO2 PPI subnetwork	0.96	>=0.20
ENSG00000112304	ACOT13 PPI subnetwork	0.28	>=0.20
ENSG00000143727	ACP1 PPI subnetwork	0.31	>=0.20
GO:0002080	acrosomal membrane	0.35	>=0.20
GO:0001669	acrosomal vesicle	0.37	>=0.20
ENSG00000103740	ACSBG1 PPI subnetwork	1	>=0.20
ENSG00000131069	ACSS2 PPI subnetwork	0.74	>=0.20
ENSG00000143632	ACTA1 PPI subnetwork	0.43	>=0.20
ENSG00000075624	ACTB PPI subnetwork	0.13	>=0.20
ENSG00000169067	ACTBL2 PPI subnetwork	0.09	>=0.20
ENSG00000184009	ACTG1 PPI subnetwork	0.08	>=0.20
ENSG00000163017	ACTG2 PPI subnetwork	0.03	>=0.20
GO:0070252	actin-mediated cell contraction	1	>=0.20
GO:0033275	actin-myosin filament sliding	1	>=0.20
GO:0003779	actin binding	0.51	>=0.20
GO:0015629	actin cytoskeleton	0.44	>=0.20
GO:0030036	actin cytoskeleton organization	0.37	>=0.20
GO:0005884	actin filament	0.86	>=0.20

GO:0030048	actin filament-based movement	1	>=0.20
GO:0030029	actin filament-based process	0.61	>=0.20
GO:0051015	actin filament binding	0.78	>=0.20
GO:0032432	actin filament bundle	0.23	>=0.20
GO:0051017	actin filament bundle assembly	0.66	>=0.20
GO:0051693	actin filament capping	0.17	>=0.20
GO:0030042	actin filament depolymerization	0.43	>=0.20
GO:0007015	actin filament organization	0.3	>=0.20
GO:0030041	actin filament polymerization	0.21	>=0.20
GO:0003785	actin monomer binding	0.11	>=0.20
GO:0008154	actin polymerization or depolymerization	0.36	>=0.20
GO:0042805	actinin binding	0.87	>=0.20
GO:0050798	activated T cell proliferation	0.7	>=0.20
GO:0007190	activation of adenylate cyclase activity	0.99	>=0.20
GO:0008635	activation of cysteine-type endopeptidase activity involved ir	1	>=0.20
GO:0002218	activation of innate immune response	0.21	>=0.20
GO:0042976	activation of Janus kinase activity	0.97	>=0.20
GO:0000187	activation of MAPK activity	0.04	>=0.20
GO:0007202	activation of phospholipase C activity	0.54	>=0.20
GO:0032147	activation of protein kinase activity	0.99	>=0.20
GO:0022804	active transmembrane transporter activity	0.26	>=0.20
GO:0017002	activin-activated receptor activity	0.69	>=0.20
GO:0048185	activin binding	0.2	>=0.20
GO:0032924	activin receptor signaling pathway	0.69	>=0.20
ENSG00000077080	ACTL6B PPI subnetwork	0.48	>=0.20
ENSG00000072110	ACTN1 PPI subnetwork	0.26	>=0.20
ENSG00000077522	ACTN2 PPI subnetwork	0.69	>=0.20
ENSG00000130402	ACTN4 PPI subnetwork	0.24	>=0.20
GO:0042641	actomyosin	0.47	>=0.20
GO:0031032	actomyosin structure organization	0.98	>=0.20
ENSG00000138107	ACTR1A PPI subnetwork	0.79	>=0.20
ENSG00000138071	ACTR2 PPI subnetwork	0.45	>=0.20
ENSG00000115091	ACTR3 PPI subnetwork	0.84	>=0.20
ENSG00000101442	ACTR5 PPI subnetwork	0.51	>=0.20
ENSG00000075089	ACTR6 PPI subnetwork	0.37	>=0.20
ENSG00000113812	ACTR8 PPI subnetwork	0.5	>=0.20
ENSG00000115170	ACVR1 PPI subnetwork	0.16	>=0.20
ENSG00000135503	ACVR1B PPI subnetwork	0.52	>=0.20
ENSG00000123612	ACVR1C PPI subnetwork	0.73	>=0.20
ENSG00000121989	ACVR2A PPI subnetwork	0.47	>=0.20
ENSG00000114739	ACVR2B PPI subnetwork	0.23	>=0.20
ENSG00000139567	ACVRL1 PPI subnetwork	0.44	>=0.20
GO:0071616	acyl-CoA biosynthetic process	0.26	>=0.20
ENSG00000143537	ADAM15 PPI subnetwork	0.45	>=0.20
ENSG00000008277	ADAM22 PPI subnetwork	0.42	>=0.20
ENSG00000042980	ADAM28 PPI subnetwork	0.17	>=0.20
ENSG00000105963	ADAP1 PPI subnetwork	0.79	>=0.20

ENSG00000163050	ADCK3 PPI subnetwork	0.44	>=0.20
ENSG00000164742	ADCY1 PPI subnetwork	0.76	>=0.20
ENSG00000078295	ADCY2 PPI subnetwork	0.65	>=0.20
ENSG00000138031	ADCY3 PPI subnetwork	0.4	>=0.20
ENSG00000173175	ADCY5 PPI subnetwork	0.51	>=0.20
ENSG00000174233	ADCY6 PPI subnetwork	0.2	>=0.20
ENSG00000155897	ADCY8 PPI subnetwork	0.03	>=0.20
ENSG00000087274	ADD1 PPI subnetwork	0.99	>=0.20
ENSG00000075340	ADD2 PPI subnetwork	0.75	>=0.20
GO:0021984	adenohypophysis development	1	>=0.20
GO:0007189	adenylate cyclase-activating G-protein coupled receptor sign	0.96	>=0.20
GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor signa	1	>=0.20
GO:0007188	adenylate cyclase-modulating G-protein coupled receptor sig	0.99	>=0.20
GO:0005912	adherens junction	0.07	>=0.20
GO:0034332	adherens junction organization	1	>=0.20
ENSG00000043591	ADRB1 PPI subnetwork	0.94	>=0.20
ENSG00000173020	ADRBK1 PPI subnetwork	0.37	>=0.20
ENSG00000130706	ADRM1 PPI subnetwork	0.73	>=0.20
GO:0030534	adult behavior	1	>=0.20
GO:0008343	adult feeding behavior	0.93	>=0.20
GO:0008344	adult locomotory behavior	1	>=0.20
GO:0007628	adult walking behavior	1	>=0.20
GO:0009060	aerobic respiration	0.86	>=0.20
ENSG00000155966	AFF2 PPI subnetwork	0.45	>=0.20
ENSG00000173744	AGFG1 PPI subnetwork	0.81	>=0.20
ENSG00000106541	AGR2 PPI subnetwork	0.26	>=0.20
ENSG00000135744	AGT PPI subnetwork	0.06	>=0.20
ENSG00000144891	AGTR1 PPI subnetwork	0.12	>=0.20
ENSG00000153207	AHCTF1 PPI subnetwork	0.76	>=0.20
ENSG00000101444	AHCY PPI subnetwork	0.44	>=0.20
ENSG00000106546	AHR PPI subnetwork	0.37	>=0.20
ENSG00000063438	AHRR PPI subnetwork	0.03	>=0.20
ENSG00000100591	AHSA1 PPI subnetwork	0.26	>=0.20
ENSG00000164022	AIMP1 PPI subnetwork	0.29	>=0.20
ENSG00000106305	AIMP2 PPI subnetwork	0.87	>=0.20
ENSG00000160224	AIRE PPI subnetwork	0.13	>=0.20
ENSG00000106992	AK1 PPI subnetwork	0.11	>=0.20
ENSG00000147853	AK3 PPI subnetwork	0.51	>=0.20
ENSG00000179841	AKAP5 PPI subnetwork	0.98	>=0.20
ENSG00000151320	AKAP6 PPI subnetwork	0.17	>=0.20
ENSG00000105127	AKAP8 PPI subnetwork	0.18	>=0.20
ENSG00000011243	AKAP8L PPI subnetwork	0.03	>=0.20
ENSG00000127914	AKAP9 PPI subnetwork	0.15	>=0.20
ENSG00000085662	AKR1B1 PPI subnetwork	0.82	>=0.20
ENSG00000204673	AKT1S1 PPI subnetwork	0.03	>=0.20
ENSG00000166971	AKTIP PPI subnetwork	0.55	>=0.20
MP:0002871	albuminuria	0.08	>=0.20

ENSG00000170017	ALCAM PPI subnetwork	0.15	>=0.20
ENSG00000111275	ALDH2 PPI subnetwork	0.11	>=0.20
ENSG00000072210	ALDH3A2 PPI subnetwork	0.13	>=0.20
GO:0004033	aldo-keto reductase (NADP) activity	0.62	>=0.20
ENSG00000149925	ALDOA PPI subnetwork	0.49	>=0.20
ENSG00000109107	ALDOC PPI subnetwork	0.93	>=0.20
ENSG00000033011	ALG1 PPI subnetwork	0.91	>=0.20
ENSG00000120697	ALG5 PPI subnetwork	0.29	>=0.20
ENSG00000159063	ALG8 PPI subnetwork	0.12	>=0.20
ENSG00000171094	ALK PPI subnetwork	0.13	>=0.20
GO:0043450	alkene biosynthetic process	0.93	>=0.20
GO:0032281	alpha-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid s	1	>=0.20
GO:0046631	alpha-beta T cell activation	0.96	>=0.20
GO:0002287	alpha-beta T cell activation involved in immune response	0.87	>=0.20
GO:0046632	alpha-beta T cell differentiation	0.72	>=0.20
GO:0002293	alpha-beta T cell differentiation involved in immune respons	0.87	>=0.20
GO:0046633	alpha-beta T cell proliferation	0.99	>=0.20
MP:0001793	altered susceptibility to infection	0.5	>=0.20
GO:0000380	alternative nuclear mRNA splicing, via spliceosome	0.89	>=0.20
GO:0001667	ameboidal cell migration	1	>=0.20
ENSG00000159461	AMFR PPI subnetwork	0.65	>=0.20
GO:0005275	amine transmembrane transporter activity	0.36	>=0.20
GO:0015837	amine transport	0.71	>=0.20
GO:0043038	amino acid activation	0.81	>=0.20
GO:0003333	amino acid transmembrane transport	0.77	>=0.20
GO:0015171	amino acid transmembrane transporter activity	0.64	>=0.20
GO:0006865	amino acid transport	0.84	>=0.20
GO:0006040	amino sugar metabolic process	0.91	>=0.20
GO:0004812	aminoacyl-tRNA ligase activity	0.51	>=0.20
GO:0006023	aminoglycan biosynthetic process	0.37	>=0.20
ENSG00000166025	AMOTL1 PPI subnetwork	0.08	>=0.20
ENSG00000078053	AMPH PPI subnetwork	0.99	>=0.20
GO:0042987	amyloid precursor protein catabolic process	0.4	>=0.20
MP:0003130	anal atresia	0.94	>=0.20
ENSG00000153107	ANAPC1 PPI subnetwork	0.84	>=0.20
ENSG00000164162	ANAPC10 PPI subnetwork	0.35	>=0.20
ENSG00000141552	ANAPC11 PPI subnetwork	0.93	>=0.20
ENSG00000176248	ANAPC2 PPI subnetwork	0.77	>=0.20
ENSG00000053900	ANAPC4 PPI subnetwork	0.81	>=0.20
ENSG00000089053	ANAPC5 PPI subnetwork	0.9	>=0.20
ENSG00000196510	ANAPC7 PPI subnetwork	0.91	>=0.20
GO:0005680	anaphase-promoting complex	0.25	>=0.20
GO:0031145	anaphase-promoting complex-dependent proteasomal ubiqu	0.91	>=0.20
GO:0060249	anatomical structure homeostasis	0.78	>=0.20
GO:0031225	anchored to membrane	0.48	>=0.20
GO:0046658	anchored to plasma membrane	0.37	>=0.20
GO:0030934	anchoring collagen	0.89	>=0.20

GO:0070161	anchoring junction	0.12	>=0.20
GO:0030521	androgen receptor signaling pathway	0.82	>=0.20
MP:0001890	anencephaly	1	>=0.20
MP:0004024	aneuploidy	0.26	>=0.20
GO:0005253	anion channel activity	1	>=0.20
GO:0008509	anion transmembrane transporter activity	0.98	>=0.20
GO:0006820	anion transport	0.98	>=0.20
GO:0015296	anion:cation symporter activity	0.98	>=0.20
MP:0002641	anisopoikilocytosis	0.59	>=0.20
ENSG00000029534	ANK1 PPI subnetwork	0.76	>=0.20
ENSG00000101745	ANKRD12 PPI subnetwork	0.54	>=0.20
ENSG00000064999	ANKS1A PPI subnetwork	0.2	>=0.20
ENSG00000163516	ANKZF1 PPI subnetwork	0.83	>=0.20
MP:0001293	anophthalmia	0.54	>=0.20
ENSG00000140350	ANP32A PPI subnetwork	0.6	>=0.20
ENSG00000136938	ANP32B PPI subnetwork	0.2	>=0.20
GO:0009948	anterior/posterior axis specification	0.99	>=0.20
GO:0009952	anterior/posterior pattern specification	1	>=0.20
GO:0006916	anti-apoptosis	0.06	>=0.20
GO:0019882	antigen processing and presentation	0.94	>=0.20
GO:0019884	antigen processing and presentation of exogenous antigen	1	>=0.20
GO:0002478	antigen processing and presentation of exogenous peptide a	1	>=0.20
GO:0048002	antigen processing and presentation of peptide antigen	0.96	>=0.20
GO:0002474	antigen processing and presentation of peptide antigen via M	0.95	>=0.20
GO:0002495	antigen processing and presentation of peptide antigen via M	1	>=0.20
GO:0002504	antigen processing and presentation of peptide or polysacch	1	>=0.20
GO:0050851	antigen receptor-mediated signaling pathway	0.88	>=0.20
GO:0015297	antiporter activity	0.97	>=0.20
ENSG00000182718	ANXA2 PPI subnetwork	0.08	>=0.20
ENSG00000196975	ANXA4 PPI subnetwork	0.06	>=0.20
ENSG00000100280	AP1B1 PPI subnetwork	0.76	>=0.20
ENSG00000166747	AP1G1 PPI subnetwork	0.34	>=0.20
ENSG00000106367	AP1S1 PPI subnetwork	0.25	>=0.20
ENSG00000152056	AP1S3 PPI subnetwork	0.57	>=0.20
ENSG00000196961	AP2A1 PPI subnetwork	0.06	>=0.20
ENSG00000183020	AP2A2 PPI subnetwork	0.33	>=0.20
ENSG00000006125	AP2B1 PPI subnetwork	0.6	>=0.20
ENSG00000177879	AP3S1 PPI subnetwork	0.81	>=0.20
ENSG00000107282	APBA1 PPI subnetwork	1	>=0.20
ENSG00000034053	APBA2 PPI subnetwork	0.89	>=0.20
ENSG00000166313	APBB1 PPI subnetwork	0.68	>=0.20
ENSG00000077420	APBB1IP PPI subnetwork	0.45	>=0.20
ENSG00000134982	APC PPI subnetwork	0.71	>=0.20
ENSG00000100823	APEX1 PPI subnetwork	0.23	>=0.20
GO:0043297	apical junction assembly	1	>=0.20
GO:0043296	apical junction complex	0.78	>=0.20
GO:0045177	apical part of cell	0.2	>=0.20

GO:0016324	apical plasma membrane	0.24	>=0.20
GO:0016327	apicolateral plasma membrane	0.84	>=0.20
ENSG00000175279	APITD1 PPI subnetwork	0.85	>=0.20
ENSG00000169621	APLF PPI subnetwork	0.91	>=0.20
ENSG00000084234	APLP2 PPI subnetwork	0.67	>=0.20
GO:0043277	apoptotic cell clearance	0.04	>=0.20
GO:0008637	apoptotic mitochondrial changes	0.96	>=0.20
GO:0048736	appendage development	1	>=0.20
GO:0035107	appendage morphogenesis	1	>=0.20
ENSG00000157500	APPL1 PPI subnetwork	0.43	>=0.20
ENSG00000136044	APPL2 PPI subnetwork	0.84	>=0.20
ENSG00000169083	AR PPI subnetwork	0.08	>=0.20
ENSG00000198576	ARC PPI subnetwork	0.48	>=0.20
ENSG00000095139	ARCN1 PPI subnetwork	0.16	>=0.20
GO:0008060	ARF GTPase activator activity	0.05	>=0.20
GO:0005086	ARF guanyl-nucleotide exchange factor activity	0.34	>=0.20
ENSG00000134287	ARF3 PPI subnetwork	0.68	>=0.20
ENSG00000165527	ARF6 PPI subnetwork	0.3	>=0.20
ENSG00000149182	ARFGAP2 PPI subnetwork	0.56	>=0.20
ENSG00000101246	ARFRP1 PPI subnetwork	0.63	>=0.20
ENSG00000175220	ARHGAP1 PPI subnetwork	0.31	>=0.20
ENSG00000075884	ARHGAP15 PPI subnetwork	0.73	>=0.20
ENSG00000134909	ARHGAP32 PPI subnetwork	0.82	>=0.20
ENSG00000160007	ARHGAP35 PPI subnetwork	0.23	>=0.20
ENSG00000006740	ARHGAP44 PPI subnetwork	1	>=0.20
ENSG00000100852	ARHGAP5 PPI subnetwork	0.27	>=0.20
ENSG00000141522	ARHGDIA PPI subnetwork	0.09	>=0.20
ENSG00000111348	ARHGDIB PPI subnetwork	0.04	>=0.20
ENSG00000076928	ARHGEF1 PPI subnetwork	0.26	>=0.20
ENSG00000130762	ARHGEF16 PPI subnetwork	0.41	>=0.20
ENSG00000110237	ARHGEF17 PPI subnetwork	0.19	>=0.20
ENSG00000116584	ARHGEF2 PPI subnetwork	0.61	>=0.20
ENSG00000129675	ARHGEF6 PPI subnetwork	0.15	>=0.20
ENSG00000102606	ARHGEF7 PPI subnetwork	0.19	>=0.20
ENSG00000117713	ARID1A PPI subnetwork	0.58	>=0.20
ENSG00000189079	ARID2 PPI subnetwork	0.21	>=0.20
ENSG00000054267	ARID4B PPI subnetwork	0.12	>=0.20
ENSG00000166233	ARIH1 PPI subnetwork	0.72	>=0.20
ENSG00000213465	ARL2 PPI subnetwork	1	>=0.20
ENSG00000143437	ARNT PPI subnetwork	0.63	>=0.20
ENSG00000172379	ARNT2 PPI subnetwork	0.32	>=0.20
ENSG00000133794	ARNTL PPI subnetwork	0.11	>=0.20
GO:0019438	aromatic compound biosynthetic process	0.63	>=0.20
ENSG00000130429	ARPC1B PPI subnetwork	0.94	>=0.20
ENSG00000163466	ARPC2 PPI subnetwork	0.25	>=0.20
ENSG00000162704	ARPC5 PPI subnetwork	0.18	>=0.20
ENSG00000136950	ARPC5L PPI subnetwork	0.41	>=0.20

MP:0008261	arrest of male meiosis	0.98	>=0.20
MP:0001155	arrest of spermatogenesis	0.91	>=0.20
MP:0008279	arrest of spermiogenesis	0.07	>=0.20
MP:0001802	arrested B cell differentiation	0.06	>=0.20
MP:0001825	arrested T cell differentiation	0.46	>=0.20
GO:0060840	artery development	0.89	>=0.20
GO:0048844	artery morphogenesis	0.87	>=0.20
GO:0004065	arylsulfatase activity	0.84	>=0.20
ENSG00000100325	ASCC2 PPI subnetwork	0.2	>=0.20
ENSG00000112249	ASCC3 PPI subnetwork	0.11	>=0.20
MP:0005324	ascites	0.39	>=0.20
ENSG00000139352	ASCL1 PPI subnetwork	0.64	>=0.20
ENSG00000111875	ASF1A PPI subnetwork	0.28	>=0.20
ENSG00000105011	ASF1B PPI subnetwork	0.32	>=0.20
ENSG00000126522	ASL PPI subnetwork	0.97	>=0.20
ENSG00000198356	ASNA1 PPI subnetwork	0.12	>=0.20
GO:0009068	aspartate family amino acid catabolic process	0.8	>=0.20
GO:0004190	aspartic-type endopeptidase activity	0.43	>=0.20
GO:0070001	aspartic-type peptidase activity	0.43	>=0.20
GO:0008306	associative learning	1	>=0.20
MP:0002675	asthenozoospermia	0.38	>=0.20
GO:0048708	astrocyte differentiation	0.95	>=0.20
MP:0003354	astrocytosis	0.09	>=0.20
MP:0008146	asymmetric rib-sternum attachment	0.38	>=0.20
GO:0032279	asymmetric synapse	1	>=0.20
ENSG00000156802	ATAD2 PPI subnetwork	0.24	>=0.20
MP:0001393	ataxia	0.99	>=0.20
MP:0001177	atelectasis	0.2	>=0.20
ENSG00000115966	ATF2 PPI subnetwork	0.07	>=0.20
ENSG00000162772	ATF3 PPI subnetwork	0.21	>=0.20
ENSG00000169136	ATF5 PPI subnetwork	0.05	>=0.20
ENSG00000170653	ATF7 PPI subnetwork	0.04	>=0.20
ENSG00000145782	ATG12 PPI subnetwork	0.52	>=0.20
ENSG00000144848	ATG3 PPI subnetwork	0.82	>=0.20
ENSG00000168397	ATG4B PPI subnetwork	0.8	>=0.20
ENSG00000057663	ATG5 PPI subnetwork	0.31	>=0.20
ENSG00000197548	ATG7 PPI subnetwork	0.99	>=0.20
ENSG00000198925	ATG9A PPI subnetwork	0.85	>=0.20
ENSG00000111676	ATN1 PPI subnetwork	0.64	>=0.20
GO:0043044	ATP-dependent chromatin remodeling	0.95	>=0.20
GO:0004003	ATP-dependent DNA helicase activity	0.96	>=0.20
GO:0008026	ATP-dependent helicase activity	0.44	>=0.20
GO:0004004	ATP-dependent RNA helicase activity	0.22	>=0.20
GO:0006754	ATP biosynthetic process	0.77	>=0.20
GO:0006200	ATP catabolic process	0.62	>=0.20
GO:0015991	ATP hydrolysis coupled proton transport	0.88	>=0.20
GO:0046034	ATP metabolic process	0.56	>=0.20

GO:0042773	ATP synthesis coupled electron transport	1	>=0.20
GO:0015986	ATP synthesis coupled proton transport	0.99	>=0.20
ENSG00000075673	ATP12A PPI subnetwork	0.08	>=0.20
ENSG00000163399	ATP1A1 PPI subnetwork	0.28	>=0.20
ENSG00000143153	ATP1B1 PPI subnetwork	0.41	>=0.20
ENSG00000174437	ATP2A2 PPI subnetwork	0.6	>=0.20
ENSG00000070961	ATP2B1 PPI subnetwork	1	>=0.20
ENSG00000157087	ATP2B2 PPI subnetwork	0.88	>=0.20
ENSG00000067842	ATP2B3 PPI subnetwork	0.67	>=0.20
ENSG00000058668	ATP2B4 PPI subnetwork	0.98	>=0.20
ENSG00000152234	ATP5A1 PPI subnetwork	0.04	>=0.20
ENSG00000165629	ATP5C1 PPI subnetwork	0.84	>=0.20
ENSG00000099624	ATP5D PPI subnetwork	1	>=0.20
ENSG00000124172	ATP5E PPI subnetwork	0.89	>=0.20
ENSG00000116459	ATP5F1 PPI subnetwork	1	>=0.20
ENSG00000159199	ATP5G1 PPI subnetwork	0.92	>=0.20
ENSG00000135390	ATP5G2 PPI subnetwork	0.91	>=0.20
ENSG00000154518	ATP5G3 PPI subnetwork	0.86	>=0.20
ENSG00000167863	ATP5H PPI subnetwork	0.92	>=0.20
ENSG00000169020	ATP5I PPI subnetwork	0.84	>=0.20
ENSG00000154723	ATP5J PPI subnetwork	0.74	>=0.20
ENSG00000167283	ATP5L PPI subnetwork	0.95	>=0.20
ENSG00000033627	ATP6V0A1 PPI subnetwork	0.88	>=0.20
ENSG00000117410	ATP6V0B PPI subnetwork	0.74	>=0.20
ENSG00000185883	ATP6V0C PPI subnetwork	0.27	>=0.20
ENSG00000159720	ATP6V0D1 PPI subnetwork	0.86	>=0.20
ENSG00000114573	ATP6V1A PPI subnetwork	0.25	>=0.20
ENSG00000147416	ATP6V1B2 PPI subnetwork	0.93	>=0.20
ENSG00000155097	ATP6V1C1 PPI subnetwork	0.56	>=0.20
ENSG00000100554	ATP6V1D PPI subnetwork	0.63	>=0.20
ENSG00000131100	ATP6V1E1 PPI subnetwork	0.65	>=0.20
ENSG00000128524	ATP6V1F PPI subnetwork	0.94	>=0.20
ENSG00000136888	ATP6V1G1 PPI subnetwork	0.88	>=0.20
ENSG00000047249	ATP6V1H PPI subnetwork	0.3	>=0.20
GO:0042623	ATPase activity, coupled	0.3	>=0.20
GO:0043492	ATPase activity, coupled to movement of substances	0.25	>=0.20
GO:0042625	ATPase activity, coupled to transmembrane movement of ior	0.33	>=0.20
GO:0015662	ATPase activity, coupled to transmembrane movement of ior	0.64	>=0.20
GO:0042626	ATPase activity, coupled to transmembrane movement of sul	0.22	>=0.20
GO:0060590	ATPase regulator activity	0.79	>=0.20
ENSG00000175054	ATR PPI subnetwork	0.26	>=0.20
MP:0010403	atrial septal defect	0.83	>=0.20
ENSG00000164053	ATRIP PPI subnetwork	0.99	>=0.20
GO:0051313	attachment of spindle microtubules to chromosome	0.99	>=0.20
GO:0008608	attachment of spindle microtubules to kinetochore	1	>=0.20
ENSG00000124788	ATXN1 PPI subnetwork	0.38	>=0.20
ENSG00000130638	ATXN10 PPI subnetwork	0.04	>=0.20

ENSG00000168488	ATXN2L PPI subnetwork	0.09	>=0.20
ENSG00000163635	ATXN7 PPI subnetwork	0.09	>=0.20
GO:0017091	AU-rich element binding	0.66	>=0.20
GO:0042491	auditory receptor cell differentiation	0.97	>=0.20
ENSG00000087586	AURKA PPI subnetwork	0.24	>=0.20
ENSG00000178999	AURKB PPI subnetwork	0.84	>=0.20
MP:0001844	autoimmune response	0.44	>=0.20
GO:0048483	autonomic nervous system development	1	>=0.20
GO:0005776	autophagic vacuole	0.24	>=0.20
GO:0000045	autophagic vacuole assembly	0.78	>=0.20
GO:0000421	autophagic vacuole membrane	0.77	>=0.20
GO:0006914	autophagy	0.65	>=0.20
ENSG00000168646	AXIN2 PPI subnetwork	0.91	>=0.20
GO:0003401	axis elongation	1	>=0.20
GO:0009798	axis specification	1	>=0.20
ENSG00000167601	AXL PPI subnetwork	0.03	>=0.20
GO:0030673	axolemma	0.99	>=0.20
GO:0030424	axon	1	>=0.20
GO:0008088	axon cargo transport	1	>=0.20
MP:0005405	axon degeneration	0.89	>=0.20
GO:0008366	axon ensheathment	1	>=0.20
GO:0032291	axon ensheathment in central nervous system	0.99	>=0.20
GO:0048675	axon extension	0.97	>=0.20
GO:0048846	axon extension involved in axon guidance	0.97	>=0.20
GO:0007411	axon guidance	1	>=0.20
GO:0033267	axon part	1	>=0.20
GO:0043679	axon terminus	1	>=0.20
GO:0007413	axonal fasciculation	1	>=0.20
GO:0005858	axonemal dynein complex	0.8	>=0.20
GO:0005930	axoneme	0.99	>=0.20
GO:0044447	axoneme part	0.93	>=0.20
GO:0007409	axonogenesis	1	>=0.20
ENSG00000163512	AZI2 PPI subnetwork	0.34	>=0.20
MP:0005159	azoospermia	0.58	>=0.20
GO:0042113	B cell activation	0.31	>=0.20
GO:0002312	B cell activation involved in immune response	1	>=0.20
GO:0001783	B cell apoptotic process	0.8	>=0.20
MP:0002023	B cell derived lymphoma	0.8	>=0.20
GO:0030183	B cell differentiation	0.13	>=0.20
GO:0001782	B cell homeostasis	0.66	>=0.20
GO:0042100	B cell proliferation	0.42	>=0.20
GO:0050853	B cell receptor signaling pathway	0.48	>=0.20
ENSG00000166710	B2M PPI subnetwork	0.2	>=0.20
ENSG00000186318	BACE1 PPI subnetwork	0.09	>=0.20
ENSG00000107262	BAG1 PPI subnetwork	0.11	>=0.20
ENSG00000112208	BAG2 PPI subnetwork	0.79	>=0.20
ENSG00000166170	BAG5 PPI subnetwork	0.48	>=0.20

ENSG00000181790	BAI1 PPI subnetwork	1	>=0.20
ENSG00000175866	BAIAP2 PPI subnetwork	0.43	>=0.20
ENSG00000030110	BAK1 PPI subnetwork	0.67	>=0.20
ENSG00000175334	BANF1 PPI subnetwork	0.26	>=0.20
ENSG00000138376	BARD1 PPI subnetwork	0.8	>=0.20
GO:0005605	basal lamina	0.34	>=0.20
GO:0009925	basal plasma membrane	0.07	>=0.20
GO:0006284	base-excision repair	0.97	>=0.20
GO:0005604	basement membrane	0.53	>=0.20
GO:0015802	basic amino acid transport	0.66	>=0.20
ENSG00000176788	BASP1 PPI subnetwork	1	>=0.20
ENSG00000087088	BAX PPI subnetwork	0.41	>=0.20
ENSG00000009954	BAZ1B PPI subnetwork	0.08	>=0.20
ENSG00000132692	BCAN PPI subnetwork	0.65	>=0.20
ENSG00000185825	BCAP31 PPI subnetwork	0.53	>=0.20
ENSG00000137936	BCAR3 PPI subnetwork	0.04	>=0.20
ENSG00000142867	BCL10 PPI subnetwork	0.11	>=0.20
ENSG00000119866	BCL11A PPI subnetwork	0.35	>=0.20
ENSG00000171791	BCL2 PPI subnetwork	0.17	>=0.20
ENSG00000171552	BCL2L1 PPI subnetwork	0.78	>=0.20
ENSG00000129473	BCL2L2 PPI subnetwork	0.88	>=0.20
ENSG00000069399	BCL3 PPI subnetwork	0.25	>=0.20
ENSG00000113916	BCL6 PPI subnetwork	0.25	>=0.20
ENSG00000110987	BCL7A PPI subnetwork	0.53	>=0.20
ENSG00000183337	BCOR PPI subnetwork	0.08	>=0.20
GO:0007610	behavior	1	>=0.20
GO:0002209	behavioral defense response	1	>=0.20
GO:0001662	behavioral fear response	1	>=0.20
MP:0000373	belly spot	0.7	>=0.20
ENSG00000178409	BEND3 PPI subnetwork	0.04	>=0.20
GO:0042537	benzene-containing compound metabolic process	0.93	>=0.20
ENSG00000105829	BET1 PPI subnetwork	0.03	>=0.20
GO:0008013	beta-catenin binding	0.37	>=0.20
GO:0048487	beta-tubulin binding	0.36	>=0.20
GO:0015838	betaine transport	0.83	>=0.20
ENSG00000182492	BGN PPI subnetwork	0.89	>=0.20
ENSG00000185963	BICD2 PPI subnetwork	0.07	>=0.20
ENSG00000015475	BID PPI subnetwork	0.78	>=0.20
MP:0001395	bidirectional circling	0.88	>=0.20
ENSG00000136717	BIN1 PPI subnetwork	0.1	>=0.20
ENSG00000147439	BIN3 PPI subnetwork	0.03	>=0.20
GO:0007339	binding of sperm to zona pellucida	0.9	>=0.20
GO:0031214	biomineral tissue development	0.95	>=0.20
ENSG00000089685	BIRC5 PPI subnetwork	0.74	>=0.20
ENSG00000115760	BIRC6 PPI subnetwork	1	>=0.20
GO:0001825	blastocyst formation	0.97	>=0.20
GO:0007350	blastoderm segmentation	1	>=0.20

MP:0002001	blindness	0.1	>=0.20
MP:0001208	blistering	0.5	>=0.20
ENSG00000136573	BLK PPI subnetwork	0.03	>=0.20
ENSG00000197299	BLM PPI subnetwork	1	>=0.20
ENSG00000095585	BLNK PPI subnetwork	0.11	>=0.20
GO:0008015	blood circulation	0.05	>=0.20
GO:0043534	blood vessel endothelial cell migration	0.17	>=0.20
GO:0001974	blood vessel remodeling	0.44	>=0.20
ENSG00000168283	BMI1 PPI subnetwork	0.38	>=0.20
GO:0030509	BMP signaling pathway	0.97	>=0.20
ENSG00000168487	BMP1 PPI subnetwork	0.8	>=0.20
ENSG00000125845	BMP2 PPI subnetwork	0.95	>=0.20
ENSG00000125378	BMP4 PPI subnetwork	0.72	>=0.20
ENSG00000153162	BMP6 PPI subnetwork	0.96	>=0.20
ENSG00000101144	BMP7 PPI subnetwork	0.63	>=0.20
ENSG00000107779	BMPR1A PPI subnetwork	0.82	>=0.20
ENSG00000138696	BMPR1B PPI subnetwork	0.98	>=0.20
GO:0007589	body fluid secretion	0.28	>=0.20
GO:0010171	body morphogenesis	1	>=0.20
GO:0060348	bone development	0.48	>=0.20
GO:0030282	bone mineralization	0.83	>=0.20
GO:0060349	bone morphogenesis	0.52	>=0.20
GO:0046849	bone remodeling	0.62	>=0.20
ENSG00000170727	BOP1 PPI subnetwork	0.52	>=0.20
MP:0004374	bowed radius	0.86	>=0.20
MP:0004358	bowed tibia	0.58	>=0.20
ENSG00000171634	BPTF PPI subnetwork	0.46	>=0.20
MP:0002544	brachydactyly	0.98	>=0.20
MP:0002543	brachyphalangia	0.93	>=0.20
ENSG00000157764	BRAF PPI subnetwork	0.15	>=0.20
GO:0007420	brain development	0.99	>=0.20
MP:0001847	brain inflammation	0.63	>=0.20
GO:0009083	branched chain family amino acid catabolic process	0.7	>=0.20
GO:0009081	branched chain family amino acid metabolic process	0.44	>=0.20
GO:0060444	branching involved in mammary gland duct morphogenesis	0.94	>=0.20
GO:0060445	branching involved in salivary gland morphogenesis	0.95	>=0.20
GO:0001658	branching involved in ureteric bud morphogenesis	0.99	>=0.20
GO:0048754	branching morphogenesis of a tube	0.92	>=0.20
ENSG00000089234	BRAP PPI subnetwork	0.24	>=0.20
ENSG00000139618	BRCA2 PPI subnetwork	0.99	>=0.20
ENSG00000204256	BRD2 PPI subnetwork	0.06	>=0.20
ENSG00000215077	BRD2 PPI subnetwork	0.06	>=0.20
ENSG00000169925	BRD3 PPI subnetwork	0.36	>=0.20
ENSG00000112983	BRD8 PPI subnetwork	0.06	>=0.20
ENSG00000185024	BRF1 PPI subnetwork	0.88	>=0.20
ENSG00000174744	BRMS1 PPI subnetwork	0.05	>=0.20
GO:0005903	brush border	0.13	>=0.20

GO:0031526	brush border membrane	0.14	>=0.20
ENSG00000185658	BRWD1 PPI subnetwork	0.82	>=0.20
ENSG00000165288	BRWD3 PPI subnetwork	0.77	>=0.20
ENSG00000164061	BSN PPI subnetwork	0.97	>=0.20
ENSG00000095564	BTAF1 PPI subnetwork	0.87	>=0.20
ENSG00000133243	BTBD2 PPI subnetwork	0.41	>=0.20
ENSG00000134717	BTF3L4 PPI subnetwork	0.83	>=0.20
ENSG00000166167	BTRC PPI subnetwork	0.36	>=0.20
ENSG00000156970	BUB1B PPI subnetwork	0.72	>=0.20
ENSG00000154473	BUB3 PPI subnetwork	0.78	>=0.20
GO:0016493	C-C chemokine receptor activity	0.39	>=0.20
GO:0018410	C-terminal protein amino acid modification	0.99	>=0.20
GO:0006501	C-terminal protein lipidation	0.97	>=0.20
ENSG00000168005	C11orf84 PPI subnetwork	0.79	>=0.20
ENSG00000087302	C14orf166 PPI subnetwork	1	>=0.20
ENSG00000141034	C17orf39 PPI subnetwork	0.27	>=0.20
ENSG00000161939	C17orf49 PPI subnetwork	0.4	>=0.20
ENSG00000172301	C17orf79 PPI subnetwork	0.5	>=0.20
ENSG00000163362	C1orf106 PPI subnetwork	0.34	>=0.20
ENSG00000154429	C1orf96 PPI subnetwork	0.48	>=0.20
ENSG00000173372	C1QA PPI subnetwork	0.15	>=0.20
ENSG00000173369	C1QB PPI subnetwork	0.05	>=0.20
ENSG00000108561	C1QBP PPI subnetwork	0.06	>=0.20
ENSG00000159189	C1QC PPI subnetwork	0.13	>=0.20
ENSG00000101331	C20orf160 PPI subnetwork	0.47	>=0.20
ENSG00000101189	C20orf20 PPI subnetwork	0.76	>=0.20
ENSG00000101084	C20orf24 PPI subnetwork	0.49	>=0.20
GO:0006700	C21-steroid hormone biosynthetic process	0.58	>=0.20
ENSG00000196872	C2orf55 PPI subnetwork	1	>=0.20
ENSG00000118491	C6orf94 PPI subnetwork	1	>=0.20
ENSG00000180190	C8orf42 PPI subnetwork	1	>=0.20
ENSG00000104267	CA2 PPI subnetwork	0.31	>=0.20
MP:0005150	cachexia	0.27	>=0.20
ENSG00000141837	CACNA1A PPI subnetwork	0.6	>=0.20
ENSG00000148408	CACNA1B PPI subnetwork	0.98	>=0.20
ENSG00000151067	CACNA1C PPI subnetwork	0.98	>=0.20
ENSG00000157388	CACNA1D PPI subnetwork	0.9	>=0.20
ENSG00000198216	CACNA1E PPI subnetwork	0.79	>=0.20
ENSG00000102001	CACNA1F PPI subnetwork	0.91	>=0.20
ENSG00000196557	CACNA1H PPI subnetwork	0.69	>=0.20
ENSG00000081248	CACNA1S PPI subnetwork	0.95	>=0.20
ENSG00000067191	CACNB1 PPI subnetwork	0.92	>=0.20
ENSG00000166862	CACNG2 PPI subnetwork	0.99	>=0.20
GO:0045296	cadherin binding	0.99	>=0.20
GO:0015030	Cajal body	0.57	>=0.20
ENSG00000172137	CALB2 PPI subnetwork	0.73	>=0.20
GO:0016339	calcium-dependent cell-cell adhesion	1	>=0.20

GO:0004198	calcium-dependent cysteine-type endopeptidase activity	0.96	>=0.20
GO:0005544	calcium-dependent phospholipid binding	0.7	>=0.20
GO:0048306	calcium-dependent protein binding	0.43	>=0.20
GO:0016338	calcium-independent cell-cell adhesion	0.99	>=0.20
GO:0015278	calcium-release channel activity	0.88	>=0.20
GO:0005227	calcium activated cation channel activity	1	>=0.20
GO:0005262	calcium channel activity	1	>=0.20
GO:0034704	calcium channel complex	1	>=0.20
GO:0005246	calcium channel regulator activity	0.6	>=0.20
GO:0017156	calcium ion-dependent exocytosis	1	>=0.20
GO:0055074	calcium ion homeostasis	0.4	>=0.20
GO:0070588	calcium ion transmembrane transport	1	>=0.20
GO:0006816	calcium ion transport	1	>=0.20
ENSG00000198668	CALM1 PPI subnetwork	0.54	>=0.20
ENSG00000143933	CALM2 PPI subnetwork	0.54	>=0.20
ENSG00000160014	CALM3 PPI subnetwork	0.54	>=0.20
ENSG00000178363	CALML3 PPI subnetwork	0.5	>=0.20
GO:0004683	calmodulin-dependent protein kinase activity	0.66	>=0.20
GO:0005516	calmodulin binding	0.97	>=0.20
ENSG00000128595	CALU PPI subnetwork	1	>=0.20
GO:0043010	camera-type eye development	1	>=0.20
GO:0048593	camera-type eye morphogenesis	1	>=0.20
GO:0060219	camera-type eye photoreceptor cell differentiation	1	>=0.20
ENSG00000134072	CAMK1 PPI subnetwork	1	>=0.20
ENSG00000183049	CAMK1D PPI subnetwork	0.91	>=0.20
ENSG00000070808	CAMK2A PPI subnetwork	0.88	>=0.20
ENSG00000058404	CAMK2B PPI subnetwork	0.96	>=0.20
ENSG00000145349	CAMK2D PPI subnetwork	0.7	>=0.20
ENSG00000148660	CAMK2G PPI subnetwork	1	>=0.20
ENSG00000164076	CAMKV PPI subnetwork	1	>=0.20
GO:0004691	cAMP-dependent protein kinase activity	0.19	>=0.20
GO:0019933	cAMP-mediated signaling	0.98	>=0.20
GO:0030552	cAMP binding	0.17	>=0.20
GO:0006171	cAMP biosynthetic process	0.99	>=0.20
GO:0006198	cAMP catabolic process	0.57	>=0.20
GO:0046058	cAMP metabolic process	0.99	>=0.20
ENSG00000111530	CAND1 PPI subnetwork	0.45	>=0.20
GO:0060070	canonical Wnt receptor signaling pathway	1	>=0.20
ENSG00000014216	CAPN1 PPI subnetwork	0.23	>=0.20
ENSG00000126247	CAPNS1 PPI subnetwork	0.24	>=0.20
ENSG00000135387	CAPRIN1 PPI subnetwork	0.17	>=0.20
ENSG00000198898	CAPZA2 PPI subnetwork	0.16	>=0.20
GO:0004089	carbonate dehydratase activity	0.52	>=0.20
GO:0004180	carboxypeptidase activity	0.09	>=0.20
ENSG00000198286	CARD11 PPI subnetwork	0.59	>=0.20
GO:0003230	cardiac atrium development	0.95	>=0.20
GO:0003209	cardiac atrium morphogenesis	0.94	>=0.20

GO:0055006	cardiac cell development	0.47	>=0.20
GO:0035051	cardiac cell differentiation	0.8	>=0.20
GO:0003205	cardiac chamber development	0.97	>=0.20
GO:0003207	cardiac chamber formation	0.86	>=0.20
GO:0003206	cardiac chamber morphogenesis	0.93	>=0.20
MP:0001625	cardiac hypertrophy	0.04	>=0.20
MP:0005608	cardiac interstitial fibrosis	0.08	>=0.20
GO:0055013	cardiac muscle cell development	0.47	>=0.20
GO:0055007	cardiac muscle cell differentiation	0.77	>=0.20
GO:0060038	cardiac muscle cell proliferation	0.99	>=0.20
GO:0060048	cardiac muscle contraction	0.96	>=0.20
GO:0048738	cardiac muscle tissue development	0.96	>=0.20
GO:0055017	cardiac muscle tissue growth	0.96	>=0.20
GO:0055008	cardiac muscle tissue morphogenesis	0.99	>=0.20
GO:0055003	cardiac myofibril assembly	0.91	>=0.20
GO:0003215	cardiac right ventricle morphogenesis	1	>=0.20
GO:0003279	cardiac septum development	0.97	>=0.20
GO:0060411	cardiac septum morphogenesis	0.85	>=0.20
GO:0003231	cardiac ventricle development	0.97	>=0.20
GO:0003211	cardiac ventricle formation	0.89	>=0.20
GO:0003208	cardiac ventricle morphogenesis	0.96	>=0.20
MP:0005330	cardiomyopathy	0.5	>=0.20
ENSG00000142453	CARM1 PPI subnetwork	0.67	>=0.20
GO:0015879	carnitine transport	0.83	>=0.20
GO:0001502	cartilage condensation	1	>=0.20
GO:0051216	cartilage development	0.92	>=0.20
ENSG00000137812	CASC5 PPI subnetwork	0.73	>=0.20
ENSG00000147044	CASK PPI subnetwork	0.65	>=0.20
ENSG00000137757	CASP5 PPI subnetwork	0.1	>=0.20
ENSG00000138794	CASP6 PPI subnetwork	0.08	>=0.20
ENSG00000165806	CASP7 PPI subnetwork	0.19	>=0.20
ENSG00000064012	CASP8 PPI subnetwork	0.08	>=0.20
ENSG00000132906	CASP9 PPI subnetwork	0.13	>=0.20
ENSG00000153113	CAST PPI subnetwork	0.42	>=0.20
MP:0001304	cataracts	0.53	>=0.20
GO:0009713	catechol-containing compound biosynthetic process	1	>=0.20
GO:0009712	catechol-containing compound metabolic process	0.99	>=0.20
GO:0042423	catecholamine biosynthetic process	1	>=0.20
GO:0006584	catecholamine metabolic process	0.99	>=0.20
GO:0050432	catecholamine secretion	0.97	>=0.20
GO:0051937	catecholamine transport	0.9	>=0.20
GO:0019829	cation-transporting ATPase activity	0.23	>=0.20
GO:0005261	cation channel activity	1	>=0.20
GO:0034703	cation channel complex	1	>=0.20
GO:0055080	cation homeostasis	0.09	>=0.20
GO:0005416	cation:amino acid symporter activity	0.88	>=0.20
GO:0015491	cation:cation antiporter activity	0.93	>=0.20

MP:0004073	caudal body truncation	0.14	>=0.20
ENSG00000105971	CAV2 PPI subnetwork	0.52	>=0.20
ENSG00000182533	CAV3 PPI subnetwork	0.15	>=0.20
ENSG00000078699	CBFA2T2 PPI subnetwork	0.9	>=0.20
ENSG00000129993	CBFA2T3 PPI subnetwork	0.99	>=0.20
ENSG00000160200	CBS PPI subnetwork	0.5	>=0.20
ENSG00000108468	CBX1 PPI subnetwork	0.17	>=0.20
ENSG00000173894	CBX2 PPI subnetwork	0.11	>=0.20
ENSG00000122565	CBX3 PPI subnetwork	0.05	>=0.20
ENSG00000141582	CBX4 PPI subnetwork	0.22	>=0.20
ENSG00000094916	CBX5 PPI subnetwork	0.38	>=0.20
ENSG00000183741	CBX6 PPI subnetwork	0.42	>=0.20
ENSG00000141570	CBX8 PPI subnetwork	0.24	>=0.20
ENSG00000144648	CCBP2 PPI subnetwork	0.35	>=0.20
ENSG00000176476	CCDC101 PPI subnetwork	0.34	>=0.20
ENSG00000168502	CCDC165 PPI subnetwork	0.77	>=0.20
ENSG00000140481	CCDC33 PPI subnetwork	0.69	>=0.20
ENSG00000175602	CCDC85B PPI subnetwork	0.58	>=0.20
ENSG00000179071	CCDC89 PPI subnetwork	0.27	>=0.20
ENSG00000137500	CCDC90B PPI subnetwork	0.38	>=0.20
ENSG00000142039	CCDC97 PPI subnetwork	0.31	>=0.20
ENSG00000110148	CCKBR PPI subnetwork	0.43	>=0.20
ENSG00000161570	CCL5 PPI subnetwork	0.17	>=0.20
ENSG00000108688	CCL7 PPI subnetwork	0.22	>=0.20
ENSG00000133101	CCNA1 PPI subnetwork	0.21	>=0.20
ENSG00000145386	CCNA2 PPI subnetwork	0.27	>=0.20
ENSG00000134057	CCNB1 PPI subnetwork	0.39	>=0.20
ENSG00000157456	CCNB2 PPI subnetwork	0.8	>=0.20
ENSG00000147082	CCNB3 PPI subnetwork	0.48	>=0.20
ENSG00000112237	CCNC PPI subnetwork	0.78	>=0.20
ENSG00000110092	CCND1 PPI subnetwork	0.16	>=0.20
ENSG00000118971	CCND2 PPI subnetwork	0.44	>=0.20
ENSG00000105173	CCNE1 PPI subnetwork	0.35	>=0.20
ENSG00000175305	CCNE2 PPI subnetwork	0.69	>=0.20
ENSG00000129315	CCNT1 PPI subnetwork	0.05	>=0.20
ENSG00000082258	CCNT2 PPI subnetwork	0.19	>=0.20
ENSG00000108100	CCNY PPI subnetwork	0.18	>=0.20
GO:0048020	CCR chemokine receptor binding	0.1	>=0.20
ENSG00000163823	CCR1 PPI subnetwork	0.19	>=0.20
ENSG00000183625	CCR3 PPI subnetwork	0.17	>=0.20
ENSG00000160791	CCR5 PPI subnetwork	0.03	>=0.20
ENSG00000129048	CCRL1 PPI subnetwork	0.14	>=0.20
ENSG00000166226	CCT2 PPI subnetwork	0.15	>=0.20
ENSG00000163468	CCT3 PPI subnetwork	0.66	>=0.20
ENSG00000115484	CCT4 PPI subnetwork	0.06	>=0.20
ENSG00000150753	CCT5 PPI subnetwork	0.72	>=0.20
ENSG00000146731	CCT6A PPI subnetwork	0.18	>=0.20

ENSG00000135624	CCT7 PPI subnetwork	0.9	>=0.20
ENSG00000156261	CCT8 PPI subnetwork	0.25	>=0.20
ENSG00000177455	CD19 PPI subnetwork	0.41	>=0.20
ENSG00000116824	CD2 PPI subnetwork	0.4	>=0.20
ENSG00000198821	CD247 PPI subnetwork	0.39	>=0.20
ENSG00000178562	CD28 PPI subnetwork	0.28	>=0.20
ENSG00000198087	CD2AP PPI subnetwork	0.31	>=0.20
ENSG00000135218	CD36 PPI subnetwork	0.14	>=0.20
ENSG00000167286	CD3D PPI subnetwork	1	>=0.20
ENSG00000198851	CD3E PPI subnetwork	0.97	>=0.20
ENSG00000160654	CD3G PPI subnetwork	1	>=0.20
GO:0035710	CD4-positive, alpha-beta T cell activation	0.68	>=0.20
GO:0043367	CD4-positive, alpha-beta T cell differentiation	0.67	>=0.20
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in imr	0.73	>=0.20
ENSG00000010610	CD4 PPI subnetwork	0.15	>=0.20
ENSG00000101017	CD40 PPI subnetwork	0.87	>=0.20
ENSG00000026508	CD44 PPI subnetwork	0.07	>=0.20
ENSG00000117335	CD46 PPI subnetwork	0.2	>=0.20
ENSG00000196776	CD47 PPI subnetwork	0.05	>=0.20
ENSG00000117091	CD48 PPI subnetwork	0.81	>=0.20
ENSG00000110448	CD5 PPI subnetwork	0.3	>=0.20
ENSG00000143119	CD53 PPI subnetwork	0.79	>=0.20
ENSG00000135404	CD63 PPI subnetwork	0.21	>=0.20
ENSG00000105369	CD79A PPI subnetwork	0.03	>=0.20
ENSG00000007312	CD79B PPI subnetwork	0.44	>=0.20
ENSG00000110651	CD81 PPI subnetwork	0.09	>=0.20
ENSG00000085117	CD82 PPI subnetwork	0.06	>=0.20
ENSG00000153563	CD8A PPI subnetwork	0.8	>=0.20
ENSG00000172116	CD8B PPI subnetwork	0.86	>=0.20
ENSG00000079335	CDC14A PPI subnetwork	0.71	>=0.20
ENSG00000130177	CDC16 PPI subnetwork	0.66	>=0.20
ENSG00000117399	CDC20 PPI subnetwork	0.78	>=0.20
ENSG00000094880	CDC23 PPI subnetwork	0.48	>=0.20
ENSG00000164045	CDC25A PPI subnetwork	0.21	>=0.20
ENSG00000101224	CDC25B PPI subnetwork	0.08	>=0.20
ENSG00000158402	CDC25C PPI subnetwork	0.73	>=0.20
ENSG00000176386	CDC26 PPI subnetwork	0.77	>=0.20
ENSG00000004897	CDC27 PPI subnetwork	0.64	>=0.20
ENSG00000070831	CDC42 PPI subnetwork	0.83	>=0.20
ENSG00000171219	CDC42BPG PPI subnetwork	0.25	>=0.20
ENSG00000093009	CDC45 PPI subnetwork	0.94	>=0.20
ENSG00000096401	CDC5L PPI subnetwork	0.86	>=0.20
ENSG00000094804	CDC6 PPI subnetwork	0.82	>=0.20
ENSG00000097046	CDC7 PPI subnetwork	0.59	>=0.20
ENSG00000134371	CDC73 PPI subnetwork	0.52	>=0.20
ENSG00000134690	CDCA8 PPI subnetwork	0.79	>=0.20
ENSG00000039068	CDH1 PPI subnetwork	0.45	>=0.20

ENSG00000170558	CDH2 PPI subnetwork	0.4	>=0.20
ENSG00000062038	CDH3 PPI subnetwork	0.51	>=0.20
ENSG00000170312	CDK1 PPI subnetwork	0.24	>=0.20
ENSG00000167258	CDK12 PPI subnetwork	0.39	>=0.20
ENSG00000117266	CDK18 PPI subnetwork	0.32	>=0.20
ENSG00000155111	CDK19 PPI subnetwork	1	>=0.20
ENSG00000123374	CDK2 PPI subnetwork	0.62	>=0.20
ENSG00000164885	CDK5 PPI subnetwork	0.93	>=0.20
ENSG00000105810	CDK6 PPI subnetwork	0.28	>=0.20
ENSG00000134058	CDK7 PPI subnetwork	0.14	>=0.20
ENSG00000132964	CDK8 PPI subnetwork	0.09	>=0.20
ENSG00000136807	CDK9 PPI subnetwork	0.32	>=0.20
ENSG00000124762	CDKN1A PPI subnetwork	0.34	>=0.20
ENSG00000111276	CDKN1B PPI subnetwork	0.42	>=0.20
ENSG00000129757	CDKN1C PPI subnetwork	0.68	>=0.20
ENSG00000147889	CDKN2A PPI subnetwork	0.84	>=0.20
ENSG00000123080	CDKN2C PPI subnetwork	0.63	>=0.20
ENSG00000167513	CDT1 PPI subnetwork	0.37	>=0.20
ENSG00000172288	CDY1 PPI subnetwork	0.32	>=0.20
ENSG00000172352	CDY1B PPI subnetwork	0.32	>=0.20
ENSG00000153046	CDYL PPI subnetwork	0.12	>=0.20
ENSG00000172216	CEBPB PPI subnetwork	0.04	>=0.20
ENSG00000149187	CELF1 PPI subnetwork	0.51	>=0.20
GO:0005913	cell-cell adherens junction	0.32	>=0.20
GO:0016337	cell-cell adhesion	1	>=0.20
GO:0044291	cell-cell contact zone	0.98	>=0.20
GO:0005911	cell-cell junction	0.41	>=0.20
GO:0007043	cell-cell junction assembly	0.99	>=0.20
GO:0045216	cell-cell junction organization	1	>=0.20
GO:0009988	cell-cell recognition	0.61	>=0.20
GO:0045168	cell-cell signaling involved in cell fate commitment	1	>=0.20
GO:0007160	cell-matrix adhesion	0.04	>=0.20
GO:0031589	cell-substrate adhesion	0.16	>=0.20
GO:0030055	cell-substrate junction	0.04	>=0.20
GO:0007044	cell-substrate junction assembly	0.71	>=0.20
GO:0002263	cell activation involved in immune response	0.83	>=0.20
GO:0033627	cell adhesion mediated by integrin	0.06	>=0.20
GO:0050839	cell adhesion molecule binding	0.95	>=0.20
GO:0044297	cell body	1	>=0.20
GO:0060326	cell chemotaxis	0.24	>=0.20
GO:0005938	cell cortex	0.06	>=0.20
GO:0044448	cell cortex part	0.08	>=0.20
GO:0007050	cell cycle arrest	0.7	>=0.20
GO:0000075	cell cycle checkpoint	0.75	>=0.20
GO:0033205	cell cycle cytokinesis	0.97	>=0.20
GO:0021533	cell differentiation in hindbrain	0.97	>=0.20
GO:0021515	cell differentiation in spinal cord	1	>=0.20

GO:0051301	cell division	0.86	>=0.20
GO:0032153	cell division site	0.66	>=0.20
GO:0032155	cell division site part	0.66	>=0.20
GO:0030313	cell envelope	1	>=0.20
GO:0045165	cell fate commitment	1	>=0.20
GO:0060795	cell fate commitment involved in formation of primary germ	1	>=0.20
GO:0001708	cell fate specification	1	>=0.20
GO:0016049	cell growth	0.23	>=0.20
GO:0034329	cell junction assembly	0.98	>=0.20
GO:0034330	cell junction organization	0.99	>=0.20
GO:0001906	cell killing	0.89	>=0.20
GO:0031252	cell leading edge	0.15	>=0.20
GO:0042074	cell migration involved in gastrulation	1	>=0.20
GO:0002042	cell migration involved in sprouting angiogenesis	0.94	>=0.20
GO:0030031	cell projection assembly	0.92	>=0.20
GO:0032838	cell projection cytoplasm	0.92	>=0.20
GO:0031253	cell projection membrane	0.45	>=0.20
GO:0021846	cell proliferation in forebrain	0.94	>=0.20
GO:0008037	cell recognition	0.97	>=0.20
GO:0045454	cell redox homeostasis	0.96	>=0.20
GO:0009986	cell surface	0.03	>=0.20
GO:0061311	cell surface receptor signaling pathway involved in heart dev	0.97	>=0.20
GO:0006081	cellular aldehyde metabolic process	0.56	>=0.20
GO:0043449	cellular alkene metabolic process	0.92	>=0.20
GO:0042401	cellular biogenic amine biosynthetic process	1	>=0.20
GO:0006874	cellular calcium ion homeostasis	0.52	>=0.20
GO:0030003	cellular cation homeostasis	0.15	>=0.20
GO:0010927	cellular component assembly involved in morphogenesis	0.98	>=0.20
GO:0022411	cellular component disassembly	0.18	>=0.20
GO:0071845	cellular component disassembly at cellular level	0.26	>=0.20
GO:0006921	cellular component disassembly involved in apoptotic proces	0.13	>=0.20
GO:0043954	cellular component maintenance	1	>=0.20
GO:0006968	cellular defense response	0.9	>=0.20
GO:0072503	cellular divalent inorganic cation homeostasis	0.45	>=0.20
GO:0045123	cellular extravasation	0.72	>=0.20
GO:0006873	cellular ion homeostasis	0.72	>=0.20
GO:0034622	cellular macromolecular complex assembly	0.53	>=0.20
GO:0034623	cellular macromolecular complex disassembly	0.89	>=0.20
GO:0006944	cellular membrane fusion	0.45	>=0.20
GO:0006875	cellular metal ion homeostasis	0.22	>=0.20
GO:0042398	cellular modified amino acid biosynthetic process	0.96	>=0.20
GO:0033059	cellular pigmentation	0.99	>=0.20
GO:0044247	cellular polysaccharide catabolic process	0.14	>=0.20
GO:0071804	cellular potassium ion transport	1	>=0.20
GO:0048610	cellular process involved in reproduction	0.93	>=0.20
GO:0044257	cellular protein catabolic process	0.69	>=0.20
GO:0043623	cellular protein complex assembly	0.3	>=0.20

GO:0043624	cellular protein complex disassembly	0.98	>=0.20
GO:0045333	cellular respiration	1	>=0.20
GO:0071214	cellular response to abiotic stimulus	0.76	>=0.20
GO:0071230	cellular response to amino acid stimulus	0.99	>=0.20
GO:0071345	cellular response to cytokine stimulus	0.18	>=0.20
GO:0071359	cellular response to dsRNA	1	>=0.20
GO:0071496	cellular response to external stimulus	0.11	>=0.20
GO:0031668	cellular response to extracellular stimulus	0.31	>=0.20
GO:0044344	cellular response to fibroblast growth factor stimulus	0.41	>=0.20
GO:0071377	cellular response to glucagon stimulus	0.7	>=0.20
GO:0071363	cellular response to growth factor stimulus	0.4	>=0.20
GO:0070301	cellular response to hydrogen peroxide	0.13	>=0.20
GO:0071241	cellular response to inorganic substance	0.06	>=0.20
GO:0071346	cellular response to interferon-gamma	0.91	>=0.20
GO:0071347	cellular response to interleukin-1	0.84	>=0.20
GO:0071260	cellular response to mechanical stimulus	0.69	>=0.20
GO:0071248	cellular response to metal ion	0.07	>=0.20
GO:0031670	cellular response to nutrient	0.93	>=0.20
GO:0031669	cellular response to nutrient levels	0.46	>=0.20
GO:0034599	cellular response to oxidative stress	0.11	>=0.20
GO:0034614	cellular response to reactive oxygen species	0.18	>=0.20
GO:0009267	cellular response to starvation	0.4	>=0.20
GO:0035967	cellular response to topologically incorrect protein	0.96	>=0.20
GO:0071356	cellular response to tumor necrosis factor	0.46	>=0.20
GO:0071357	cellular response to type I interferon	0.99	>=0.20
GO:0034620	cellular response to unfolded protein	0.97	>=0.20
GO:0035924	cellular response to vascular endothelial growth factor stimu	0.16	>=0.20
GO:0071295	cellular response to vitamin	1	>=0.20
GO:0071305	cellular response to vitamin D	0.9	>=0.20
GO:0034080	CenH3-containing nucleosome assembly at centromere	0.99	>=0.20
ENSG00000115163	CENPA PPI subnetwork	0.71	>=0.20
ENSG00000145241	CENPC1 PPI subnetwork	0.62	>=0.20
ENSG00000138778	CENPE PPI subnetwork	0.78	>=0.20
ENSG00000153044	CENPH PPI subnetwork	0.78	>=0.20
ENSG00000102384	CENPI PPI subnetwork	0.8	>=0.20
ENSG00000123219	CENPK PPI subnetwork	0.82	>=0.20
ENSG00000120334	CENPL PPI subnetwork	0.76	>=0.20
ENSG00000100162	CENPM PPI subnetwork	0.82	>=0.20
ENSG00000166451	CENPN PPI subnetwork	0.82	>=0.20
ENSG00000138092	CENPO PPI subnetwork	0.82	>=0.20
ENSG00000188312	CENPP PPI subnetwork	0.8	>=0.20
ENSG00000031691	CENPQ PPI subnetwork	0.8	>=0.20
ENSG00000102901	CENPT PPI subnetwork	0.88	>=0.20
GO:0022010	central nervous system myelination	0.99	>=0.20
GO:0021955	central nervous system neuron axonogenesis	1	>=0.20
GO:0021954	central nervous system neuron development	1	>=0.20
GO:0021953	central nervous system neuron differentiation	1	>=0.20

GO:0021952	central nervous system projection neuron axonogenesis	1	>=0.20
MP:0009404	centrally nucleated skeletal muscle fibers	0.55	>=0.20
GO:0005814	centriole	0.73	>=0.20
GO:0007099	centriole replication	0.97	>=0.20
GO:0005721	centromeric heterochromatin	0.08	>=0.20
GO:0005813	centrosome	0.27	>=0.20
GO:0007098	centrosome cycle	0.82	>=0.20
GO:0051298	centrosome duplication	0.94	>=0.20
GO:0051297	centrosome organization	0.95	>=0.20
ENSG00000126001	CEP250 PPI subnetwork	0.08	>=0.20
ENSG00000138180	CEP55 PPI subnetwork	0.58	>=0.20
ENSG00000114107	CEP70 PPI subnetwork	0.6	>=0.20
ENSG00000134255	CEPT1 PPI subnetwork	0.16	>=0.20
ENSG00000147869	CER1 PPI subnetwork	1	>=0.20
GO:0046513	ceramide biosynthetic process	0.99	>=0.20
GO:0006672	ceramide metabolic process	0.6	>=0.20
GO:0021697	cerebellar cortex formation	0.75	>=0.20
GO:0021549	cerebellum development	0.74	>=0.20
GO:0021795	cerebral cortex cell migration	0.83	>=0.20
GO:0021987	cerebral cortex development	0.99	>=0.20
GO:0021895	cerebral cortex neuron differentiation	1	>=0.20
GO:0021799	cerebral cortex radially oriented cell migration	0.65	>=0.20
MP:0004620	cervical vertebral fusion	0.99	>=0.20
MP:0004615	cervical vertebral transformation	0.77	>=0.20
ENSG00000153140	CETN3 PPI subnetwork	0.95	>=0.20
ENSG00000153774	CFDP1 PPI subnetwork	0.28	>=0.20
ENSG00000172757	CFL1 PPI subnetwork	0.17	>=0.20
ENSG00000165410	CFL2 PPI subnetwork	0.26	>=0.20
ENSG00000003402	CFLAR PPI subnetwork	0.6	>=0.20
ENSG00000001626	CFTR PPI subnetwork	0.07	>=0.20
GO:0030553	cGMP binding	0.89	>=0.20
GO:0006182	cGMP biosynthetic process	1	>=0.20
ENSG00000143375	CGN PPI subnetwork	0.05	>=0.20
ENSG00000167670	CHAF1A PPI subnetwork	0.1	>=0.20
ENSG00000159259	CHAF1B PPI subnetwork	0.67	>=0.20
ENSG00000198824	CHAMP1 PPI subnetwork	0.07	>=0.20
GO:0015267	channel activity	1	>=0.20
GO:0016247	channel regulator activity	0.98	>=0.20
GO:0061077	chaperone-mediated protein folding	0.86	>=0.20
GO:0051087	chaperone binding	0.36	>=0.20
GO:0051085	chaperone mediated protein folding requiring cofactor	0.95	>=0.20
ENSG00000106554	CHCHD3 PPI subnetwork	0.51	>=0.20
ENSG00000153922	CHD1 PPI subnetwork	0.04	>=0.20
ENSG00000170004	CHD3 PPI subnetwork	0.64	>=0.20
ENSG00000177200	CHD9 PPI subnetwork	0.43	>=0.20
ENSG00000149554	CHEK1 PPI subnetwork	0.42	>=0.20
ENSG00000183765	CHEK2 PPI subnetwork	0.2	>=0.20

GO:0042056	chemoattractant activity	0.46	>=0.20
GO:0008009	chemokine activity	0.06	>=0.20
GO:0042033	chemokine biosynthetic process	1	>=0.20
GO:0050755	chemokine metabolic process	0.93	>=0.20
GO:0032602	chemokine production	0.81	>=0.20
GO:0004950	chemokine receptor activity	0.47	>=0.20
GO:0042379	chemokine receptor binding	0.04	>=0.20
ENSG00000085872	CHERP PPI subnetwork	0.25	>=0.20
GO:0005254	chloride channel activity	1	>=0.20
GO:0034707	chloride channel complex	1	>=0.20
GO:0015108	chloride transmembrane transporter activity	0.19	>=0.20
GO:0006821	chloride transport	1	>=0.20
ENSG00000188419	CHM PPI subnetwork	0.07	>=0.20
ENSG00000115561	CHMP3 PPI subnetwork	1	>=0.20
ENSG00000101421	CHMP4B PPI subnetwork	0.71	>=0.20
ENSG00000176108	CHMP6 PPI subnetwork	0.81	>=0.20
GO:0002063	chondrocyte development	0.96	>=0.20
GO:0002062	chondrocyte differentiation	0.66	>=0.20
MP:0002657	chondrodystrophy	0.84	>=0.20
GO:0030204	chondroitin sulfate metabolic process	0.61	>=0.20
GO:0050654	chondroitin sulfate proteoglycan metabolic process	0.47	>=0.20
GO:0043009	chordate embryonic development	0.64	>=0.20
ENSG00000168539	CHRM1 PPI subnetwork	0.98	>=0.20
ENSG00000181072	CHRM2 PPI subnetwork	1	>=0.20
GO:0031497	chromatin assembly	0.96	>=0.20
GO:0006333	chromatin assembly or disassembly	0.9	>=0.20
GO:0003682	chromatin binding	0.13	>=0.20
GO:0031498	chromatin disassembly	0.66	>=0.20
GO:0031490	chromatin DNA binding	0.42	>=0.20
GO:0016568	chromatin modification	0.25	>=0.20
GO:0006325	chromatin organization	0.32	>=0.20
GO:0006338	chromatin remodeling	0.3	>=0.20
GO:0031055	chromatin remodeling at centromere	0.99	>=0.20
GO:0016585	chromatin remodeling complex	0.14	>=0.20
GO:0006342	chromatin silencing	0.78	>=0.20
MP:0008866	chromosomal instability	0.99	>=0.20
GO:0044427	chromosomal part	0.15	>=0.20
MP:0004028	chromosome breakage	0.54	>=0.20
GO:0030261	chromosome condensation	0.44	>=0.20
GO:0050000	chromosome localization	0.98	>=0.20
GO:0070192	chromosome organization involved in meiosis	1	>=0.20
GO:0007059	chromosome segregation	0.88	>=0.20
GO:0000775	chromosome, centromeric region	0.5	>=0.20
GO:0000781	chromosome, telomeric region	0.82	>=0.20
GO:0002544	chronic inflammatory response	0.64	>=0.20
ENSG00000127586	CHTF18 PPI subnetwork	0.96	>=0.20
ENSG00000144021	CIAO1 PPI subnetwork	0.2	>=0.20

ENSG00000005194	CIAPIN1 PPI subnetwork	0.97	>=0.20
GO:0001539	ciliary or flagellar motility	0.98	>=0.20
GO:0035253	ciliary rootlet	0.98	>=0.20
GO:0005929	cilium	0.98	>=0.20
GO:0042384	cilium assembly	0.99	>=0.20
GO:0035085	cilium axoneme	0.99	>=0.20
GO:0060271	cilium morphogenesis	0.99	>=0.20
GO:0044441	cilium part	1	>=0.20
ENSG00000138433	CIR1 PPI subnetwork	0.12	>=0.20
ENSG00000099622	CIRBP PPI subnetwork	0.27	>=0.20
GO:0007623	circadian rhythm	0.5	>=0.20
GO:0042745	circadian sleep/wake cycle	0.99	>=0.20
MP:0001394	circling	0.97	>=0.20
GO:0003013	circulatory system process	0.04	>=0.20
GO:0005801	cis-Golgi network	0.61	>=0.20
GO:0016859	cis-trans isomerase activity	0.07	>=0.20
ENSG00000114737	CISH PPI subnetwork	0.06	>=0.20
ENSG00000122966	CIT PPI subnetwork	0.22	>=0.20
ENSG00000164442	CITED2 PPI subnetwork	0.46	>=0.20
ENSG00000136026	CKAP4 PPI subnetwork	0.77	>=0.20
ENSG00000175216	CKAP5 PPI subnetwork	0.91	>=0.20
ENSG00000104879	CKM PPI subnetwork	0.42	>=0.20
ENSG00000074054	CLASP1 PPI subnetwork	0.22	>=0.20
ENSG00000163539	CLASP2 PPI subnetwork	0.86	>=0.20
GO:0030136	clathrin-coated vesicle	0.46	>=0.20
GO:0030118	clathrin coat	0.04	>=0.20
GO:0030665	clathrin coated vesicle membrane	0.99	>=0.20
GO:0060198	clathrin sculpted vesicle	0.99	>=0.20
GO:0030125	clathrin vesicle coat	0.23	>=0.20
ENSG00000175505	CLCF1 PPI subnetwork	0.06	>=0.20
ENSG00000013297	CLDN11 PPI subnetwork	0.1	>=0.20
GO:0032154	cleavage furrow	0.58	>=0.20
MP:0000111	cleft palate	0.99	>=0.20
MP:0009890	cleft secondary palate	0.98	>=0.20
ENSG00000130779	CLIP1 PPI subnetwork	0.7	>=0.20
ENSG00000106665	CLIP2 PPI subnetwork	0.95	>=0.20
ENSG00000113240	CLK4 PPI subnetwork	0.03	>=0.20
ENSG00000074201	CLNS1A PPI subnetwork	0.67	>=0.20
ENSG00000134852	CLOCK PPI subnetwork	0.37	>=0.20
MP:0003996	clonic seizures	1	>=0.20
ENSG00000172409	CLP1 PPI subnetwork	0.04	>=0.20
ENSG00000162129	CLPB PPI subnetwork	0.89	>=0.20
ENSG00000171603	CLSTN1 PPI subnetwork	0.9	>=0.20
ENSG00000139182	CLSTN3 PPI subnetwork	0.87	>=0.20
ENSG00000122705	CLTA PPI subnetwork	0.23	>=0.20
ENSG00000175416	CLTB PPI subnetwork	0.1	>=0.20
ENSG00000141367	CLTC PPI subnetwork	0.29	>=0.20

ENSG00000070371	CLTCL1 PPI subnetwork	0.04	>=0.20
ENSG00000120885	CLU PPI subnetwork	0.16	>=0.20
ENSG00000103351	CLUAP1 PPI subnetwork	0.89	>=0.20
ENSG00000169714	CNBP PPI subnetwork	0.36	>=0.20
ENSG00000133313	CNDP2 PPI subnetwork	0.09	>=0.20
ENSG00000143771	CNIH4 PPI subnetwork	0.49	>=0.20
ENSG00000142675	CNKSR1 PPI subnetwork	0.23	>=0.20
ENSG00000149970	CNKSR2 PPI subnetwork	1	>=0.20
ENSG00000130176	CNN1 PPI subnetwork	0.76	>=0.20
ENSG00000080802	CNOT4 PPI subnetwork	0.83	>=0.20
ENSG00000113300	CNOT6 PPI subnetwork	0.03	>=0.20
ENSG00000198791	CNOT7 PPI subnetwork	0.59	>=0.20
ENSG00000155508	CNOT8 PPI subnetwork	0.08	>=0.20
ENSG00000173786	CNP PPI subnetwork	1	>=0.20
MP:0006082	CNS inflammation	0.82	>=0.20
ENSG00000122756	CNTFR PPI subnetwork	0.35	>=0.20
ENSG00000018236	CNTN1 PPI subnetwork	0.97	>=0.20
ENSG00000108797	CNTNAP1 PPI subnetwork	0.89	>=0.20
ENSG00000174469	CNTNAP2 PPI subnetwork	0.86	>=0.20
GO:0048475	coated membrane	0.12	>=0.20
GO:0030135	coated vesicle	0.29	>=0.20
GO:0030662	coated vesicle membrane	0.83	>=0.20
GO:0090102	cochlea development	1	>=0.20
GO:0090103	cochlea morphogenesis	0.99	>=0.20
MP:0002857	cochlear ganglion degeneration	0.78	>=0.20
MP:0004362	cochlear hair cell degeneration	0.2	>=0.20
MP:0004398	cochlear inner hair cell degeneration	0.76	>=0.20
MP:0004404	cochlear outer hair cell degeneration	0.61	>=0.20
GO:0009109	coenzyme catabolic process	0.85	>=0.20
GO:0051187	cofactor catabolic process	0.7	>=0.20
ENSG00000136152	COG3 PPI subnetwork	0.22	>=0.20
ENSG00000103051	COG4 PPI subnetwork	0.21	>=0.20
ENSG00000164597	COG5 PPI subnetwork	0.41	>=0.20
ENSG00000133103	COG6 PPI subnetwork	0.2	>=0.20
ENSG00000213380	COG8 PPI subnetwork	0.73	>=0.20
GO:0050890	cognition	1	>=0.20
GO:0008278	cohesin complex	0.97	>=0.20
MP:0009238	coiled sperm flagellum	0.94	>=0.20
ENSG00000065618	COL17A1 PPI subnetwork	0.37	>=0.20
ENSG00000108821	COL1A1 PPI subnetwork	0.32	>=0.20
ENSG00000139219	COL2A1 PPI subnetwork	0.18	>=0.20
ENSG00000168542	COL3A1 PPI subnetwork	0.97	>=0.20
ENSG00000169031	COL4A3 PPI subnetwork	0.72	>=0.20
ENSG00000081052	COL4A4 PPI subnetwork	0.26	>=0.20
ENSG00000188153	COL4A5 PPI subnetwork	0.06	>=0.20
ENSG00000142156	COL6A1 PPI subnetwork	0.52	>=0.20
ENSG00000114270	COL7A1 PPI subnetwork	0.52	>=0.20

GO:0005581	collagen	0.42	>=0.20
GO:0005518	collagen binding	0.08	>=0.20
GO:0032964	collagen biosynthetic process	0.44	>=0.20
GO:0030574	collagen catabolic process	0.99	>=0.20
GO:0030199	collagen fibril organization	1	>=0.20
GO:0032963	collagen metabolic process	0.62	>=0.20
ENSG00000173163	COMMD1 PPI subnetwork	0.76	>=0.20
ENSG00000145781	COMMD10 PPI subnetwork	0.26	>=0.20
ENSG00000105664	COMP PPI subnetwork	0.78	>=0.20
GO:0043218	compact myelin	0.99	>=0.20
MP:0011093	complete embryonic lethality at implantation	0.13	>=0.20
MP:0011094	complete embryonic lethality before implantation	0.1	>=0.20
MP:0011083	complete lethality at weaning	0.89	>=0.20
MP:0011087	complete neonatal lethality	0.77	>=0.20
MP:0011089	complete perinatal lethality	0.67	>=0.20
MP:0011085	complete postnatal lethality	0.49	>=0.20
MP:0011100	complete preweaning lethality	0.26	>=0.20
GO:0000793	condensed chromosome	0.64	>=0.20
GO:0000777	condensed chromosome kinetochore	0.75	>=0.20
GO:0000940	condensed chromosome outer kinetochore	0.73	>=0.20
GO:0000779	condensed chromosome, centromeric region	0.69	>=0.20
GO:0000794	condensed nuclear chromosome	0.81	>=0.20
GO:0000780	condensed nuclear chromosome, centromeric region	0.82	>=0.20
MP:0006138	congestive heart failure	0.18	>=0.20
GO:0005922	connexon complex	0.27	>=0.20
GO:0043292	contractile fiber	0.75	>=0.20
GO:0044449	contractile fiber part	0.79	>=0.20
GO:0060026	convergent extension	1	>=0.20
MP:0000947	convulsive seizures	1	>=0.20
ENSG00000122218	COPA PPI subnetwork	0.04	>=0.20
ENSG00000129083	COPB1 PPI subnetwork	0.15	>=0.20
ENSG00000105669	COPE PPI subnetwork	0.28	>=0.20
ENSG00000181789	COPG PPI subnetwork	0.39	>=0.20
ENSG00000158623	COPG2 PPI subnetwork	0.33	>=0.20
GO:0030137	COPI-coated vesicle	0.34	>=0.20
GO:0035964	COPI-coated vesicle budding	0.46	>=0.20
GO:0030663	COPI coated vesicle membrane	0.06	>=0.20
GO:0048205	COPI coating of Golgi vesicle	0.46	>=0.20
GO:0030126	COPI vesicle coat	0.12	>=0.20
ENSG00000138663	COPS4 PPI subnetwork	0.51	>=0.20
ENSG00000121022	COPS5 PPI subnetwork	0.39	>=0.20
ENSG00000168090	COPS6 PPI subnetwork	0.09	>=0.20
ENSG00000111652	COPS7A PPI subnetwork	0.91	>=0.20
ENSG00000198612	COPS8 PPI subnetwork	0.87	>=0.20
ENSG00000111481	COPZ1 PPI subnetwork	0.07	>=0.20
GO:0001047	core promoter binding	0.52	>=0.20
GO:0001046	core promoter sequence-specific DNA binding	0.81	>=0.20

GO:0015026	coreceptor activity	0.18	>=0.20
MP:0001314	corneal opacity	0.77	>=0.20
MP:0005543	corneal thinning	0.93	>=0.20
MP:0005542	corneal vascularization	0.5	>=0.20
GO:0001533	cornified envelope	0.67	>=0.20
ENSG00000172725	CORO1B PPI subnetwork	0.69	>=0.20
ENSG00000110880	CORO1C PPI subnetwork	0.49	>=0.20
ENSG00000167549	CORO6 PPI subnetwork	0.6	>=0.20
GO:0030864	cortical actin cytoskeleton	0.44	>=0.20
GO:0030863	cortical cytoskeleton	0.19	>=0.20
GO:0043034	costamere	0.92	>=0.20
GO:0006613	cotranslational protein targeting to membrane	0.71	>=0.20
GO:0016569	covalent chromatin modification	0.34	>=0.20
ENSG00000131143	COX4I1 PPI subnetwork	1	>=0.20
ENSG00000178741	COX5A PPI subnetwork	0.99	>=0.20
ENSG00000135940	COX5B PPI subnetwork	0.91	>=0.20
ENSG00000126267	COX6B1 PPI subnetwork	0.95	>=0.20
ENSG00000164919	COX6C PPI subnetwork	1	>=0.20
ENSG00000127184	COX7C PPI subnetwork	1	>=0.20
ENSG00000109472	CPE PPI subnetwork	0.99	>=0.20
ENSG00000071894	CPSF1 PPI subnetwork	0.07	>=0.20
ENSG00000160917	CPSF4 PPI subnetwork	0.08	>=0.20
ENSG00000117322	CR2 PPI subnetwork	0.45	>=0.20
GO:0021545	cranial nerve development	1	>=0.20
GO:0021602	cranial nerve morphogenesis	1	>=0.20
GO:0060363	cranial suture morphogenesis	1	>=0.20
GO:0097094	craniofacial suture morphogenesis	1	>=0.20
ENSG00000134376	CRB1 PPI subnetwork	0.92	>=0.20
ENSG00000118260	CREB1 PPI subnetwork	0.22	>=0.20
ENSG00000182809	CRIP2 PPI subnetwork	0.23	>=0.20
ENSG00000167193	CRK PPI subnetwork	0.94	>=0.20
ENSG00000099942	CRKL PPI subnetwork	0.14	>=0.20
ENSG00000105662	CRTC1 PPI subnetwork	0.08	>=0.20
ENSG00000109846	CRYAB PPI subnetwork	0.41	>=0.20
MP:0002286	cryptorchism	0.98	>=0.20
ENSG00000009307	CSDE1 PPI subnetwork	0.23	>=0.20
ENSG00000124207	CSE1L PPI subnetwork	0.23	>=0.20
ENSG00000184371	CSF1 PPI subnetwork	0.4	>=0.20
ENSG00000182578	CSF1R PPI subnetwork	0.07	>=0.20
ENSG00000164400	CSF2 PPI subnetwork	0.1	>=0.20
ENSG00000198223	CSF2RA PPI subnetwork	0.22	>=0.20
ENSG00000100368	CSF2RB PPI subnetwork	0.09	>=0.20
ENSG00000108342	CSF3 PPI subnetwork	0.12	>=0.20
ENSG00000119535	CSF3R PPI subnetwork	0.1	>=0.20
ENSG00000136488	CSH1 PPI subnetwork	0.06	>=0.20
ENSG00000183117	CSMD1 PPI subnetwork	0.3	>=0.20
ENSG00000113712	CSNK1A1 PPI subnetwork	0.12	>=0.20

ENSG00000180138	CSNK1A1L PPI subnetwork	0.71	>=0.20
ENSG00000204435	CSNK2B PPI subnetwork	0.13	>=0.20
ENSG00000206406	CSNK2B PPI subnetwork	0.13	>=0.20
ENSG00000129170	CSRP3 PPI subnetwork	0.3	>=0.20
ENSG00000121552	CSTA PPI subnetwork	0.37	>=0.20
ENSG00000160213	CSTB PPI subnetwork	0.07	>=0.20
ENSG00000101811	CSTF2 PPI subnetwork	0.04	>=0.20
ENSG00000159692	CTBP1 PPI subnetwork	0.15	>=0.20
ENSG00000175029	CTBP2 PPI subnetwork	0.37	>=0.20
ENSG00000102974	CTCF PPI subnetwork	0.62	>=0.20
ENSG00000060069	CTDP1 PPI subnetwork	0.04	>=0.20
ENSG00000150281	CTF1 PPI subnetwork	0.12	>=0.20
ENSG00000118523	CTGF PPI subnetwork	0.73	>=0.20
ENSG00000116761	CTH PPI subnetwork	0.83	>=0.20
ENSG00000044115	CTNNA1 PPI subnetwork	0.4	>=0.20
ENSG00000066032	CTNNA2 PPI subnetwork	0.8	>=0.20
ENSG00000168036	CTNNB1 PPI subnetwork	0.23	>=0.20
ENSG00000178585	CTNNBIP1 PPI subnetwork	0.05	>=0.20
ENSG00000198561	CTNND1 PPI subnetwork	0.12	>=0.20
ENSG00000198730	CTR9 PPI subnetwork	0.19	>=0.20
ENSG00000064601	CTSA PPI subnetwork	0.05	>=0.20
ENSG00000085733	CTTN PPI subnetwork	0.44	>=0.20
ENSG00000077063	CTTNBP2 PPI subnetwork	0.26	>=0.20
ENSG00000143079	CTTNBP2NL PPI subnetwork	0.33	>=0.20
ENSG00000055130	CUL1 PPI subnetwork	0.24	>=0.20
ENSG00000108094	CUL2 PPI subnetwork	0.47	>=0.20
ENSG00000036257	CUL3 PPI subnetwork	0.85	>=0.20
GO:0080008	CUL4 RING ubiquitin ligase complex	1	>=0.20
ENSG00000139842	CUL4A PPI subnetwork	0.94	>=0.20
ENSG00000158290	CUL4B PPI subnetwork	0.77	>=0.20
ENSG00000166266	CUL5 PPI subnetwork	0.55	>=0.20
GO:0031461	cullin-RING ubiquitin ligase complex	0.59	>=0.20
MP:0003051	curly tail	0.76	>=0.20
ENSG00000107562	CXCL12 PPI subnetwork	0.57	>=0.20
ENSG00000163464	CXCR1 PPI subnetwork	0.17	>=0.20
ENSG00000180871	CXCR2 PPI subnetwork	0.47	>=0.20
ENSG00000186810	CXCR3 PPI subnetwork	0.51	>=0.20
MP:0001575	cyanosis	0.34	>=0.20
ENSG00000159348	CYB5R1 PPI subnetwork	0.44	>=0.20
ENSG00000179091	CYC1 PPI subnetwork	0.89	>=0.20
GO:0019935	cyclic-nucleotide-mediated signaling	0.95	>=0.20
GO:0004112	cyclic-nucleotide phosphodiesterase activity	0.55	>=0.20
GO:0004690	cyclic nucleotide-dependent protein kinase activity	0.22	>=0.20
GO:0030551	cyclic nucleotide binding	0.66	>=0.20
GO:0009190	cyclic nucleotide biosynthetic process	1	>=0.20
GO:0009214	cyclic nucleotide catabolic process	0.67	>=0.20
GO:0009187	cyclic nucleotide metabolic process	0.99	>=0.20

GO:0000307	cyclin-dependent protein kinase holoenzyme complex	0.9	>=0.20
ENSG00000068793	CYFIP1 PPI subnetwork	0.93	>=0.20
ENSG00000055163	CYFIP2 PPI subnetwork	0.77	>=0.20
ENSG00000142871	CYR61 PPI subnetwork	0.15	>=0.20
GO:0008656	cysteine-type endopeptidase activator activity involved in ap	0.95	>=0.20
GO:0043028	cysteine-type endopeptidase regulator activity involved in ap	0.83	>=0.20
GO:0004129	cytochrome-c oxidase activity	0.99	>=0.20
GO:0019221	cytokine-mediated signaling pathway	0.24	>=0.20
GO:0005125	cytokine activity	0.36	>=0.20
GO:0019955	cytokine binding	0.03	>=0.20
GO:0042089	cytokine biosynthetic process	0.09	>=0.20
GO:0002367	cytokine production involved in immune response	0.52	>=0.20
GO:0004896	cytokine receptor activity	0.2	>=0.20
GO:0005126	cytokine receptor binding	0.15	>=0.20
GO:0050663	cytokine secretion	0.5	>=0.20
GO:0000910	cytokinesis	0.93	>=0.20
GO:0005868	cytoplasmic dynein complex	0.74	>=0.20
GO:0005881	cytoplasmic microtubule	0.48	>=0.20
GO:0000932	cytoplasmic mRNA processing body	0.22	>=0.20
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	0.66	>=0.20
GO:0030659	cytoplasmic vesicle membrane	0.91	>=0.20
GO:0008093	cytoskeletal adaptor activity	0.3	>=0.20
GO:0030705	cytoskeleton-dependent intracellular transport	1	>=0.20
GO:0051480	cytosolic calcium ion homeostasis	0.77	>=0.20
GO:0022625	cytosolic large ribosomal subunit	0.67	>=0.20
GO:0044445	cytosolic part	0.2	>=0.20
GO:0022626	cytosolic ribosome	0.86	>=0.20
GO:0022627	cytosolic small ribosomal subunit	0.92	>=0.20
ENSG00000153071	DAB2 PPI subnetwork	0.39	>=0.20
ENSG00000165659	DACH1 PPI subnetwork	0.98	>=0.20
ENSG00000129562	DAD1 PPI subnetwork	0.94	>=0.20
ENSG00000173402	DAG1 PPI subnetwork	0.6	>=0.20
GO:0003684	damaged DNA binding	0.96	>=0.20
ENSG00000196730	DAPK1 PPI subnetwork	0.98	>=0.20
ENSG00000167657	DAPK3 PPI subnetwork	0.16	>=0.20
ENSG00000204209	DAXX PPI subnetwork	0.24	>=0.20
ENSG00000206206	DAXX PPI subnetwork	0.24	>=0.20
ENSG00000206279	DAXX PPI subnetwork	0.24	>=0.20
ENSG00000006634	DBF4 PPI subnetwork	0.93	>=0.20
ENSG00000137992	DBT PPI subnetwork	0.46	>=0.20
ENSG00000136485	DCAF7 PPI subnetwork	0.13	>=0.20
ENSG00000156136	DCK PPI subnetwork	0.56	>=0.20
ENSG00000133083	DCLK1 PPI subnetwork	1	>=0.20
ENSG00000011465	DCN PPI subnetwork	0.16	>=0.20
ENSG00000151065	DCP1B PPI subnetwork	0.59	>=0.20
ENSG00000204843	DCTN1 PPI subnetwork	0.42	>=0.20
ENSG00000175203	DCTN2 PPI subnetwork	0.84	>=0.20

ENSG00000179958	DCTPP1 PPI subnetwork	0.44	>=0.20
ENSG00000167986	DDB1 PPI subnetwork	0.49	>=0.20
ENSG00000134574	DDB2 PPI subnetwork	0.65	>=0.20
ENSG00000013573	DDX11 PPI subnetwork	1	>=0.20
ENSG00000100201	DDX17 PPI subnetwork	0.33	>=0.20
ENSG00000157349	DDX19B PPI subnetwork	0.9	>=0.20
ENSG00000064703	DDX20 PPI subnetwork	0.13	>=0.20
ENSG00000089737	DDX24 PPI subnetwork	0.69	>=0.20
ENSG00000124228	DDX27 PPI subnetwork	0.5	>=0.20
ENSG00000215301	DDX3X PPI subnetwork	0.08	>=0.20
ENSG00000198231	DDX42 PPI subnetwork	0.92	>=0.20
ENSG00000145833	DDX46 PPI subnetwork	0.3	>=0.20
ENSG00000107625	DDX50 PPI subnetwork	0.61	>=0.20
ENSG00000123064	DDX54 PPI subnetwork	0.85	>=0.20
ENSG00000111364	DDX55 PPI subnetwork	0.7	>=0.20
ENSG00000136271	DDX56 PPI subnetwork	0.83	>=0.20
ENSG00000110367	DDX6 PPI subnetwork	0.51	>=0.20
MP:0001967	deafness	0.49	>=0.20
GO:0005035	death receptor activity	0.73	>=0.20
GO:0046697	decidualization	0.22	>=0.20
ENSG00000104325	DECR1 PPI subnetwork	0.26	>=0.20
MP:0005656	decreased aggression	0.85	>=0.20
MP:0003862	decreased aggression towards males	1	>=0.20
MP:0002335	decreased airway responsiveness	0.1	>=0.20
MP:0001364	decreased anxiety-related response	0.99	>=0.20
MP:0004978	decreased B-1 B cell number	0.15	>=0.20
MP:0008168	decreased B-1a cell number	0.27	>=0.20
MP:0005093	decreased B cell proliferation	0.07	>=0.20
MP:0009703	decreased birth body size	0.19	>=0.20
MP:0005566	decreased blood urea nitrogen level	0.9	>=0.20
MP:0010124	decreased bone mineral content	0.15	>=0.20
MP:0000063	decreased bone mineral density	0.2	>=0.20
MP:0004993	decreased bone resorption	0.21	>=0.20
MP:0000774	decreased brain size	0.66	>=0.20
MP:0004765	decreased brainstem auditory evoked potential	0.99	>=0.20
MP:0005140	decreased cardiac muscle contractility	0.19	>=0.20
MP:0001539	decreased caudal vertebrae number	0.88	>=0.20
MP:0008075	decreased CD4-positive T cell number	0.04	>=0.20
MP:0008079	decreased CD8-positive T cell number	0.16	>=0.20
MP:0001982	decreased chemically-elicited antinociception	0.99	>=0.20
MP:0000167	decreased chondrocyte cell number	0.25	>=0.20
MP:0002664	decreased circulating adrenocorticotropin level	0.65	>=0.20
MP:0002696	decreased circulating glucagon level	0.79	>=0.20
MP:0008578	decreased circulating interferon-gamma level	0.15	>=0.20
MP:0008642	decreased circulating interleukin-1 beta level	0.16	>=0.20
MP:0008603	decreased circulating interleukin-4 level	0.72	>=0.20
MP:0003148	decreased cochlear coiling	1	>=0.20

MP:0000135	decreased compact bone thickness	0.19	>=0.20
MP:0000781	decreased corpus callosum size	1	>=0.20
MP:0008525	decreased cranium height	0.31	>=0.20
MP:0008127	decreased dendritic cell number	0.34	>=0.20
MP:0011448	decreased dopaminergic neuron number	0.72	>=0.20
MP:0005089	decreased double-negative T cell number	0.18	>=0.20
MP:0005092	decreased double-positive T cell number	0.04	>=0.20
MP:0003910	decreased eating behavior	0.31	>=0.20
MP:0005012	decreased eosinophil cell number	0.25	>=0.20
MP:0001417	decreased exploration in new environment	0.94	>=0.20
MP:0008174	decreased follicular B cell number	0.04	>=0.20
MP:0008347	decreased gamma-delta T cell number	0.89	>=0.20
MP:0000334	decreased granulocyte number	0.93	>=0.20
MP:0010053	decreased grip strength	0.77	>=0.20
MP:0005136	decreased growth hormone level	0.99	>=0.20
MP:0000379	decreased hair follicle number	0.11	>=0.20
MP:0005333	decreased heart rate	0.33	>=0.20
MP:0001807	decreased IgA level	0.76	>=0.20
MP:0002492	decreased IgE level	0.51	>=0.20
MP:0001805	decreased IgG level	0.11	>=0.20
MP:0008495	decreased IgG1 level	0.24	>=0.20
MP:0008496	decreased IgG2a level	0.58	>=0.20
MP:0008497	decreased IgG2b level	0.63	>=0.20
MP:0008498	decreased IgG3 level	0.56	>=0.20
MP:0001806	decreased IgM level	0.35	>=0.20
MP:0008215	decreased immature B cell number	0.05	>=0.20
MP:0002460	decreased immunoglobulin level	0.28	>=0.20
MP:0009038	decreased inferior colliculus size	0.99	>=0.20
MP:0001876	decreased inflammatory response	0.05	>=0.20
MP:0003059	decreased insulin secretion	0.71	>=0.20
MP:0008567	decreased interferon-gamma secretion	0.24	>=0.20
MP:0008658	decreased interleukin-1 beta secretion	0.09	>=0.20
MP:0008661	decreased interleukin-10 secretion	0.04	>=0.20
MP:0008670	decreased interleukin-12b secretion	0.03	>=0.20
MP:0008673	decreased interleukin-13 secretion	0.13	>=0.20
MP:0008682	decreased interleukin-17 secretion	0.67	>=0.20
MP:0008688	decreased interleukin-2 secretion	0.39	>=0.20
MP:0008700	decreased interleukin-4 secretion	0.53	>=0.20
MP:0008703	decreased interleukin-5 secretion	0.9	>=0.20
MP:0008332	decreased lactotroph cell number	0.77	>=0.20
MP:0004686	decreased length of long bones	0.05	>=0.20
MP:0003402	decreased liver weight	0.03	>=0.20
MP:0005016	decreased lymphocyte cell number	0.13	>=0.20
MP:0003884	decreased macrophage cell number	0.39	>=0.20
MP:0004901	decreased male germ cell number	0.98	>=0.20
MP:0008182	decreased marginal zone B cell number	0.12	>=0.20
MP:0000336	decreased mast cell number	0.07	>=0.20

MP:0008211	decreased mature B cell number	0.08	>=0.20
MP:0002682	decreased mature ovarian follicle number	0.52	>=0.20
MP:0004876	decreased mean systemic arterial blood pressure	0.61	>=0.20
MP:0008050	decreased memory T cell number	0.99	>=0.20
MP:0001273	decreased metastatic potential	0.15	>=0.20
MP:0006400	decreased molar number	1	>=0.20
MP:0000939	decreased motor neuron number	0.96	>=0.20
MP:0004567	decreased myocardial fiber number	0.64	>=0.20
MP:0011290	decreased nephron number	0.93	>=0.20
MP:0004981	decreased neuronal precursor cell number	0.87	>=0.20
MP:0003990	decreased neurotransmitter release	0.99	>=0.20
MP:0000222	decreased neutrophil cell number	0.17	>=0.20
MP:0008045	decreased NK cell number	0.58	>=0.20
MP:0008040	decreased NK T cell number	0.8	>=0.20
MP:0005431	decreased oocyte number	1	>=0.20
MP:0004989	decreased osteoblast cell number	0.23	>=0.20
MP:0004985	decreased osteoclast cell number	0.17	>=0.20
MP:0002920	decreased paired-pulse facilitation	1	>=0.20
MP:0003339	decreased pancreatic beta cell number	0.31	>=0.20
MP:0008133	decreased Peyer's patch number	0.91	>=0.20
MP:0008098	decreased plasma cell number	0.8	>=0.20
MP:0004725	decreased platelet serotonin level	0.92	>=0.20
MP:0009142	decreased prepulse inhibition	0.73	>=0.20
MP:0008392	decreased primordial germ cell number	0.85	>=0.20
MP:0000880	decreased Purkinje cell number	0.74	>=0.20
MP:0004974	decreased regulatory T cell number	0.11	>=0.20
MP:0004505	decreased renal glomerulus number	0.31	>=0.20
MP:0004486	decreased response of heart to induced stress	0.03	>=0.20
MP:0001327	decreased retinal photoreceptor cell number	0.86	>=0.20
MP:0003345	decreased rib number	0.93	>=0.20
MP:0009764	decreased sensitivity to induced morbidity/mortality	0.08	>=0.20
MP:0000966	decreased sensory neuron number	0.98	>=0.20
MP:0008083	decreased single-positive T cell number	0.97	>=0.20
MP:0004819	decreased skeletal muscle mass	0.2	>=0.20
MP:0003089	decreased skin tensile strength	0.6	>=0.20
MP:0008482	decreased spleen germinal center number	0.77	>=0.20
MP:0008479	decreased spleen white pulp amount	0.2	>=0.20
MP:0009339	decreased splenocyte number	0.11	>=0.20
MP:0001489	decreased startle reflex	0.99	>=0.20
MP:0005341	decreased susceptibility to atherosclerosis	0.04	>=0.20
MP:0004804	decreased susceptibility to autoimmune diabetes	0.09	>=0.20
MP:0004800	decreased susceptibility to experimental autoimmune encep	0.48	>=0.20
MP:0008539	decreased susceptibility to induced colitis	0.13	>=0.20
MP:0006059	decreased susceptibility to ischemic brain injury	0.14	>=0.20
MP:0005026	decreased susceptibility to parasitic infection	0.04	>=0.20
MP:0002887	decreased susceptibility to pharmacologically induced seizur	1	>=0.20
MP:0002410	decreased susceptibility to viral infection	0.05	>=0.20

MP:0009790	decreased susceptibility to viral infection induced morbidity/	0.35	>=0.20
MP:0005018	decreased T cell number	0.18	>=0.20
MP:0005095	decreased T cell proliferation	0.05	>=0.20
MP:0004852	decreased testis weight	0.53	>=0.20
MP:0003998	decreased thermal nociceptive threshold	0.94	>=0.20
MP:0000715	decreased thymocyte number	0.29	>=0.20
MP:0009907	decreased tongue size	1	>=0.20
MP:0008190	decreased transitional stage B cell number	0.06	>=0.20
MP:0003447	decreased tumor growth/size	0.11	>=0.20
MP:0006020	decreased tympanic ring size	1	>=0.20
MP:0002988	decreased urine osmolality	0.19	>=0.20
MP:0006317	decreased urine sodium level	0.22	>=0.20
MP:0005598	decreased ventricle muscle contractility	0.03	>=0.20
MP:0002757	decreased vertical activity	0.99	>=0.20
MP:0005079	defective cytotoxic T cell cytolysis	0.94	>=0.20
GO:0042742	defense response to bacterium	0.58	>=0.20
GO:0050832	defense response to fungus	0.95	>=0.20
GO:0051607	defense response to virus	0.33	>=0.20
GO:0060216	definitive hemopoiesis	0.93	>=0.20
MP:0001429	dehydration	0.42	>=0.20
ENSG00000124795	DEK PPI subnetwork	0.25	>=0.20
MP:0000060	delayed bone ossification	0.26	>=0.20
MP:0003419	delayed endochondral bone ossification	0.42	>=0.20
MP:0002621	delayed neural tube closure	0.7	>=0.20
GO:0005251	delayed rectifier potassium channel activity	0.93	>=0.20
MP:0002908	delayed wound healing	0.13	>=0.20
MP:0000921	demyelination	0.8	>=0.20
GO:0030425	dendrite	1	>=0.20
GO:0016358	dendrite development	1	>=0.20
GO:0048813	dendrite morphogenesis	1	>=0.20
GO:0002407	dendritic cell chemotaxis	0.74	>=0.20
GO:0043198	dendritic shaft	1	>=0.20
GO:0043197	dendritic spine	1	>=0.20
GO:0044327	dendritic spine head	1	>=0.20
GO:0060997	dendritic spine morphogenesis	0.99	>=0.20
GO:0097061	dendritic spine organization	0.99	>=0.20
ENSG00000174485	DENND4A PPI subnetwork	0.11	>=0.20
GO:0004536	deoxyribonuclease activity	0.99	>=0.20
GO:0009264	deoxyribonucleotide catabolic process	0.92	>=0.20
GO:0009262	deoxyribonucleotide metabolic process	0.99	>=0.20
ENSG00000100150	DEPDC5 PPI subnetwork	0.84	>=0.20
GO:0016311	dephosphorylation	0.6	>=0.20
ENSG00000175084	DES PPI subnetwork	0.33	>=0.20
GO:0030057	desmosome	0.59	>=0.20
GO:0009582	detection of abiotic stimulus	1	>=0.20
GO:0016045	detection of bacterium	0.29	>=0.20
GO:0009593	detection of chemical stimulus	0.81	>=0.20

GO:0050907	detection of chemical stimulus involved in sensory perceptio	0.96	>=0.20
GO:0050911	detection of chemical stimulus involved in sensory perceptio	0.97	>=0.20
GO:0050912	detection of chemical stimulus involved in sensory perceptio	0.94	>=0.20
GO:0009581	detection of external stimulus	1	>=0.20
GO:0009583	detection of light stimulus	1	>=0.20
GO:0050962	detection of light stimulus involved in sensory perception	0.81	>=0.20
GO:0050908	detection of light stimulus involved in visual perception	0.81	>=0.20
GO:0051606	detection of stimulus	0.97	>=0.20
GO:0050906	detection of stimulus involved in sensory perception	1	>=0.20
GO:0009584	detection of visible light	0.98	>=0.20
GO:0008340	determination of adult lifespan	1	>=0.20
GO:0009855	determination of bilateral symmetry	1	>=0.20
GO:0061371	determination of heart left/right asymmetry	0.93	>=0.20
GO:0007368	determination of left/right symmetry	0.99	>=0.20
GO:0046545	development of primary female sexual characteristics	0.62	>=0.20
GO:0046546	development of primary male sexual characteristics	0.81	>=0.20
GO:0045137	development of primary sexual characteristics	0.78	>=0.20
GO:0048588	developmental cell growth	0.93	>=0.20
GO:0048589	developmental growth	0.62	>=0.20
GO:0060560	developmental growth involved in morphogenesis	0.94	>=0.20
GO:0031128	developmental induction	1	>=0.20
GO:0021700	developmental maturation	0.6	>=0.20
GO:0048066	developmental pigmentation	0.98	>=0.20
GO:0003006	developmental process involved in reproduction	0.77	>=0.20
MP:0000644	dextrocardia	1	>=0.20
ENSG00000100056	DGCR14 PPI subnetwork	0.65	>=0.20
ENSG00000149091	DGKZ PPI subnetwork	0.16	>=0.20
ENSG00000139549	DHH PPI subnetwork	0.59	>=0.20
ENSG00000100867	DHRS2 PPI subnetwork	0.17	>=0.20
ENSG00000100612	DHRS7 PPI subnetwork	0.35	>=0.20
ENSG00000132153	DHX30 PPI subnetwork	0.11	>=0.20
ENSG00000135829	DHX9 PPI subnetwork	0.06	>=0.20
GO:0004143	diacylglycerol kinase activity	1	>=0.20
ENSG00000131504	DIAPH1 PPI subnetwork	0.35	>=0.20
ENSG00000147202	DIAPH2 PPI subnetwork	0.12	>=0.20
ENSG00000100697	DICER1 PPI subnetwork	0.35	>=0.20
GO:0021536	diencephalon development	1	>=0.20
GO:0007586	digestion	0.35	>=0.20
GO:0055123	digestive system development	0.99	>=0.20
GO:0048565	digestive tract development	1	>=0.20
GO:0048546	digestive tract morphogenesis	0.96	>=0.20
MP:0002795	dilated cardiomyopathy	0.27	>=0.20
MP:0003140	dilated heart atrium	0.62	>=0.20
MP:0002754	dilated heart right ventricle	0.05	>=0.20
MP:0000825	dilated lateral ventricles	0.84	>=0.20
MP:0009050	dilated proximal convoluted tubules	0.86	>=0.20
MP:0002705	dilated renal tubules	0.33	>=0.20

MP:0010856	dilated respiratory conducting tubes	0.98	>=0.20
MP:0000371	diluted coat color	0.32	>=0.20
GO:0034312	diol biosynthetic process	1	>=0.20
GO:0034311	diol metabolic process	0.99	>=0.20
GO:0016805	dipeptidase activity	0.72	>=0.20
GO:0008239	dipeptidyl-peptidase activity	0.84	>=0.20
ENSG00000165023	DIRAS2 PPI subnetwork	1	>=0.20
ENSG00000162946	DISC1 PPI subnetwork	0.92	>=0.20
MP:0006397	disorganized long bone epiphyseal plate	0.03	>=0.20
MP:0009254	disorganized pancreatic islets	0.74	>=0.20
MP:0008586	disorganized photoreceptor outer segment	0.66	>=0.20
MP:0001328	disorganized retinal layers	0.97	>=0.20
MP:0002427	disproportionate dwarf	0.14	>=0.20
MP:0001270	distended abdomen	0.93	>=0.20
GO:0015036	disulfide oxidoreductase activity	0.07	>=0.20
GO:0072507	divalent inorganic cation homeostasis	0.34	>=0.20
GO:0072509	divalent inorganic cation transmembrane transporter activity	0.99	>=0.20
GO:0072511	divalent inorganic cation transport	1	>=0.20
GO:0070838	divalent metal ion transport	1	>=0.20
ENSG00000075711	DLG1 PPI subnetwork	1	>=0.20
ENSG00000150672	DLG2 PPI subnetwork	1	>=0.20
ENSG00000082458	DLG3 PPI subnetwork	1	>=0.20
ENSG00000132535	DLG4 PPI subnetwork	1	>=0.20
ENSG00000170579	DLGAP1 PPI subnetwork	0.96	>=0.20
ENSG00000198010	DLGAP2 PPI subnetwork	1	>=0.20
ENSG00000116544	DLGAP3 PPI subnetwork	0.7	>=0.20
ENSG00000119689	DLST PPI subnetwork	0.17	>=0.20
ENSG00000115844	DLX2 PPI subnetwork	0.99	>=0.20
ENSG00000105880	DLX5 PPI subnetwork	1	>=0.20
ENSG00000178028	DMAP1 PPI subnetwork	0.32	>=0.20
ENSG00000198947	DMD PPI subnetwork	0.99	>=0.20
GO:0008094	DNA-dependent ATPase activity	0.99	>=0.20
GO:0006261	DNA-dependent DNA replication	0.97	>=0.20
GO:0006270	DNA-dependent DNA replication initiation	0.98	>=0.20
GO:0003887	DNA-directed DNA polymerase activity	0.78	>=0.20
GO:0003899	DNA-directed RNA polymerase activity	0.98	>=0.20
GO:0000428	DNA-directed RNA polymerase complex	0.96	>=0.20
GO:0005665	DNA-directed RNA polymerase II, core complex	0.54	>=0.20
GO:0016591	DNA-directed RNA polymerase II, holoenzyme	0.47	>=0.20
GO:0006305	DNA alkylation	0.61	>=0.20
GO:0008301	DNA binding, bending	0.31	>=0.20
GO:0071897	DNA biosynthetic process	0.77	>=0.20
GO:0006308	DNA catabolic process	0.75	>=0.20
GO:0071103	DNA conformation change	0.77	>=0.20
GO:0000077	DNA damage checkpoint	0.82	>=0.20
GO:0030330	DNA damage response, signal transduction by p53 class med	0.78	>=0.20
GO:0006977	DNA damage response, signal transduction by p53 class med	0.91	>=0.20

GO:0042771	DNA damage response, signal transduction by p53 class med	0.93	>=0.20
GO:0008630	DNA damage response, signal transduction resulting in induc	0.99	>=0.20
GO:0032508	DNA duplex unwinding	0.82	>=0.20
GO:0044349	DNA excision	1	>=0.20
GO:0032392	DNA geometric change	0.82	>=0.20
GO:0003678	DNA helicase activity	0.78	>=0.20
GO:0033202	DNA helicase complex	0.22	>=0.20
GO:0015074	DNA integration	0.88	>=0.20
GO:0031570	DNA integrity checkpoint	0.83	>=0.20
GO:0006266	DNA ligation	0.97	>=0.20
GO:0006306	DNA methylation	0.61	>=0.20
GO:0043046	DNA methylation involved in gamete generation	1	>=0.20
GO:0006323	DNA packaging	0.88	>=0.20
GO:0034061	DNA polymerase activity	0.7	>=0.20
GO:0042575	DNA polymerase complex	0.78	>=0.20
GO:0006310	DNA recombination	0.92	>=0.20
GO:0006281	DNA repair	0.86	>=0.20
GO:0006260	DNA replication	0.81	>=0.20
GO:0006336	DNA replication-independent nucleosome assembly	0.99	>=0.20
GO:0034724	DNA replication-independent nucleosome organization	0.99	>=0.20
GO:0000076	DNA replication checkpoint	1	>=0.20
GO:0000217	DNA secondary structure binding	0.55	>=0.20
GO:0022616	DNA strand elongation	0.99	>=0.20
GO:0006271	DNA strand elongation involved in DNA replication	1	>=0.20
ENSG00000138346	DNA2 PPI subnetwork	0.84	>=0.20
ENSG00000114841	DNAH1 PPI subnetwork	0.73	>=0.20
ENSG00000007174	DNAH9 PPI subnetwork	0.37	>=0.20
ENSG00000103423	DNAJA3 PPI subnetwork	0.33	>=0.20
ENSG00000132002	DNAJB1 PPI subnetwork	0.43	>=0.20
ENSG00000105993	DNAJB6 PPI subnetwork	0.13	>=0.20
ENSG00000059769	DNAJC25 PPI subnetwork	0.76	>=0.20
ENSG00000163879	DNALI1 PPI subnetwork	0.66	>=0.20
ENSG00000106976	DNM1 PPI subnetwork	0.24	>=0.20
ENSG00000079805	DNM2 PPI subnetwork	0.11	>=0.20
ENSG00000197959	DNM3 PPI subnetwork	0.98	>=0.20
ENSG00000107554	DNMBP PPI subnetwork	0.86	>=0.20
ENSG00000130816	DNMT1 PPI subnetwork	0.59	>=0.20
ENSG00000119772	DNMT3A PPI subnetwork	0.19	>=0.20
ENSG00000088305	DNMT3B PPI subnetwork	0.69	>=0.20
ENSG00000067334	DNTTIP2 PPI subnetwork	0.19	>=0.20
ENSG00000150760	DOCK1 PPI subnetwork	0.35	>=0.20
ENSG00000116641	DOCK7 PPI subnetwork	0.89	>=0.20
ENSG00000115325	DOK1 PPI subnetwork	0.34	>=0.20
ENSG00000147443	DOK2 PPI subnetwork	0.81	>=0.20
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	0.9	>=0.20
GO:0042417	dopamine metabolic process	1	>=0.20
GO:0007212	dopamine receptor signaling pathway	1	>=0.20

GO:0015872	dopamine transport	0.91	>=0.20
GO:0021516	dorsal spinal cord development	1	>=0.20
GO:0009950	dorsal/ventral axis specification	0.99	>=0.20
GO:0021904	dorsal/ventral neural tube patterning	0.99	>=0.20
GO:0009953	dorsal/ventral pattern formation	1	>=0.20
GO:0006302	double-strand break repair	0.93	>=0.20
GO:0000724	double-strand break repair via homologous recombination	0.91	>=0.20
GO:0006303	double-strand break repair via nonhomologous end joining	0.96	>=0.20
GO:0003690	double-stranded DNA binding	0.24	>=0.20
GO:0003725	double-stranded RNA binding	0.88	>=0.20
MP:0000284	double outlet heart right ventricle	0.45	>=0.20
ENSG00000092964	DPYSL2 PPI subnetwork	1	>=0.20
ENSG00000175550	DRAP1 PPI subnetwork	0.98	>=0.20
ENSG00000149295	DRD2 PPI subnetwork	0.96	>=0.20
ENSG00000185721	DRG1 PPI subnetwork	0.19	>=0.20
ENSG00000113360	DROSHA PPI subnetwork	0.45	>=0.20
GO:0008144	drug binding	0.15	>=0.20
GO:0015238	drug transmembrane transporter activity	0.61	>=0.20
GO:0015893	drug transport	0.97	>=0.20
ENSG00000136982	DSCC1 PPI subnetwork	0.94	>=0.20
ENSG00000149636	DSN1 PPI subnetwork	0.79	>=0.20
ENSG00000096696	DSP PPI subnetwork	0.12	>=0.20
ENSG00000151914	DST PPI subnetwork	0.58	>=0.20
ENSG00000125868	DSTN PPI subnetwork	0.04	>=0.20
ENSG00000133059	DSTYK PPI subnetwork	0.15	>=0.20
ENSG00000134769	DTNA PPI subnetwork	0.88	>=0.20
ENSG00000168393	DTYMK PPI subnetwork	0.99	>=0.20
ENSG00000120129	DUSP1 PPI subnetwork	0.92	>=0.20
ENSG00000111266	DUSP16 PPI subnetwork	0.99	>=0.20
ENSG00000189037	DUSP21 PPI subnetwork	0.39	>=0.20
ENSG00000120875	DUSP4 PPI subnetwork	0.48	>=0.20
ENSG00000139318	DUSP6 PPI subnetwork	0.97	>=0.20
ENSG00000164086	DUSP7 PPI subnetwork	0.83	>=0.20
ENSG00000197102	DYNC1H1 PPI subnetwork	0.5	>=0.20
ENSG00000158560	DYNC1I1 PPI subnetwork	0.17	>=0.20
ENSG00000077380	DYNC1I2 PPI subnetwork	0.21	>=0.20
GO:0030286	dynein complex	0.72	>=0.20
ENSG00000121083	DYNLL2 PPI subnetwork	0.96	>=0.20
ENSG00000127334	DYRK2 PPI subnetwork	0.03	>=0.20
MP:0000752	dystrophic muscle	0.86	>=0.20
GO:0016010	dystrophin-associated glycoprotein complex	0.99	>=0.20
GO:0070888	E-box binding	0.86	>=0.20
ENSG00000101412	E2F1 PPI subnetwork	0.84	>=0.20
ENSG00000007968	E2F2 PPI subnetwork	0.56	>=0.20
ENSG00000112242	E2F3 PPI subnetwork	0.55	>=0.20
ENSG00000205250	E2F4 PPI subnetwork	0.04	>=0.20
ENSG00000133740	E2F5 PPI subnetwork	0.13	>=0.20

ENSG00000169016	E2F6 PPI subnetwork	0.45	>=0.20
ENSG00000144597	EAF1 PPI subnetwork	0.51	>=0.20
GO:0043583	ear development	1	>=0.20
GO:0042471	ear morphogenesis	1	>=0.20
MP:0008008	early cellular replicative senescence	0.31	>=0.20
GO:0005769	early endosome	0.21	>=0.20
GO:0031901	early endosome membrane	0.92	>=0.20
GO:0045022	early endosome to late endosome transport	0.73	>=0.20
GO:0042755	eating behavior	0.9	>=0.20
ENSG00000164330	EBF1 PPI subnetwork	0.51	>=0.20
ENSG00000117395	EBNA1BP2 PPI subnetwork	0.54	>=0.20
GO:0007398	ectoderm development	0.57	>=0.20
MP:0000885	ectopic Purkinje cell	0.95	>=0.20
ENSG00000179151	EDC3 PPI subnetwork	0.07	>=0.20
ENSG00000151617	EDNRA PPI subnetwork	0.54	>=0.20
ENSG00000136160	EDNRB PPI subnetwork	0.69	>=0.20
ENSG00000102189	EEA1 PPI subnetwork	0.21	>=0.20
ENSG00000074266	EED PPI subnetwork	0.83	>=0.20
ENSG00000101210	EEF1A2 PPI subnetwork	0.09	>=0.20
ENSG00000114942	EEF1B2 PPI subnetwork	0.19	>=0.20
ENSG00000124802	EEF1E1 PPI subnetwork	0.94	>=0.20
ENSG00000169242	EFNA1 PPI subnetwork	0.97	>=0.20
ENSG00000125266	EFNB2 PPI subnetwork	0.96	>=0.20
ENSG00000100842	EFS PPI subnetwork	0.05	>=0.20
ENSG00000108883	EFTUD2 PPI subnetwork	0.03	>=0.20
ENSG00000181090	EHMT1 PPI subnetwork	0.31	>=0.20
ENSG00000173674	EIF1AX PPI subnetwork	0.88	>=0.20
ENSG00000198692	EIF1AY PPI subnetwork	0.78	>=0.20
ENSG00000114784	EIF1B PPI subnetwork	0.42	>=0.20
ENSG00000144895	EIF2A PPI subnetwork	0.81	>=0.20
ENSG00000086232	EIF2AK1 PPI subnetwork	0.23	>=0.20
ENSG00000055332	EIF2AK2 PPI subnetwork	0.21	>=0.20
ENSG00000172071	EIF2AK3 PPI subnetwork	0.3	>=0.20
ENSG00000145191	EIF2B5 PPI subnetwork	0.18	>=0.20
ENSG00000125977	EIF2S2 PPI subnetwork	0.86	>=0.20
ENSG00000130741	EIF2S3 PPI subnetwork	0.61	>=0.20
ENSG00000107581	EIF3A PPI subnetwork	0.59	>=0.20
ENSG00000106263	EIF3B PPI subnetwork	0.92	>=0.20
ENSG00000184110	EIF3C PPI subnetwork	0.44	>=0.20
ENSG00000205609	EIF3CL PPI subnetwork	0.65	>=0.20
ENSG00000100353	EIF3D PPI subnetwork	0.8	>=0.20
ENSG00000104408	EIF3E PPI subnetwork	0.43	>=0.20
ENSG00000175390	EIF3F PPI subnetwork	0.96	>=0.20
ENSG00000130811	EIF3G PPI subnetwork	0.93	>=0.20
ENSG00000147677	EIF3H PPI subnetwork	0.87	>=0.20
ENSG00000084623	EIF3I PPI subnetwork	0.72	>=0.20
ENSG00000104131	EIF3J PPI subnetwork	0.87	>=0.20

ENSG00000178982	EIF3K PPI subnetwork	0.89	>=0.20
ENSG00000100129	EIF3L PPI subnetwork	0.75	>=0.20
ENSG00000156976	EIF4A2 PPI subnetwork	0.59	>=0.20
ENSG00000141543	EIF4A3 PPI subnetwork	0.07	>=0.20
ENSG00000063046	EIF4B PPI subnetwork	0.74	>=0.20
ENSG00000151247	EIF4E PPI subnetwork	0.23	>=0.20
ENSG00000135930	EIF4E2 PPI subnetwork	0.11	>=0.20
ENSG00000187840	EIF4EBP1 PPI subnetwork	0.41	>=0.20
ENSG00000110321	EIF4G2 PPI subnetwork	0.21	>=0.20
ENSG00000106682	EIF4H PPI subnetwork	0.95	>=0.20
ENSG00000100664	EIF5 PPI subnetwork	0.84	>=0.20
ENSG00000132507	EIF5A PPI subnetwork	0.41	>=0.20
ENSG00000158417	EIF5B PPI subnetwork	0.62	>=0.20
GO:0022900	electron transport chain	1	>=0.20
GO:0007204	elevation of cytosolic calcium ion concentration	0.84	>=0.20
ENSG00000120690	ELF1 PPI subnetwork	0.23	>=0.20
ENSG00000163435	ELF3 PPI subnetwork	0.59	>=0.20
ENSG00000105656	ELL PPI subnetwork	0.25	>=0.20
ENSG00000118985	ELL2 PPI subnetwork	0.89	>=0.20
ENSG00000049540	ELN PPI subnetwork	0.52	>=0.20
ENSG00000130165	ELOF1 PPI subnetwork	0.26	>=0.20
ENSG00000012660	ELOVL5 PPI subnetwork	0.55	>=0.20
ENSG00000134014	ELP3 PPI subnetwork	0.21	>=0.20
ENSG00000109911	ELP4 PPI subnetwork	0.65	>=0.20
GO:0009792	embryo development ending in birth or egg hatching	0.62	>=0.20
GO:0007566	embryo implantation	0.96	>=0.20
GO:0035113	embryonic appendage morphogenesis	1	>=0.20
GO:0031076	embryonic camera-type eye development	1	>=0.20
GO:0048596	embryonic camera-type eye morphogenesis	0.88	>=0.20
GO:0048701	embryonic cranial skeleton morphogenesis	1	>=0.20
GO:0048566	embryonic digestive tract development	1	>=0.20
GO:0048557	embryonic digestive tract morphogenesis	0.51	>=0.20
GO:0042733	embryonic digit morphogenesis	1	>=0.20
GO:0001838	embryonic epithelial tube formation	1	>=0.20
GO:0048048	embryonic eye morphogenesis	0.95	>=0.20
GO:0035115	embryonic forelimb morphogenesis	1	>=0.20
GO:0035050	embryonic heart tube development	0.87	>=0.20
GO:0003143	embryonic heart tube morphogenesis	0.93	>=0.20
GO:0035162	embryonic hemopoiesis	0.23	>=0.20
GO:0035116	embryonic hindlimb morphogenesis	1	>=0.20
GO:0030326	embryonic limb morphogenesis	1	>=0.20
GO:0048598	embryonic morphogenesis	0.99	>=0.20
GO:0048568	embryonic organ development	0.95	>=0.20
GO:0048562	embryonic organ morphogenesis	1	>=0.20
GO:0009880	embryonic pattern specification	0.98	>=0.20
GO:0072498	embryonic skeletal joint development	1	>=0.20
GO:0048706	embryonic skeletal system development	1	>=0.20

GO:0048704	embryonic skeletal system morphogenesis	1	>=0.20
MP:0001958	emphysema	0.9	>=0.20
GO:0003197	endocardial cushion development	1	>=0.20
GO:0003203	endocardial cushion morphogenesis	1	>=0.20
GO:0060350	endochondral bone morphogenesis	0.5	>=0.20
GO:0001958	endochondral ossification	0.78	>=0.20
GO:0031018	endocrine pancreas development	0.85	>=0.20
GO:0035270	endocrine system development	1	>=0.20
GO:0030666	endocytic vesicle membrane	0.27	>=0.20
GO:0004520	endodeoxyribonuclease activity	0.92	>=0.20
GO:0007492	endoderm development	0.8	>=0.20
GO:0001706	endoderm formation	0.55	>=0.20
ENSG00000167136	ENDOG PPI subnetwork	0.43	>=0.20
GO:0033116	endoplasmic reticulum-Golgi intermediate compartment me	0.19	>=0.20
GO:0007029	endoplasmic reticulum organization	0.85	>=0.20
GO:0030968	endoplasmic reticulum unfolded protein response	0.97	>=0.20
GO:0016891	endoribonuclease activity, producing 5'-phosphomonoesters	0.98	>=0.20
GO:0044440	endosomal part	0.05	>=0.20
GO:0016197	endosomal transport	0.19	>=0.20
GO:0010008	endosome membrane	0.04	>=0.20
GO:0008333	endosome to lysosome transport	0.43	>=0.20
GO:0045446	endothelial cell differentiation	0.41	>=0.20
GO:0001935	endothelial cell proliferation	0.16	>=0.20
GO:0003158	endothelium development	0.26	>=0.20
GO:0015988	energy coupled proton transport, against electrochemical gra	0.88	>=0.20
GO:0015985	energy coupled proton transport, down electrochemical grac	0.99	>=0.20
GO:0015980	energy derivation by oxidation of organic compounds	0.41	>=0.20
GO:0006112	energy reserve metabolic process	0.03	>=0.20
ENSG00000106991	ENG PPI subnetwork	0.72	>=0.20
MP:0009746	enhanced behavioral response to xenobiotic	0.92	>=0.20
MP:0009453	enhanced contextual conditioning behavior	0.99	>=0.20
MP:0003008	enhanced long term potentiation	1	>=0.20
MP:0002919	enhanced paired-pulse facilitation	1	>=0.20
MP:0002724	enhanced wound healing	0.38	>=0.20
GO:0035326	enhancer binding	0.91	>=0.20
GO:0001158	enhancer sequence-specific DNA binding	0.95	>=0.20
MP:0000274	enlarged heart	0.15	>=0.20
MP:0008725	enlarged heart atrium	0.87	>=0.20
MP:0008535	enlarged lateral ventricles	0.95	>=0.20
MP:0000652	enlarged sebaceous gland	0.3	>=0.20
MP:0008536	enlarged third ventricle	1	>=0.20
MP:0000709	enlarged thymus	0.09	>=0.20
ENSG00000007816	ENSG00000007816 PPI subnetwork	0.78	>=0.20
ENSG00000013455	ENSG00000013455 PPI subnetwork	0.3	>=0.20
ENSG00000056678	ENSG00000056678 PPI subnetwork	0.72	>=0.20
ENSG00000085365	ENSG00000085365 PPI subnetwork	0.69	>=0.20
ENSG00000091073	ENSG00000091073 PPI subnetwork	0.44	>=0.20

ENSG00000091436	ENSG00000091436 PPI subnetwork	0.31	>=0.20
ENSG00000099389	ENSG00000099389 PPI subnetwork	0.44	>=0.20
ENSG00000099725	ENSG00000099725 PPI subnetwork	0.83	>=0.20
ENSG00000099882	ENSG00000099882 PPI subnetwork	0.49	>=0.20
ENSG00000102391	ENSG00000102391 PPI subnetwork	0.88	>=0.20
ENSG00000104637	ENSG00000104637 PPI subnetwork	0.75	>=0.20
ENSG00000104725	ENSG00000104725 PPI subnetwork	0.81	>=0.20
ENSG00000105216	ENSG00000105216 PPI subnetwork	0.04	>=0.20
ENSG00000105663	ENSG00000105663 PPI subnetwork	0.45	>=0.20
ENSG00000108504	ENSG00000108504 PPI subnetwork	0.61	>=0.20
ENSG00000108819	ENSG00000108819 PPI subnetwork	0.5	>=0.20
ENSG00000111788	ENSG00000111788 PPI subnetwork	1	>=0.20
ENSG00000112049	ENSG00000112049 PPI subnetwork	0.51	>=0.20
ENSG00000112526	ENSG00000112526 PPI subnetwork	0.06	>=0.20
ENSG00000112727	ENSG00000112727 PPI subnetwork	0.68	>=0.20
ENSG00000115128	ENSG00000115128 PPI subnetwork	0.12	>=0.20
ENSG00000115254	ENSG00000115254 PPI subnetwork	0.81	>=0.20
ENSG00000115953	ENSG00000115953 PPI subnetwork	0.94	>=0.20
ENSG00000117242	ENSG00000117242 PPI subnetwork	0.59	>=0.20
ENSG00000120247	ENSG00000120247 PPI subnetwork	0.09	>=0.20
ENSG00000121031	ENSG00000121031 PPI subnetwork	0.08	>=0.20
ENSG00000124097	ENSG00000124097 PPI subnetwork	0.92	>=0.20
ENSG00000124642	ENSG00000124642 PPI subnetwork	0.41	>=0.20
ENSG00000126005	ENSG00000126005 PPI subnetwork	0.28	>=0.20
ENSG00000127388	ENSG00000127388 PPI subnetwork	0.57	>=0.20
ENSG00000128692	ENSG00000128692 PPI subnetwork	0.6	>=0.20
ENSG00000130041	ENSG00000130041 PPI subnetwork	0.72	>=0.20
ENSG00000130288	ENSG00000130288 PPI subnetwork	0.95	>=0.20
ENSG00000133511	ENSG00000133511 PPI subnetwork	0.9	>=0.20
ENSG00000134602	ENSG00000134602 PPI subnetwork	0.44	>=0.20
ENSG00000136149	ENSG00000136149 PPI subnetwork	0.98	>=0.20
ENSG00000137379	ENSG00000137379 PPI subnetwork	0.12	>=0.20
ENSG00000138396	ENSG00000138396 PPI subnetwork	0.95	>=0.20
ENSG00000139239	ENSG00000139239 PPI subnetwork	0.27	>=0.20
ENSG00000146143	ENSG00000146143 PPI subnetwork	0.92	>=0.20
ENSG00000146677	ENSG00000146677 PPI subnetwork	0.99	>=0.20
ENSG00000147877	ENSG00000147877 PPI subnetwork	0.09	>=0.20
ENSG00000152268	ENSG00000152268 PPI subnetwork	0.64	>=0.20
ENSG00000157152	ENSG00000157152 PPI subnetwork	0.98	>=0.20
ENSG00000157344	ENSG00000157344 PPI subnetwork	0.53	>=0.20
ENSG00000159113	ENSG00000159113 PPI subnetwork	0.34	>=0.20
ENSG00000159186	ENSG00000159186 PPI subnetwork	1	>=0.20
ENSG00000160695	ENSG00000160695 PPI subnetwork	0.1	>=0.20
ENSG00000160916	ENSG00000160916 PPI subnetwork	0.08	>=0.20
ENSG00000162290	ENSG00000162290 PPI subnetwork	0.88	>=0.20
ENSG00000165178	ENSG00000165178 PPI subnetwork	0.21	>=0.20
ENSG00000167674	ENSG00000167674 PPI subnetwork	0.6	>=0.20

ENSG00000168399	ENSG00000168399 PPI subnetwork	0.84	>=0.20
ENSG00000168593	ENSG00000168593 PPI subnetwork	0.91	>=0.20
ENSG00000170847	ENSG00000170847 PPI subnetwork	0.63	>=0.20
ENSG00000171549	ENSG00000171549 PPI subnetwork	0.87	>=0.20
ENSG00000173534	ENSG00000173534 PPI subnetwork	0.63	>=0.20
ENSG00000173636	ENSG00000173636 PPI subnetwork	0.69	>=0.20
ENSG00000173867	ENSG00000173867 PPI subnetwork	0.49	>=0.20
ENSG00000174622	ENSG00000174622 PPI subnetwork	0.83	>=0.20
ENSG00000174766	ENSG00000174766 PPI subnetwork	0.96	>=0.20
ENSG00000175333	ENSG00000175333 PPI subnetwork	0.93	>=0.20
ENSG00000176534	ENSG00000176534 PPI subnetwork	0.89	>=0.20
ENSG00000178458	ENSG00000178458 PPI subnetwork	0.68	>=0.20
ENSG00000179036	ENSG00000179036 PPI subnetwork	0.72	>=0.20
ENSG00000179899	ENSG00000179899 PPI subnetwork	0.26	>=0.20
ENSG00000182498	ENSG00000182498 PPI subnetwork	0.38	>=0.20
ENSG00000182520	ENSG00000182520 PPI subnetwork	0.87	>=0.20
ENSG00000182754	ENSG00000182754 PPI subnetwork	0.61	>=0.20
ENSG00000183093	ENSG00000183093 PPI subnetwork	0.55	>=0.20
ENSG00000185214	ENSG00000185214 PPI subnetwork	0.77	>=0.20
ENSG00000186809	ENSG00000186809 PPI subnetwork	0.09	>=0.20
ENSG00000186831	ENSG00000186831 PPI subnetwork	0.32	>=0.20
ENSG00000186842	ENSG00000186842 PPI subnetwork	0.93	>=0.20
ENSG00000186879	ENSG00000186879 PPI subnetwork	0.62	>=0.20
ENSG00000187558	ENSG00000187558 PPI subnetwork	0.68	>=0.20
ENSG00000187953	ENSG00000187953 PPI subnetwork	0.65	>=0.20
ENSG00000188170	ENSG00000188170 PPI subnetwork	0.16	>=0.20
ENSG00000188459	ENSG00000188459 PPI subnetwork	0.32	>=0.20
ENSG00000189162	ENSG00000189162 PPI subnetwork	0.11	>=0.20
ENSG00000196084	ENSG00000196084 PPI subnetwork	0.06	>=0.20
ENSG00000196285	ENSG00000196285 PPI subnetwork	0.48	>=0.20
ENSG00000196501	ENSG00000196501 PPI subnetwork	0.69	>=0.20
ENSG00000196656	ENSG00000196656 PPI subnetwork	0.7	>=0.20
ENSG00000196681	ENSG00000196681 PPI subnetwork	0.89	>=0.20
ENSG00000197303	ENSG00000197303 PPI subnetwork	0.78	>=0.20
ENSG00000197373	ENSG00000197373 PPI subnetwork	0.74	>=0.20
ENSG00000197558	ENSG00000197558 PPI subnetwork	0.57	>=0.20
ENSG00000197597	ENSG00000197597 PPI subnetwork	0.69	>=0.20
ENSG00000198618	ENSG00000198618 PPI subnetwork	0.03	>=0.20
ENSG00000198637	ENSG00000198637 PPI subnetwork	0.89	>=0.20
ENSG00000198641	ENSG00000198641 PPI subnetwork	0.82	>=0.20
ENSG00000198744	ENSG00000198744 PPI subnetwork	0.9	>=0.20
ENSG00000198802	ENSG00000198802 PPI subnetwork	0.05	>=0.20
ENSG00000198868	ENSG00000198868 PPI subnetwork	0.98	>=0.20
ENSG00000203283	ENSG00000203283 PPI subnetwork	0.17	>=0.20
ENSG00000204133	ENSG00000204133 PPI subnetwork	0.8	>=0.20
ENSG00000204218	ENSG00000204218 PPI subnetwork	0.72	>=0.20
ENSG00000204261	ENSG00000204261 PPI subnetwork	0.51	>=0.20

ENSG00000204273	ENSG00000204273 PPI subnetwork	0.84	>=0.20
ENSG00000204523	ENSG00000204523 PPI subnetwork	0.05	>=0.20
ENSG00000206088	ENSG00000206088 PPI subnetwork	0.3	>=0.20
ENSG00000206156	ENSG00000206156 PPI subnetwork	0.05	>=0.20
ENSG00000206210	ENSG00000206210 PPI subnetwork	0.74	>=0.20
ENSG00000206211	ENSG00000206211 PPI subnetwork	0.83	>=0.20
ENSG00000206212	ENSG00000206212 PPI subnetwork	0.38	>=0.20
ENSG00000206215	ENSG00000206215 PPI subnetwork	0.05	>=0.20
ENSG00000206229	ENSG00000206229 PPI subnetwork	0.94	>=0.20
ENSG00000206232	ENSG00000206232 PPI subnetwork	0.51	>=0.20
ENSG00000206233	ENSG00000206233 PPI subnetwork	0.63	>=0.20
ENSG00000206234	ENSG00000206234 PPI subnetwork	0.73	>=0.20
ENSG00000206293	ENSG00000206293 PPI subnetwork	0.94	>=0.20
ENSG00000206294	ENSG00000206294 PPI subnetwork	0.77	>=0.20
ENSG00000206296	ENSG00000206296 PPI subnetwork	0.51	>=0.20
ENSG00000206300	ENSG00000206300 PPI subnetwork	0.13	>=0.20
ENSG00000206328	ENSG00000206328 PPI subnetwork	0.93	>=0.20
ENSG00000206385	ENSG00000206385 PPI subnetwork	0.92	>=0.20
ENSG00000206413	ENSG00000206413 PPI subnetwork	0.97	>=0.20
ENSG00000206419	ENSG00000206419 PPI subnetwork	0.55	>=0.20
ENSG00000206429	ENSG00000206429 PPI subnetwork	0.83	>=0.20
ENSG00000206443	ENSG00000206443 PPI subnetwork	0.87	>=0.20
ENSG00000206456	ENSG00000206456 PPI subnetwork	0.83	>=0.20
ENSG00000206476	ENSG00000206476 PPI subnetwork	0.71	>=0.20
ENSG00000211592	ENSG00000211592 PPI subnetwork	0.04	>=0.20
ENSG00000211614	ENSG00000211614 PPI subnetwork	0.14	>=0.20
ENSG00000211735	ENSG00000211735 PPI subnetwork	1	>=0.20
ENSG00000211739	ENSG00000211739 PPI subnetwork	1	>=0.20
ENSG00000211762	ENSG00000211762 PPI subnetwork	1	>=0.20
ENSG00000211790	ENSG00000211790 PPI subnetwork	1	>=0.20
ENSG00000211799	ENSG00000211799 PPI subnetwork	1	>=0.20
ENSG00000211810	ENSG00000211810 PPI subnetwork	1	>=0.20
ENSG00000211889	ENSG00000211889 PPI subnetwork	1	>=0.20
ENSG00000211895	ENSG00000211895 PPI subnetwork	0.34	>=0.20
ENSG00000212664	ENSG00000212664 PPI subnetwork	0.97	>=0.20
ENSG00000212695	ENSG00000212695 PPI subnetwork	0.91	>=0.20
ENSG00000212802	ENSG00000212802 PPI subnetwork	0.96	>=0.20
ENSG00000212868	ENSG00000212868 PPI subnetwork	0.99	>=0.20
ENSG00000212869	ENSG00000212869 PPI subnetwork	0.98	>=0.20
ENSG00000212870	ENSG00000212870 PPI subnetwork	0.96	>=0.20
ENSG00000212871	ENSG00000212871 PPI subnetwork	0.98	>=0.20
ENSG00000212872	ENSG00000212872 PPI subnetwork	0.98	>=0.20
ENSG00000212874	ENSG00000212874 PPI subnetwork	0.99	>=0.20
ENSG00000212875	ENSG00000212875 PPI subnetwork	0.97	>=0.20
ENSG00000212876	ENSG00000212876 PPI subnetwork	0.99	>=0.20
ENSG00000213496	ENSG00000213496 PPI subnetwork	0.96	>=0.20
ENSG00000213611	ENSG00000213611 PPI subnetwork	0.91	>=0.20

ENSG00000214122	ENSG00000214122 PPI subnetwork	0.49	>=0.20
ENSG00000214133	ENSG00000214133 PPI subnetwork	0.33	>=0.20
ENSG00000214528	ENSG00000214528 PPI subnetwork	0.77	>=0.20
ENSG00000214826	ENSG00000214826 PPI subnetwork	1	>=0.20
ENSG00000215120	ENSG00000215120 PPI subnetwork	0.09	>=0.20
ENSG00000215467	ENSG00000215467 PPI subnetwork	0.87	>=0.20
ENSG00000215476	ENSG00000215476 PPI subnetwork	0.71	>=0.20
ENSG00000215694	ENSG00000215694 PPI subnetwork	0.99	>=0.20
ENSG00000215697	ENSG00000215697 PPI subnetwork	0.8	>=0.20
ENSG00000215699	ENSG00000215699 PPI subnetwork	0.2	>=0.20
ENSG00000215719	ENSG00000215719 PPI subnetwork	0.48	>=0.20
ENSG00000215727	ENSG00000215727 PPI subnetwork	0.48	>=0.20
ENSG00000215760	ENSG00000215760 PPI subnetwork	0.1	>=0.20
ENSG00000215769	ENSG00000215769 PPI subnetwork	0.17	>=0.20
ENSG00000215778	ENSG00000215778 PPI subnetwork	0.03	>=0.20
ENSG00000215902	ENSG00000215902 PPI subnetwork	0.89	>=0.20
GO:0007272	ensheathment of neurons	1	>=0.20
GO:0048484	enteric nervous system development	1	>=0.20
ENSG00000198018	ENTPD7 PPI subnetwork	0.51	>=0.20
GO:0008047	enzyme activator activity	0.03	>=0.20
ENSG00000183495	EP400 PPI subnetwork	0.13	>=0.20
ENSG00000159023	EPB41 PPI subnetwork	0.12	>=0.20
ENSG00000088367	EPB41L1 PPI subnetwork	0.78	>=0.20
ENSG00000079819	EPB41L2 PPI subnetwork	1	>=0.20
ENSG00000082397	EPB41L3 PPI subnetwork	0.41	>=0.20
ENSG00000120616	EPC1 PPI subnetwork	0.38	>=0.20
ENSG00000135999	EPC2 PPI subnetwork	0.31	>=0.20
ENSG00000119888	EPCAM PPI subnetwork	0.4	>=0.20
ENSG00000044524	EPHA3 PPI subnetwork	0.32	>=0.20
ENSG00000135333	EPHA7 PPI subnetwork	0.03	>=0.20
ENSG00000196411	EPHB4 PPI subnetwork	0.31	>=0.20
ENSG00000106123	EPHB6 PPI subnetwork	0.39	>=0.20
GO:0005003	ephrin receptor activity	0.88	>=0.20
GO:0046875	ephrin receptor binding	0.29	>=0.20
GO:0048013	ephrin receptor signaling pathway	0.99	>=0.20
GO:0009913	epidermal cell differentiation	0.81	>=0.20
GO:0005154	epidermal growth factor receptor binding	0.43	>=0.20
GO:0007173	epidermal growth factor receptor signaling pathway	0.33	>=0.20
MP:0001222	epidermal hyperplasia	0.44	>=0.20
GO:0008544	epidermis development	0.69	>=0.20
GO:0048730	epidermis morphogenesis	1	>=0.20
GO:0002064	epithelial cell development	0.39	>=0.20
GO:0030855	epithelial cell differentiation	0.27	>=0.20
GO:0003382	epithelial cell morphogenesis	0.95	>=0.20
GO:0050673	epithelial cell proliferation	0.45	>=0.20
GO:0001837	epithelial to mesenchymal transition	1	>=0.20
GO:0060441	epithelial tube branching involved in lung morphogenesis	1	>=0.20

GO:0072175	epithelial tube formation	1	>=0.20
GO:0060562	epithelial tube morphogenesis	0.98	>=0.20
GO:0060429	epithelium development	0.77	>=0.20
ENSG00000063245	EPN1 PPI subnetwork	0.96	>=0.20
ENSG00000072134	EPN2 PPI subnetwork	0.57	>=0.20
ENSG00000130427	EPO PPI subnetwork	0.08	>=0.20
ENSG00000187266	EPOR PPI subnetwork	0.08	>=0.20
ENSG00000085832	EPS15 PPI subnetwork	0.43	>=0.20
ENSG00000127527	EPS15L1 PPI subnetwork	0.59	>=0.20
ENSG00000138018	EPT1 PPI subnetwork	0.45	>=0.20
GO:0030433	ER-associated protein catabolic process	0.96	>=0.20
GO:0006984	ER-nucleus signaling pathway	0.65	>=0.20
ENSG00000112851	ERBB2IP PPI subnetwork	0.83	>=0.20
ENSG00000065361	ERBB3 PPI subnetwork	0.1	>=0.20
ENSG00000178568	ERBB4 PPI subnetwork	0.06	>=0.20
ENSG00000187672	ERC2 PPI subnetwork	1	>=0.20
ENSG00000012061	ERCC1 PPI subnetwork	0.78	>=0.20
ENSG00000175595	ERCC4 PPI subnetwork	0.99	>=0.20
ENSG00000134899	ERCC5 PPI subnetwork	0.86	>=0.20
ENSG00000186871	ERCC6L PPI subnetwork	0.83	>=0.20
ENSG00000100632	ERH PPI subnetwork	0.05	>=0.20
ENSG00000104626	ERI1 PPI subnetwork	0.2	>=0.20
GO:0070371	ERK1 and ERK2 cascade	0.9	>=0.20
ENSG00000107566	ERLIN1 PPI subnetwork	0.26	>=0.20
ENSG00000023318	ERP44 PPI subnetwork	0.86	>=0.20
ENSG00000116285	ERRFI1 PPI subnetwork	0.33	>=0.20
GO:0030218	erythrocyte differentiation	0.03	>=0.20
GO:0034101	erythrocyte homeostasis	0.05	>=0.20
ENSG00000141446	ESCO1 PPI subnetwork	0.94	>=0.20
GO:0030010	establishment of cell polarity	0.99	>=0.20
GO:0051303	establishment of chromosome localization	0.98	>=0.20
GO:0032401	establishment of melanosome localization	1	>=0.20
GO:0040001	establishment of mitotic spindle localization	0.9	>=0.20
GO:0000132	establishment of mitotic spindle orientation	0.84	>=0.20
GO:0051656	establishment of organelle localization	0.81	>=0.20
GO:0051905	establishment of pigment granule localization	1	>=0.20
GO:0001736	establishment of planar polarity	1	>=0.20
GO:0090177	establishment of planar polarity involved in neural tube closu	1	>=0.20
GO:0042249	establishment of planar polarity of embryonic epithelium	1	>=0.20
GO:0072655	establishment of protein localization in mitochondrion	0.97	>=0.20
GO:0072594	establishment of protein localization to organelle	0.63	>=0.20
GO:0051236	establishment of RNA localization	0.51	>=0.20
GO:0051293	establishment of spindle localization	0.87	>=0.20
GO:0051294	establishment of spindle orientation	0.84	>=0.20
GO:0007164	establishment of tissue polarity	0.99	>=0.20
GO:0051650	establishment of vesicle localization	0.71	>=0.20
GO:0035088	establishment or maintenance of apical/basal cell polarity	1	>=0.20

GO:0061245	establishment or maintenance of bipolar cell polarity	1	>=0.20
GO:0007163	establishment or maintenance of cell polarity	1	>=0.20
ENSG00000134954	ETS1 PPI subnetwork	0.04	>=0.20
ENSG00000006468	ETV1 PPI subnetwork	0.18	>=0.20
ENSG00000139083	ETV6 PPI subnetwork	0.15	>=0.20
ENSG00000010030	ETV7 PPI subnetwork	0.84	>=0.20
GO:0005852	eukaryotic translation initiation factor 3 complex	0.97	>=0.20
ENSG00000196405	EVL PPI subnetwork	0.22	>=0.20
ENSG00000167880	EVPL PPI subnetwork	0.71	>=0.20
ENSG00000182944	EWSR1 PPI subnetwork	0.75	>=0.20
GO:0005231	excitatory extracellular ligand-gated ion channel activity	1	>=0.20
GO:0060076	excitatory synapse	0.98	>=0.20
GO:0007588	excretion	0.99	>=0.20
MP:0000914	exencephaly	0.8	>=0.20
ENSG00000174371	EXO1 PPI subnetwork	0.64	>=0.20
ENSG00000090989	EXOC1 PPI subnetwork	0.76	>=0.20
ENSG00000112685	EXOC2 PPI subnetwork	0.9	>=0.20
ENSG00000180104	EXOC3 PPI subnetwork	0.86	>=0.20
ENSG00000131558	EXOC4 PPI subnetwork	0.88	>=0.20
ENSG00000070367	EXOC5 PPI subnetwork	0.28	>=0.20
ENSG00000138190	EXOC6 PPI subnetwork	0.9	>=0.20
ENSG00000182473	EXOC7 PPI subnetwork	0.82	>=0.20
ENSG00000116903	EXOC8 PPI subnetwork	0.46	>=0.20
GO:0035272	exocrine system development	0.97	>=0.20
GO:0006887	exocytosis	0.23	>=0.20
GO:0035145	exon-exon junction complex	0.59	>=0.20
GO:0004527	exonuclease activity	0.99	>=0.20
GO:0016796	exonuclease activity, active with either ribo- or deoxyribonuc	1	>=0.20
GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process i	0.99	>=0.20
GO:0004532	exoribonuclease activity	0.93	>=0.20
GO:0016896	exoribonuclease activity, producing 5'-phosphomonoesters	0.94	>=0.20
ENSG00000130713	EXOSC2 PPI subnetwork	0.87	>=0.20
ENSG00000120699	EXOSC8 PPI subnetwork	0.93	>=0.20
ENSG00000123737	EXOSC9 PPI subnetwork	0.93	>=0.20
GO:0000178	exosome (RNase complex)	0.96	>=0.20
GO:0030312	external encapsulating structure	1	>=0.20
GO:0044462	external encapsulating structure part	1	>=0.20
GO:0005234	extracellular-glutamate-gated ion channel activity	1	>=0.20
GO:0005230	extracellular ligand-gated ion channel activity	1	>=0.20
GO:0031012	extracellular matrix	0.86	>=0.20
GO:0050840	extracellular matrix binding	0.23	>=0.20
GO:0030198	extracellular matrix organization	0.98	>=0.20
GO:0044420	extracellular matrix part	0.59	>=0.20
GO:0005201	extracellular matrix structural constituent	0.84	>=0.20
GO:0043062	extracellular structure organization	0.98	>=0.20
GO:0031234	extrinsic to internal side of plasma membrane	0.95	>=0.20
GO:0019898	extrinsic to membrane	0.56	>=0.20

GO:0019897	extrinsic to plasma membrane	0.42	>=0.20
ENSG00000104313	EYA1 PPI subnetwork	0.96	>=0.20
GO:0001654	eye development	1	>=0.20
GO:0048592	eye morphogenesis	1	>=0.20
GO:0042462	eye photoreceptor cell development	1	>=0.20
GO:0001754	eye photoreceptor cell differentiation	1	>=0.20
MP:0005176	eyelids fail to open	0.97	>=0.20
MP:0001302	eyelids open at birth	0.73	>=0.20
ENSG00000106462	EZH2 PPI subnetwork	0.05	>=0.20
ENSG00000092820	EZR PPI subnetwork	0.15	>=0.20
ENSG00000158769	F11R PPI subnetwork	0.37	>=0.20
ENSG00000164251	F2RL1 PPI subnetwork	0.83	>=0.20
ENSG00000164220	F2RL2 PPI subnetwork	0.18	>=0.20
ENSG00000117480	FAAH PPI subnetwork	0.18	>=0.20
ENSG00000164687	FABP5 PPI subnetwork	0.96	>=0.20
GO:0060324	face development	0.99	>=0.20
GO:0060325	face morphogenesis	1	>=0.20
ENSG00000168040	FADD PPI subnetwork	0.74	>=0.20
ENSG00000185104	FAF1 PPI subnetwork	0.55	>=0.20
ENSG00000113194	FAF2 PPI subnetwork	0.48	>=0.20
MP:0004251	failure of heart looping	0.05	>=0.20
MP:0009886	failure of palatal shelf elevation	0.94	>=0.20
MP:0001693	failure of primitive streak formation	0.92	>=0.20
MP:0000121	failure of tooth eruption	0.15	>=0.20
MP:0002663	failure to form blastocele	0.29	>=0.20
MP:0001696	failure to gastrulate	0.03	>=0.20
ENSG00000138439	FAM117B PPI subnetwork	0.6	>=0.20
ENSG00000048828	FAM120A PPI subnetwork	0.18	>=0.20
ENSG00000148468	FAM171A1 PPI subnetwork	0.92	>=0.20
ENSG00000106125	FAM188B PPI subnetwork	0.49	>=0.20
ENSG00000143093	FAM40A PPI subnetwork	0.93	>=0.20
ENSG00000189319	FAM53B PPI subnetwork	0.21	>=0.20
ENSG00000120709	FAM53C PPI subnetwork	0.13	>=0.20
ENSG00000204361	FAM55B PPI subnetwork	0.31	>=0.20
ENSG00000147689	FAM83A PPI subnetwork	0.04	>=0.20
ENSG00000133477	FAM83F PPI subnetwork	0.06	>=0.20
ENSG00000119812	FAM98A PPI subnetwork	0.03	>=0.20
ENSG00000187741	FANCA PPI subnetwork	0.1	>=0.20
ENSG00000158169	FANCC PPI subnetwork	0.99	>=0.20
ENSG00000144554	FANCD2 PPI subnetwork	0.74	>=0.20
ENSG00000187790	FANCM PPI subnetwork	1	>=0.20
GO:0043240	Fanconi anaemia nuclear complex	0.93	>=0.20
ENSG00000026103	FAS PPI subnetwork	0.7	>=0.20
GO:0005916	fascia adherens	0.77	>=0.20
ENSG00000117560	FASLG PPI subnetwork	0.73	>=0.20
GO:0006775	fat-soluble vitamin metabolic process	0.33	>=0.20
GO:0045444	fat cell differentiation	0.12	>=0.20

ENSG00000083857	FAT1 PPI subnetwork	0.89	>=0.20
GO:0046949	fatty-acyl-CoA biosynthetic process	0.23	>=0.20
GO:0035337	fatty-acyl-CoA metabolic process	0.23	>=0.20
ENSG00000149806	FAU PPI subnetwork	0.88	>=0.20
ENSG00000105202	FBL PPI subnetwork	0.3	>=0.20
ENSG00000077942	FBLN1 PPI subnetwork	0.03	>=0.20
ENSG00000163520	FBLN2 PPI subnetwork	0.22	>=0.20
ENSG00000166147	FBN1 PPI subnetwork	0.5	>=0.20
ENSG00000161040	FBXL13 PPI subnetwork	0.83	>=0.20
ENSG00000138081	FBXO11 PPI subnetwork	0.52	>=0.20
ENSG00000072803	FBXW11 PPI subnetwork	0.51	>=0.20
ENSG00000174989	FBXW8 PPI subnetwork	0.04	>=0.20
ENSG00000158869	FCER1G PPI subnetwork	0.65	>=0.20
ENSG00000119616	FCF1 PPI subnetwork	0.95	>=0.20
GO:0042596	fear response	1	>=0.20
GO:0007631	feeding behavior	1	>=0.20
GO:0007292	female gamete generation	0.37	>=0.20
GO:0008585	female gonad development	0.71	>=0.20
GO:0046660	female sex differentiation	0.51	>=0.20
ENSG00000168496	FEN1 PPI subnetwork	0.9	>=0.20
ENSG00000151422	FER PPI subnetwork	0.06	>=0.20
GO:0015682	ferric iron transport	0.56	>=0.20
GO:0009566	fertilization	0.99	>=0.20
GO:0001660	fever generation	0.99	>=0.20
ENSG00000149557	FEZ1 PPI subnetwork	0.64	>=0.20
ENSG00000139132	FGD4 PPI subnetwork	0.96	>=0.20
ENSG00000070193	FGF10 PPI subnetwork	0.18	>=0.20
ENSG00000129682	FGF13 PPI subnetwork	0.78	>=0.20
ENSG00000158815	FGF17 PPI subnetwork	0.21	>=0.20
ENSG00000156427	FGF18 PPI subnetwork	0.21	>=0.20
ENSG00000162344	FGF19 PPI subnetwork	0.21	>=0.20
ENSG00000078579	FGF20 PPI subnetwork	0.35	>=0.20
ENSG00000070388	FGF22 PPI subnetwork	0.21	>=0.20
ENSG00000118972	FGF23 PPI subnetwork	0.24	>=0.20
ENSG00000186895	FGF3 PPI subnetwork	0.3	>=0.20
ENSG00000075388	FGF4 PPI subnetwork	0.2	>=0.20
ENSG00000138675	FGF5 PPI subnetwork	0.27	>=0.20
ENSG00000111241	FGF6 PPI subnetwork	0.21	>=0.20
ENSG00000140285	FGF7 PPI subnetwork	0.12	>=0.20
ENSG00000107831	FGF8 PPI subnetwork	0.21	>=0.20
ENSG00000102678	FGF9 PPI subnetwork	0.41	>=0.20
ENSG00000077782	FGFR1 PPI subnetwork	0.5	>=0.20
ENSG00000213066	FGFR1OP PPI subnetwork	0.61	>=0.20
ENSG00000160867	FGFR4 PPI subnetwork	0.95	>=0.20
ENSG00000189283	FHIT PPI subnetwork	0.05	>=0.20
GO:0005583	fibrillar collagen	0.85	>=0.20
GO:0005104	fibroblast growth factor receptor binding	0.97	>=0.20

GO:0008543	fibroblast growth factor receptor signaling pathway	0.76	>=0.20
GO:0001968	fibronectin binding	0.07	>=0.20
GO:0030175	filopodium	0.54	>=0.20
GO:0046847	filopodium assembly	0.88	>=0.20
GO:0031527	filopodium membrane	0.98	>=0.20
ENSG00000145216	FIP1L1 PPI subnetwork	0.2	>=0.20
ENSG00000088832	FKBP1A PPI subnetwork	0.94	>=0.20
ENSG00000096060	FKBP5 PPI subnetwork	0.22	>=0.20
GO:0019861	flagellum	0.86	>=0.20
GO:0044460	flagellum part	0.69	>=0.20
ENSG00000143520	FLG2 PPI subnetwork	0.17	>=0.20
ENSG00000177731	FLII PPI subnetwork	0.44	>=0.20
ENSG00000196924	FLNA PPI subnetwork	0.13	>=0.20
ENSG00000136068	FLNB PPI subnetwork	0.14	>=0.20
ENSG00000132589	FLOT2 PPI subnetwork	0.07	>=0.20
ENSG00000037280	FLT4 PPI subnetwork	0.06	>=0.20
GO:0042044	fluid transport	0.96	>=0.20
ENSG00000184922	FMNL1 PPI subnetwork	0.13	>=0.20
ENSG00000187239	FNBP1 PPI subnetwork	1	>=0.20
ENSG00000168522	FNTA PPI subnetwork	0.9	>=0.20
GO:0090077	foam cell differentiation	0.04	>=0.20
GO:0048041	focal adhesion assembly	0.68	>=0.20
GO:0006760	folic acid-containing compound metabolic process	0.78	>=0.20
GO:0021885	forebrain cell migration	0.93	>=0.20
GO:0030900	forebrain development	1	>=0.20
GO:0021872	forebrain generation of neurons	1	>=0.20
GO:0021879	forebrain neuron differentiation	1	>=0.20
GO:0021871	forebrain regionalization	1	>=0.20
GO:0035136	forelimb morphogenesis	1	>=0.20
GO:0001704	formation of primary germ layer	0.89	>=0.20
ENSG00000125740	FOSB PPI subnetwork	0.18	>=0.20
ENSG00000175592	FOSL1 PPI subnetwork	0.08	>=0.20
ENSG00000075426	FOSL2 PPI subnetwork	0.03	>=0.20
GO:0009378	four-way junction helicase activity	0.43	>=0.20
ENSG00000129514	FOXA1 PPI subnetwork	0.56	>=0.20
ENSG00000125798	FOXA2 PPI subnetwork	0.96	>=0.20
ENSG00000176165	FOXG1 PPI subnetwork	0.41	>=0.20
MP:0000061	fragile skeleton	0.7	>=0.20
GO:0005109	frizzled binding	1	>=0.20
ENSG00000166225	FRS2 PPI subnetwork	0.87	>=0.20
ENSG00000137218	FRS3 PPI subnetwork	0.77	>=0.20
GO:0006000	fructose metabolic process	0.07	>=0.20
ENSG00000073910	FRY PPI subnetwork	0.3	>=0.20
ENSG00000075539	FRYL PPI subnetwork	0.21	>=0.20
ENSG00000075618	FSCN1 PPI subnetwork	0.53	>=0.20
ENSG00000108592	FTSJ3 PPI subnetwork	0.64	>=0.20
ENSG00000162613	FUBP1 PPI subnetwork	1	>=0.20

GO:0006004	fucose metabolic process	0.99	>=0.20
GO:0008417	fucosyltransferase activity	0.84	>=0.20
ENSG00000140564	FURIN PPI subnetwork	0.93	>=0.20
ENSG00000089280	FUS PPI subnetwork	0.06	>=0.20
MP:0010701	fusion of atlas and odontoid process	0.27	>=0.20
MP:0004568	fusion of glossopharyngeal and vagus nerve	0.2	>=0.20
MP:0004613	fusion of vertebral arches	0.99	>=0.20
ENSG00000082074	FYB PPI subnetwork	0.87	>=0.20
ENSG00000010810	FYN PPI subnetwork	0.35	>=0.20
ENSG00000157240	FZD1 PPI subnetwork	1	>=0.20
ENSG00000111432	FZD10 PPI subnetwork	0.99	>=0.20
ENSG00000180340	FZD2 PPI subnetwork	1	>=0.20
ENSG00000104290	FZD3 PPI subnetwork	0.99	>=0.20
ENSG00000174804	FZD4 PPI subnetwork	1	>=0.20
ENSG00000163251	FZD5 PPI subnetwork	0.95	>=0.20
ENSG00000164930	FZD6 PPI subnetwork	0.99	>=0.20
ENSG00000155760	FZD7 PPI subnetwork	1	>=0.20
ENSG00000177283	FZD8 PPI subnetwork	0.98	>=0.20
ENSG00000188763	FZD9 PPI subnetwork	0.99	>=0.20
ENSG00000105325	FZR1 PPI subnetwork	0.51	>=0.20
GO:0031683	G-protein beta/gamma-subunit complex binding	0.89	>=0.20
GO:0007213	G-protein coupled acetylcholine receptor signaling pathway	1	>=0.20
GO:0008227	G-protein coupled amine receptor activity	1	>=0.20
GO:0001637	G-protein coupled chemoattractant receptor activity	0.47	>=0.20
GO:0001608	G-protein coupled nucleotide receptor activity	0.94	>=0.20
GO:0008528	G-protein coupled peptide receptor activity	0.44	>=0.20
GO:0045028	G-protein coupled purinergic nucleotide receptor activity	0.94	>=0.20
GO:0004930	G-protein coupled receptor activity	0.91	>=0.20
GO:0001664	G-protein coupled receptor binding	0.6	>=0.20
GO:0007187	G-protein coupled receptor signaling pathway, coupled to cy	0.99	>=0.20
GO:0051318	G1 phase	0.21	>=0.20
GO:0000080	G1 phase of mitotic cell cycle	0.11	>=0.20
GO:0071779	G1/S transition checkpoint	0.93	>=0.20
GO:0000082	G1/S transition of mitotic cell cycle	0.94	>=0.20
GO:0031576	G2/M transition checkpoint	0.63	>=0.20
GO:0000086	G2/M transition of mitotic cell cycle	0.62	>=0.20
ENSG00000145907	G3BP1 PPI subnetwork	0.11	>=0.20
ENSG00000138757	G3BP2 PPI subnetwork	0.38	>=0.20
ENSG00000033327	GAB2 PPI subnetwork	0.13	>=0.20
GO:0004890	GABA-A receptor activity	1	>=0.20
GO:0016917	GABA receptor activity	1	>=0.20
ENSG00000170296	GABARAP PPI subnetwork	0.34	>=0.20
ENSG00000139112	GABARAPL1 PPI subnetwork	0.78	>=0.20
ENSG00000034713	GABARAPL2 PPI subnetwork	0.03	>=0.20
ENSG00000204681	GABBR1 PPI subnetwork	0.82	>=0.20
ENSG00000206466	GABBR1 PPI subnetwork	0.82	>=0.20
ENSG00000206511	GABBR1 PPI subnetwork	0.82	>=0.20

ENSG00000154727	GABPA PPI subnetwork	0.65	>=0.20
ENSG00000104064	GABPB1 PPI subnetwork	0.91	>=0.20
ENSG00000022355	GABRA1 PPI subnetwork	1	>=0.20
ENSG00000151834	GABRA2 PPI subnetwork	1	>=0.20
ENSG00000163288	GABRB1 PPI subnetwork	1	>=0.20
ENSG00000145864	GABRB2 PPI subnetwork	1	>=0.20
ENSG00000166206	GABRB3 PPI subnetwork	1	>=0.20
ENSG00000113327	GABRG2 PPI subnetwork	1	>=0.20
ENSG00000178950	GAK PPI subnetwork	0.14	>=0.20
GO:0008378	galactosyltransferase activity	0.88	>=0.20
GO:0007276	gamete generation	0.9	>=0.20
GO:0007214	gamma-aminobutyric acid signaling pathway	1	>=0.20
GO:0015812	gamma-aminobutyric acid transport	1	>=0.20
GO:0045295	gamma-catenin binding	0.86	>=0.20
GO:0000930	gamma-tubulin complex	0.76	>=0.20
ENSG00000127688	GAN PPI subnetwork	0.19	>=0.20
ENSG00000089597	GANAB PPI subnetwork	0.17	>=0.20
GO:0001573	ganglioside metabolic process	0.92	>=0.20
GO:0005921	gap junction	0.21	>=0.20
GO:0005243	gap junction channel activity	0.52	>=0.20
ENSG00000172020	GAP43 PPI subnetwork	0.99	>=0.20
ENSG00000111640	GAPDH PPI subnetwork	0.26	>=0.20
ENSG00000165219	GAPVD1 PPI subnetwork	0.17	>=0.20
ENSG00000106105	GARS PPI subnetwork	0.39	>=0.20
ENSG00000159131	GART PPI subnetwork	0.38	>=0.20
GO:0015669	gas transport	1	>=0.20
ENSG00000007237	GAS7 PPI subnetwork	0.18	>=0.20
GO:0007369	gastrulation	0.87	>=0.20
GO:0001702	gastrulation with mouth forming second	0.92	>=0.20
ENSG00000102145	GATA1 PPI subnetwork	0.05	>=0.20
ENSG00000179348	GATA2 PPI subnetwork	0.03	>=0.20
ENSG00000136574	GATA4 PPI subnetwork	0.17	>=0.20
ENSG00000167491	GATAD2A PPI subnetwork	0.5	>=0.20
ENSG00000143614	GATAD2B PPI subnetwork	0.54	>=0.20
GO:0022836	gated channel activity	1	>=0.20
ENSG00000160844	GATS PPI subnetwork	0.42	>=0.20
ENSG00000146729	GBAS PPI subnetwork	0.75	>=0.20
ENSG00000145321	GC PPI subnetwork	0.44	>=0.20
ENSG00000164404	GDF9 PPI subnetwork	0.88	>=0.20
ENSG00000203879	GDI1 PPI subnetwork	0.09	>=0.20
ENSG00000057608	GDI2 PPI subnetwork	0.12	>=0.20
GO:0019003	GDP binding	0.46	>=0.20
ENSG00000179409	GEMIN4 PPI subnetwork	0.3	>=0.20
ENSG00000082516	GEMIN5 PPI subnetwork	0.71	>=0.20
ENSG00000152147	GEMIN6 PPI subnetwork	0.86	>=0.20
ENSG00000142252	GEMIN7 PPI subnetwork	0.93	>=0.20
GO:0016458	gene silencing	0.71	>=0.20

GO:0035195	gene silencing by miRNA	0.97	>=0.20
GO:0031047	gene silencing by RNA	0.97	>=0.20
GO:0003001	generation of a signal involved in cell-cell signaling	0.68	>=0.20
GO:0006091	generation of precursor metabolites and energy	0.15	>=0.20
GO:0048806	genitalia development	0.96	>=0.20
GO:0007281	germ cell development	0.95	>=0.20
GO:0043073	germ cell nucleus	1	>=0.20
GO:0060293	germ plasm	0.95	>=0.20
GO:0002467	germinal center formation	0.67	>=0.20
ENSG00000165702	GFI1B PPI subnetwork	0.83	>=0.20
ENSG00000198380	GFPT1 PPI subnetwork	0.21	>=0.20
ENSG00000125447	GGA3 PPI subnetwork	0.36	>=0.20
ENSG00000204120	GIGYF2 PPI subnetwork	0.56	>=0.20
ENSG00000101003	GINS1 PPI subnetwork	0.92	>=0.20
ENSG00000131153	GINS2 PPI subnetwork	0.92	>=0.20
ENSG00000147536	GINS4 PPI subnetwork	0.74	>=0.20
ENSG00000123159	GIPC1 PPI subnetwork	0.38	>=0.20
ENSG00000108262	GIT1 PPI subnetwork	0.99	>=0.20
ENSG00000139436	GIT2 PPI subnetwork	0.28	>=0.20
ENSG00000152661	GJA1 PPI subnetwork	0.26	>=0.20
GO:0048732	gland development	0.95	>=0.20
GO:0022612	gland morphogenesis	0.92	>=0.20
ENSG00000119392	GLE1 PPI subnetwork	0.8	>=0.20
ENSG00000090863	GLG1 PPI subnetwork	0.29	>=0.20
ENSG00000111087	GLI1 PPI subnetwork	0.41	>=0.20
ENSG00000074047	GLI2 PPI subnetwork	0.64	>=0.20
ENSG00000106571	GLI3 PPI subnetwork	0.62	>=0.20
GO:0021782	glial cell development	0.82	>=0.20
GO:0010001	glial cell differentiation	0.8	>=0.20
GO:0021781	glial cell fate commitment	1	>=0.20
GO:0042063	gliogenesis	0.78	>=0.20
MP:0002183	gliosis	0.31	>=0.20
GO:0032835	glomerulus development	0.83	>=0.20
GO:0072012	glomerulus vasculature development	0.98	>=0.20
ENSG00000139433	GLTP PPI subnetwork	1	>=0.20
GO:0009251	glucan catabolic process	0.14	>=0.20
GO:0008211	glucocorticoid metabolic process	0.58	>=0.20
GO:0006041	glucosamine metabolic process	0.96	>=0.20
GO:0006007	glucose catabolic process	0.03	>=0.20
GO:0015758	glucose transport	0.16	>=0.20
GO:0015926	glucosidase activity	0.12	>=0.20
GO:0015020	glucuronosyltransferase activity	0.86	>=0.20
ENSG00000148672	GLUD1 PPI subnetwork	0.77	>=0.20
GO:0008066	glutamate receptor activity	1	>=0.20
GO:0035254	glutamate receptor binding	1	>=0.20
GO:0007215	glutamate receptor signaling pathway	1	>=0.20
GO:0014047	glutamate secretion	1	>=0.20

GO:0009065	glutamine family amino acid catabolic process	0.58	>=0.20
GO:0006749	glutathione metabolic process	0.84	>=0.20
GO:0004602	glutathione peroxidase activity	0.22	>=0.20
GO:0004364	glutathione transferase activity	0.71	>=0.20
GO:0006071	glycerol metabolic process	0.28	>=0.20
GO:0016594	glycine binding	0.74	>=0.20
GO:0005980	glycogen catabolic process	0.14	>=0.20
GO:0009247	glycolipid biosynthetic process	0.98	>=0.20
GO:0006664	glycolipid metabolic process	0.66	>=0.20
GO:0001948	glycoprotein binding	0.22	>=0.20
GO:0009101	glycoprotein biosynthetic process	0.67	>=0.20
GO:0006516	glycoprotein catabolic process	0.67	>=0.20
GO:0009100	glycoprotein metabolic process	0.71	>=0.20
GO:0006024	glycosaminoglycan biosynthetic process	0.22	>=0.20
GO:0006688	glycosphingolipid biosynthetic process	0.99	>=0.20
GO:0006687	glycosphingolipid metabolic process	0.85	>=0.20
GO:0070085	glycosylation	0.96	>=0.20
ENSG00000162419	GMEB1 PPI subnetwork	0.92	>=0.20
ENSG00000197045	GMFB PPI subnetwork	0.12	>=0.20
ENSG00000112312	GMNN PPI subnetwork	0.72	>=0.20
GO:0019002	GMP binding	0.93	>=0.20
ENSG00000088256	GNA11 PPI subnetwork	0.5	>=0.20
ENSG00000156049	GNA14 PPI subnetwork	0.73	>=0.20
ENSG00000060558	GNA15 PPI subnetwork	0.88	>=0.20
ENSG00000127955	GNAI1 PPI subnetwork	0.78	>=0.20
ENSG00000114353	GNAI2 PPI subnetwork	0.51	>=0.20
ENSG00000065135	GNAI3 PPI subnetwork	0.55	>=0.20
ENSG00000141404	GNAL PPI subnetwork	0.99	>=0.20
ENSG00000087258	GNAO1 PPI subnetwork	0.27	>=0.20
ENSG00000156052	GNAQ PPI subnetwork	0.56	>=0.20
ENSG00000087460	GNAS PPI subnetwork	0.58	>=0.20
ENSG00000128266	GNAZ PPI subnetwork	0.99	>=0.20
ENSG00000078369	GNB1 PPI subnetwork	0.98	>=0.20
ENSG00000204628	GNB2L1 PPI subnetwork	0.35	>=0.20
ENSG00000111664	GNB3 PPI subnetwork	0.91	>=0.20
ENSG00000114450	GNB4 PPI subnetwork	0.98	>=0.20
ENSG00000127920	GNG11 PPI subnetwork	0.94	>=0.20
ENSG00000127588	GNG13 PPI subnetwork	0.85	>=0.20
ENSG00000162188	GNG3 PPI subnetwork	0.88	>=0.20
ENSG00000168243	GNG4 PPI subnetwork	0.88	>=0.20
ENSG00000174021	GNG5 PPI subnetwork	0.95	>=0.20
ENSG00000167414	GNG8 PPI subnetwork	0.83	>=0.20
ENSG00000127928	GNGT1 PPI subnetwork	0.87	>=0.20
ENSG00000167083	GNGT2 PPI subnetwork	1	>=0.20
ENSG00000204590	GNL1 PPI subnetwork	0.35	>=0.20
ENSG00000206412	GNL1 PPI subnetwork	0.35	>=0.20
ENSG00000206492	GNL1 PPI subnetwork	0.35	>=0.20

ENSG00000134697	GNL2 PPI subnetwork	0.63	>=0.20
ENSG00000167110	GOLGA2 PPI subnetwork	0.29	>=0.20
ENSG00000090615	GOLGA3 PPI subnetwork	0.08	>=0.20
GO:0005798	Golgi-associated vesicle	0.06	>=0.20
GO:0030660	Golgi-associated vesicle membrane	0.33	>=0.20
GO:0031985	Golgi cisterna	0.2	>=0.20
GO:0032580	Golgi cisterna membrane	0.34	>=0.20
GO:0000139	Golgi membrane	0.43	>=0.20
GO:0007030	Golgi organization	0.73	>=0.20
GO:0005795	Golgi stack	0.22	>=0.20
GO:0006893	Golgi to plasma membrane transport	0.99	>=0.20
GO:0017119	Golgi transport complex	0.5	>=0.20
GO:0048200	Golgi transport vesicle coating	0.46	>=0.20
GO:0048194	Golgi vesicle budding	0.55	>=0.20
GO:0048193	Golgi vesicle transport	0.23	>=0.20
GO:0008406	gonad development	0.65	>=0.20
ENSG00000114745	GORASP1 PPI subnetwork	0.07	>=0.20
ENSG00000108433	GOSR2 PPI subnetwork	0.03	>=0.20
ENSG00000125166	GOT2 PPI subnetwork	0.56	>=0.20
ENSG00000171723	GPHN PPI subnetwork	0.88	>=0.20
GO:0006506	GPI anchor biosynthetic process	0.95	>=0.20
GO:0006505	GPI anchor metabolic process	0.91	>=0.20
ENSG00000198932	GPRASP1 PPI subnetwork	0.84	>=0.20
ENSG00000204175	GPRIN2 PPI subnetwork	0.15	>=0.20
ENSG00000169727	GPS1 PPI subnetwork	0.6	>=0.20
ENSG00000161835	GRASP PPI subnetwork	0.98	>=0.20
ENSG00000106070	GRB10 PPI subnetwork	0.31	>=0.20
ENSG00000155511	GRIA1 PPI subnetwork	0.97	>=0.20
ENSG00000120251	GRIA2 PPI subnetwork	0.99	>=0.20
ENSG00000152578	GRIA4 PPI subnetwork	0.91	>=0.20
ENSG00000152208	GRID2 PPI subnetwork	1	>=0.20
ENSG00000164418	GRIK2 PPI subnetwork	0.51	>=0.20
ENSG00000176884	GRIN1 PPI subnetwork	0.88	>=0.20
ENSG00000183454	GRIN2A PPI subnetwork	0.97	>=0.20
ENSG00000150086	GRIN2B PPI subnetwork	0.94	>=0.20
ENSG00000198785	GRIN3A PPI subnetwork	0.96	>=0.20
ENSG00000155974	GRIP1 PPI subnetwork	1	>=0.20
ENSG00000198873	GRK5 PPI subnetwork	0.72	>=0.20
ENSG00000152822	GRM1 PPI subnetwork	0.91	>=0.20
ENSG00000168959	GRM5 PPI subnetwork	0.81	>=0.20
ENSG00000196277	GRM7 PPI subnetwork	0.42	>=0.20
GO:0030426	growth cone	0.99	>=0.20
GO:0008083	growth factor activity	0.33	>=0.20
GO:0070851	growth factor receptor binding	0.3	>=0.20
GO:0044110	growth involved in symbiotic interaction	0.93	>=0.20
GO:0044117	growth of symbiont in host	0.93	>=0.20
GO:0044116	growth of symbiont involved in interaction with host	0.93	>=0.20

ENSG00000109519	GRPEL1 PPI subnetwork	0.32	>=0.20
ENSG00000105447	GRWD1 PPI subnetwork	0.93	>=0.20
ENSG00000177602	GSG2 PPI subnetwork	0.14	>=0.20
ENSG00000105723	GSK3A PPI subnetwork	0.05	>=0.20
ENSG00000148180	GSN PPI subnetwork	0.36	>=0.20
ENSG00000189369	GSPT2 PPI subnetwork	0.94	>=0.20
ENSG00000197448	GSTK1 PPI subnetwork	0.27	>=0.20
ENSG00000134184	GSTM1 PPI subnetwork	0.63	>=0.20
ENSG00000134202	GSTM3 PPI subnetwork	0.45	>=0.20
ENSG00000084207	GSTP1 PPI subnetwork	0.54	>=0.20
ENSG00000165417	GTF2A1 PPI subnetwork	0.58	>=0.20
ENSG00000140307	GTF2A2 PPI subnetwork	0.61	>=0.20
ENSG00000137947	GTF2B PPI subnetwork	0.39	>=0.20
ENSG00000153767	GTF2E1 PPI subnetwork	0.81	>=0.20
ENSG00000197265	GTF2E2 PPI subnetwork	0.87	>=0.20
ENSG00000125651	GTF2F1 PPI subnetwork	0.05	>=0.20
ENSG00000110768	GTF2H1 PPI subnetwork	0.27	>=0.20
ENSG00000145736	GTF2H2 PPI subnetwork	0.38	>=0.20
ENSG00000183474	GTF2H2C PPI subnetwork	0.78	>=0.20
ENSG00000111358	GTF2H3 PPI subnetwork	0.64	>=0.20
ENSG00000213780	GTF2H4 PPI subnetwork	0.71	>=0.20
ENSG00000122034	GTF3A PPI subnetwork	0.97	>=0.20
ENSG00000077235	GTF3C1 PPI subnetwork	0.71	>=0.20
ENSG00000115207	GTF3C2 PPI subnetwork	0.25	>=0.20
ENSG00000119041	GTF3C3 PPI subnetwork	0.55	>=0.20
ENSG00000125484	GTF3C4 PPI subnetwork	0.83	>=0.20
ENSG00000148308	GTF3C5 PPI subnetwork	0.97	>=0.20
GO:0005525	GTP binding	0.63	>=0.20
GO:0006184	GTP catabolic process	0.78	>=0.20
GO:0046039	GTP metabolic process	0.78	>=0.20
GO:0005096	GTPase activator activity	0.21	>=0.20
GO:0003924	GTPase activity	0.84	>=0.20
GO:0051020	GTPase binding	0.73	>=0.20
GO:0030695	GTPase regulator activity	0.38	>=0.20
ENSG00000107937	GTPBP4 PPI subnetwork	0.53	>=0.20
GO:0005085	guanyl-nucleotide exchange factor activity	0.3	>=0.20
GO:0019001	guanyl nucleotide binding	0.65	>=0.20
GO:0032561	guanyl ribonucleotide binding	0.65	>=0.20
GO:0004385	guanylate kinase activity	1	>=0.20
ENSG00000145649	GZMA PPI subnetwork	0.87	>=0.20
ENSG00000189060	H1F0 PPI subnetwork	0.89	>=0.20
ENSG00000184897	H1FX PPI subnetwork	0.04	>=0.20
ENSG00000105968	H2AFV PPI subnetwork	0.83	>=0.20
ENSG00000188486	H2AFX PPI subnetwork	0.6	>=0.20
ENSG00000164032	H2AFZ PPI subnetwork	0.8	>=0.20
ENSG00000163041	H3F3A PPI subnetwork	0.48	>=0.20
ENSG00000132475	H3F3B PPI subnetwork	0.48	>=0.20

GO:0043189	H4/H2A histone acetyltransferase complex	0.34	>=0.20
ENSG00000130956	HABP4 PPI subnetwork	0.91	>=0.20
ENSG00000084754	HADHA PPI subnetwork	0.1	>=0.20
ENSG00000138029	HADHB PPI subnetwork	0.17	>=0.20
GO:0042633	hair cycle	0.98	>=0.20
GO:0022405	hair cycle process	0.98	>=0.20
GO:0001942	hair follicle development	0.98	>=0.20
GO:0031069	hair follicle morphogenesis	1	>=0.20
MP:0009243	hairpin sperm flagellum	0.63	>=0.20
ENSG00000113196	HAND1 PPI subnetwork	0.46	>=0.20
ENSG00000164107	HAND2 PPI subnetwork	0.27	>=0.20
ENSG00000173805	HAP1 PPI subnetwork	0.96	>=0.20
ENSG00000105509	HAS1 PPI subnetwork	0.51	>=0.20
ENSG00000134248	HBXIP PPI subnetwork	0.68	>=0.20
ENSG00000068024	HDAC4 PPI subnetwork	0.12	>=0.20
ENSG00000108840	HDAC5 PPI subnetwork	0.53	>=0.20
ENSG00000094631	HDAC6 PPI subnetwork	0.06	>=0.20
ENSG00000147099	HDAC8 PPI subnetwork	0.5	>=0.20
ENSG00000048052	HDAC9 PPI subnetwork	0.55	>=0.20
MP:0001410	head bobbing	0.99	>=0.20
GO:0060322	head development	0.99	>=0.20
GO:0060323	head morphogenesis	1	>=0.20
MP:0002730	head shaking	0.97	>=0.20
MP:0005191	head tilt	0.94	>=0.20
MP:0005307	head tossing	0.89	>=0.20
GO:0060047	heart contraction	0.84	>=0.20
GO:0007507	heart development	0.7	>=0.20
GO:0060419	heart growth	0.91	>=0.20
MP:0002740	heart hypoplasia	0.67	>=0.20
MP:0002625	heart left ventricle hypertrophy	0.29	>=0.20
GO:0001947	heart looping	0.93	>=0.20
GO:0003007	heart morphogenesis	0.97	>=0.20
GO:0003015	heart process	0.82	>=0.20
MP:0000276	heart right ventricle hypertrophy	0.37	>=0.20
GO:0003170	heart valve development	0.85	>=0.20
GO:0003179	heart valve morphogenesis	0.83	>=0.20
GO:0031649	heat generation	0.99	>=0.20
GO:0031072	heat shock protein binding	0.32	>=0.20
ENSG00000008869	HEATR5B PPI subnetwork	1	>=0.20
ENSG00000013583	HEBP1 PPI subnetwork	0.7	>=0.20
ENSG00000198265	HELZ PPI subnetwork	0.34	>=0.20
GO:0015002	heme-copper terminal oxidase activity	0.99	>=0.20
GO:0006783	heme biosynthetic process	0.86	>=0.20
GO:0042168	heme metabolic process	0.76	>=0.20
GO:0031581	hemidesmosome assembly	0.78	>=0.20
GO:0020027	hemoglobin metabolic process	0.36	>=0.20
GO:0043395	heparan sulfate proteoglycan binding	0.13	>=0.20

GO:0015012	heparan sulfate proteoglycan biosynthetic process	0.75	>=0.20
GO:0034483	heparan sulfate sulfotransferase activity	0.9	>=0.20
ENSG00000128731	HERC2 PPI subnetwork	0.96	>=0.20
MP:0000757	herniated abdominal wall	0.85	>=0.20
MP:0003924	herniated diaphragm	0.07	>=0.20
GO:0018130	heterocycle biosynthetic process	0.61	>=0.20
GO:0030530	heterogeneous nuclear ribonucleoprotein complex	0.03	>=0.20
GO:0005834	heterotrimeric G-protein complex	1	>=0.20
GO:0015149	hexose transmembrane transporter activity	0.04	>=0.20
GO:0008645	hexose transport	0.16	>=0.20
ENSG00000164683	HEY1 PPI subnetwork	0.83	>=0.20
ENSG00000135547	HEY2 PPI subnetwork	0.37	>=0.20
ENSG00000185359	HGS PPI subnetwork	0.75	>=0.20
ENSG00000198130	HIBCH PPI subnetwork	0.88	>=0.20
ENSG00000181061	HIGD1A PPI subnetwork	0.08	>=0.20
GO:0030902	hindbrain development	0.97	>=0.20
GO:0035137	hindlimb morphogenesis	1	>=0.20
MP:0000755	hindlimb paralysis	0.82	>=0.20
ENSG00000130787	HIP1R PPI subnetwork	0.35	>=0.20
ENSG00000163349	HIPK1 PPI subnetwork	0.53	>=0.20
ENSG00000064393	HIPK2 PPI subnetwork	0.94	>=0.20
GO:0035329	hippo signaling cascade	0.96	>=0.20
GO:0021766	hippocampus development	0.84	>=0.20
ENSG00000100084	HIRA PPI subnetwork	0.87	>=0.20
ENSG00000184357	HIST1H1B PPI subnetwork	0.61	>=0.20
ENSG00000124575	HIST1H1D PPI subnetwork	0.16	>=0.20
ENSG00000137259	HIST1H2AB PPI subnetwork	0.47	>=0.20
ENSG00000180573	HIST1H2AC PPI subnetwork	0.4	>=0.20
ENSG00000196866	HIST1H2AD PPI subnetwork	0.41	>=0.20
ENSG00000168274	HIST1H2AE PPI subnetwork	0.47	>=0.20
ENSG00000196787	HIST1H2AG PPI subnetwork	0.41	>=0.20
ENSG00000184825	HIST1H2AH PPI subnetwork	0.41	>=0.20
ENSG00000196747	HIST1H2AI PPI subnetwork	0.41	>=0.20
ENSG00000184348	HIST1H2AK PPI subnetwork	0.41	>=0.20
ENSG00000198374	HIST1H2AL PPI subnetwork	0.41	>=0.20
ENSG00000146047	HIST1H2BA PPI subnetwork	0.26	>=0.20
ENSG00000196226	HIST1H2BB PPI subnetwork	0.63	>=0.20
ENSG00000180596	HIST1H2BC PPI subnetwork	0.72	>=0.20
ENSG00000158373	HIST1H2BD PPI subnetwork	0.65	>=0.20
ENSG00000197697	HIST1H2BE PPI subnetwork	0.73	>=0.20
ENSG00000197846	HIST1H2BF PPI subnetwork	0.72	>=0.20
ENSG00000187990	HIST1H2BG PPI subnetwork	0.72	>=0.20
ENSG00000197459	HIST1H2BH PPI subnetwork	0.22	>=0.20
ENSG00000168242	HIST1H2BI PPI subnetwork	0.72	>=0.20
ENSG00000124635	HIST1H2BJ PPI subnetwork	0.68	>=0.20
ENSG00000197903	HIST1H2BK PPI subnetwork	0.69	>=0.20
ENSG00000185130	HIST1H2BL PPI subnetwork	0.61	>=0.20

ENSG00000196374	HIST1H2BM PPI subnetwork	0.57	>=0.20
ENSG00000196331	HIST1H2BO PPI subnetwork	0.29	>=0.20
ENSG00000198366	HIST1H3A PPI subnetwork	0.68	>=0.20
ENSG00000124693	HIST1H3B PPI subnetwork	0.68	>=0.20
ENSG00000196532	HIST1H3C PPI subnetwork	0.68	>=0.20
ENSG00000197409	HIST1H3D PPI subnetwork	0.68	>=0.20
ENSG00000196966	HIST1H3E PPI subnetwork	0.68	>=0.20
ENSG00000203813	HIST1H3H PPI subnetwork	0.56	>=0.20
ENSG00000182572	HIST1H3I PPI subnetwork	0.68	>=0.20
ENSG00000197153	HIST1H3J PPI subnetwork	0.68	>=0.20
ENSG00000196176	HIST1H4A PPI subnetwork	0.1	>=0.20
ENSG00000124529	HIST1H4B PPI subnetwork	0.1	>=0.20
ENSG00000197061	HIST1H4C PPI subnetwork	0.1	>=0.20
ENSG00000188987	HIST1H4D PPI subnetwork	0.1	>=0.20
ENSG00000198518	HIST1H4E PPI subnetwork	0.1	>=0.20
ENSG00000198327	HIST1H4F PPI subnetwork	0.1	>=0.20
ENSG00000158406	HIST1H4H PPI subnetwork	0.1	>=0.20
ENSG00000198339	HIST1H4I PPI subnetwork	0.1	>=0.20
ENSG00000197238	HIST1H4J PPI subnetwork	0.1	>=0.20
ENSG00000197914	HIST1H4K PPI subnetwork	0.1	>=0.20
ENSG00000198558	HIST1H4L PPI subnetwork	0.1	>=0.20
ENSG00000183558	HIST2H2AA3 PPI subnetwork	0.4	>=0.20
ENSG00000203812	HIST2H2AA4 PPI subnetwork	0.4	>=0.20
ENSG00000184270	HIST2H2AB PPI subnetwork	0.39	>=0.20
ENSG00000184678	HIST2H2BE PPI subnetwork	0.29	>=0.20
ENSG00000203814	HIST2H2BF PPI subnetwork	0.64	>=0.20
ENSG00000203852	HIST2H3A PPI subnetwork	0.55	>=0.20
ENSG00000203811	HIST2H3C PPI subnetwork	0.23	>=0.20
ENSG00000183598	HIST2H3D PPI subnetwork	0.23	>=0.20
ENSG00000183941	HIST2H4A PPI subnetwork	0.1	>=0.20
ENSG00000182217	HIST2H4B PPI subnetwork	0.1	>=0.20
ENSG00000181218	HIST3H2A PPI subnetwork	0.53	>=0.20
ENSG00000196890	HIST3H2BB PPI subnetwork	0.75	>=0.20
ENSG00000168148	HIST3H3 PPI subnetwork	0.45	>=0.20
ENSG00000197837	HIST4H4 PPI subnetwork	0.1	>=0.20
GO:0018024	histone-lysine N-methyltransferase activity	0.09	>=0.20
GO:0016573	histone acetylation	0.79	>=0.20
GO:0004402	histone acetyltransferase activity	0.38	>=0.20
GO:0000123	histone acetyltransferase complex	0.14	>=0.20
GO:0042393	histone binding	0.04	>=0.20
GO:0031078	histone deacetylase activity (H3-K14 specific)	0.95	>=0.20
GO:0032129	histone deacetylase activity (H3-K9 specific)	0.92	>=0.20
GO:0034739	histone deacetylase activity (H4-K16 specific)	0.95	>=0.20
GO:0042826	histone deacetylase binding	0.25	>=0.20
GO:0000118	histone deacetylase complex	0.6	>=0.20
GO:0043486	histone exchange	0.98	>=0.20
GO:0043968	histone H2A acetylation	0.98	>=0.20

GO:0033522	histone H2A ubiquitination	1	>=0.20
GO:0051568	histone H3-K4 methylation	0.64	>=0.20
GO:0051567	histone H3-K9 methylation	0.53	>=0.20
GO:0043966	histone H3 acetylation	0.64	>=0.20
GO:0043967	histone H4 acetylation	0.72	>=0.20
GO:0034968	histone lysine methylation	0.5	>=0.20
GO:0016571	histone methylation	0.48	>=0.20
GO:0016570	histone modification	0.26	>=0.20
GO:0016574	histone ubiquitination	1	>=0.20
ENSG00000010818	HIVEP2 PPI subnetwork	0.47	>=0.20
ENSG00000206503	HLA-A PPI subnetwork	0.69	>=0.20
ENSG00000206505	HLA-A PPI subnetwork	0.47	>=0.20
ENSG00000206450	HLA-B PPI subnetwork	0.7	>=0.20
ENSG00000206452	HLA-C PPI subnetwork	0.53	>=0.20
ENSG00000204257	HLA-DMA PPI subnetwork	0.94	>=0.20
ENSG00000196735	HLA-DQA1 PPI subnetwork	0.73	>=0.20
ENSG00000179344	HLA-DQB1 PPI subnetwork	0.78	>=0.20
ENSG00000206308	HLA-DRA PPI subnetwork	0.32	>=0.20
ENSG00000206240	HLA-DRB1 PPI subnetwork	0.58	>=0.20
ENSG00000206306	HLA-DRB1 PPI subnetwork	0.58	>=0.20
ENSG00000204592	HLA-E PPI subnetwork	0.97	>=0.20
ENSG00000206493	HLA-E PPI subnetwork	0.97	>=0.20
ENSG00000137403	HLA-F PPI subnetwork	0.93	>=0.20
ENSG00000204642	HLA-F PPI subnetwork	0.93	>=0.20
ENSG00000206509	HLA-F PPI subnetwork	0.87	>=0.20
ENSG00000204632	HLA-G PPI subnetwork	0.87	>=0.20
ENSG00000206506	HLA-G PPI subnetwork	0.87	>=0.20
ENSG00000071794	HLTF PPI subnetwork	0.99	>=0.20
ENSG00000137309	HMGA1 PPI subnetwork	0.09	>=0.20
ENSG00000149948	HMGA2 PPI subnetwork	0.25	>=0.20
ENSG00000164104	HMGB2 PPI subnetwork	0.98	>=0.20
ENSG00000100292	HMOX1 PPI subnetwork	0.23	>=0.20
ENSG00000170144	HNRNPA3 PPI subnetwork	0.1	>=0.20
ENSG00000092199	HNRNPC PPI subnetwork	0.09	>=0.20
ENSG00000169045	HNRNPH1 PPI subnetwork	0.05	>=0.20
ENSG00000126945	HNRNPH2 PPI subnetwork	0.07	>=0.20
ENSG00000104824	HNRNPL PPI subnetwork	0.04	>=0.20
ENSG00000099783	HNRNPM PPI subnetwork	0.05	>=0.20
ENSG00000125944	HNRNPR PPI subnetwork	0.08	>=0.20
ENSG00000105323	HNRNPUL1 PPI subnetwork	0.06	>=0.20
ENSG00000152795	HNRPDL PPI subnetwork	0.1	>=0.20
MP:0005157	holoprosencephaly	0.97	>=0.20
GO:0048872	homeostasis of number of cells	0.05	>=0.20
ENSG00000152413	HOMER1 PPI subnetwork	1	>=0.20
ENSG00000051128	HOMER3 PPI subnetwork	0.67	>=0.20
GO:0007156	homophilic cell adhesion	1	>=0.20
ENSG00000168172	HOOK3 PPI subnetwork	1	>=0.20

GO:0009755	hormone-mediated signaling pathway	0.15	>=0.20
GO:0005179	hormone activity	0.31	>=0.20
GO:0042446	hormone biosynthetic process	0.53	>=0.20
GO:0046879	hormone secretion	0.38	>=0.20
GO:0009914	hormone transport	0.3	>=0.20
ENSG00000078399	HOXA9 PPI subnetwork	0.26	>=0.20
ENSG00000120087	HOXB7 PPI subnetwork	0.47	>=0.20
ENSG00000037965	HOXC8 PPI subnetwork	0.69	>=0.20
ENSG00000174775	HRAS PPI subnetwork	0.08	>=0.20
ENSG00000117594	HSD11B1 PPI subnetwork	0.71	>=0.20
ENSG00000149084	HSD17B12 PPI subnetwork	0.35	>=0.20
ENSG00000185122	HSF1 PPI subnetwork	0.27	>=0.20
ENSG00000102878	HSF4 PPI subnetwork	0.11	>=0.20
ENSG00000165868	HSPA12A PPI subnetwork	1	>=0.20
ENSG00000204390	HSPA1L PPI subnetwork	0.12	>=0.20
ENSG00000173110	HSPA6 PPI subnetwork	0.7	>=0.20
ENSG00000113013	HSPA9 PPI subnetwork	0.14	>=0.20
ENSG00000106211	HSPB1 PPI subnetwork	0.31	>=0.20
ENSG00000152137	HSPB8 PPI subnetwork	0.51	>=0.20
ENSG00000133265	HSPBP1 PPI subnetwork	0.92	>=0.20
ENSG00000142798	HSPG2 PPI subnetwork	0.06	>=0.20
ENSG00000120694	HSPH1 PPI subnetwork	0.06	>=0.20
ENSG00000102241	HTATSF1 PPI subnetwork	0.6	>=0.20
ENSG00000166033	HTRA1 PPI subnetwork	0.6	>=0.20
ENSG00000197386	HTT PPI subnetwork	0.16	>=0.20
MP:0001505	hunched posture	0.08	>=0.20
GO:0005540	hyaluronic acid binding	0.23	>=0.20
MP:0001891	hydroencephaly	0.9	>=0.20
GO:0015078	hydrogen ion transmembrane transporter activity	0.93	>=0.20
GO:0046933	hydrogen ion transporting ATP synthase activity, rotational m	0.24	>=0.20
GO:0042744	hydrogen peroxide catabolic process	0.25	>=0.20
GO:0042743	hydrogen peroxide metabolic process	0.06	>=0.20
GO:0006818	hydrogen transport	0.99	>=0.20
GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzing trans	0.27	>=0.20
GO:0016814	hydrolase activity, acting on carbon-nitrogen (but not peptid	0.31	>=0.20
MP:0000519	hydronephrosis	0.92	>=0.20
MP:0000536	hydroureter	1	>=0.20
ENSG00000149428	HYOU1 PPI subnetwork	0.89	>=0.20
MP:0001399	hyperactivity	0.72	>=0.20
MP:0005407	hyperalgesia	0.75	>=0.20
MP:0000194	hypercalcemia	0.58	>=0.20
MP:0001566	hyperphosphatemia	0.98	>=0.20
MP:0001402	hypoactivity	0.54	>=0.20
MP:0003043	hypoalgesia	0.86	>=0.20
MP:0001596	hypotension	0.08	>=0.20
GO:0007249	I-kappaB kinase/NF-kappaB cascade	0.31	>=0.20
GO:0070411	I-SMAD binding	0.37	>=0.20

GO:0031674	I band	0.67	>=0.20
ENSG00000196305	IARS PPI subnetwork	0.46	>=0.20
ENSG00000067704	IARS2 PPI subnetwork	0.03	>=0.20
ENSG00000105371	ICAM4 PPI subnetwork	0.15	>=0.20
ENSG00000105376	ICAM5 PPI subnetwork	0.12	>=0.20
GO:0046456	icosanoid biosynthetic process	0.97	>=0.20
GO:0006690	icosanoid metabolic process	0.95	>=0.20
GO:0004953	icosanoid receptor activity	0.04	>=0.20
ENSG00000125968	ID1 PPI subnetwork	0.82	>=0.20
ENSG00000115738	ID2 PPI subnetwork	0.62	>=0.20
ENSG00000117318	ID3 PPI subnetwork	0.27	>=0.20
ENSG00000172201	ID4 PPI subnetwork	0.78	>=0.20
ENSG00000166411	IDH3A PPI subnetwork	0.22	>=0.20
ENSG00000067829	IDH3G PPI subnetwork	0.35	>=0.20
ENSG00000148377	IDI2 PPI subnetwork	0.38	>=0.20
ENSG00000185745	IFIT1 PPI subnetwork	0.17	>=0.20
ENSG00000119917	IFIT3 PPI subnetwork	0.39	>=0.20
ENSG00000186803	IFNA10 PPI subnetwork	0.09	>=0.20
ENSG00000147885	IFNA16 PPI subnetwork	0.09	>=0.20
ENSG00000188379	IFNA2 PPI subnetwork	0.09	>=0.20
ENSG00000137080	IFNA21 PPI subnetwork	0.09	>=0.20
ENSG00000147873	IFNA5 PPI subnetwork	0.09	>=0.20
ENSG00000120235	IFNA6 PPI subnetwork	0.06	>=0.20
ENSG00000120242	IFNA8 PPI subnetwork	0.09	>=0.20
ENSG00000142166	IFNAR1 PPI subnetwork	0.23	>=0.20
ENSG00000159110	IFNAR2 PPI subnetwork	0.34	>=0.20
ENSG00000171855	IFNB1 PPI subnetwork	0.08	>=0.20
ENSG00000184995	IFNE PPI subnetwork	0.09	>=0.20
ENSG00000111537	IFNG PPI subnetwork	0.05	>=0.20
ENSG00000027697	IFNGR1 PPI subnetwork	0.33	>=0.20
ENSG00000159128	IFNGR2 PPI subnetwork	0.31	>=0.20
ENSG00000147896	IFNK PPI subnetwork	0.09	>=0.20
ENSG00000177047	IFNW1 PPI subnetwork	0.09	>=0.20
ENSG00000089289	IGBP1 PPI subnetwork	0.7	>=0.20
ENSG00000159217	IGF2BP1 PPI subnetwork	0.07	>=0.20
ENSG00000073792	IGF2BP2 PPI subnetwork	0.22	>=0.20
ENSG00000163453	IGFBP7 PPI subnetwork	0.76	>=0.20
ENSG00000104365	IKBKB PPI subnetwork	0.09	>=0.20
ENSG00000143466	IKBKE PPI subnetwork	0.03	>=0.20
ENSG00000073009	IKBKG PPI subnetwork	0.37	>=0.20
ENSG00000185811	IKZF1 PPI subnetwork	0.83	>=0.20
ENSG00000110324	IL10RA PPI subnetwork	0.31	>=0.20
ENSG00000095752	IL11 PPI subnetwork	0.06	>=0.20
ENSG00000137070	IL11RA PPI subnetwork	0.33	>=0.20
ENSG00000096996	IL12RB1 PPI subnetwork	0.45	>=0.20
ENSG00000081985	IL12RB2 PPI subnetwork	0.37	>=0.20
ENSG00000131724	IL13RA1 PPI subnetwork	0.39	>=0.20

ENSG00000123496	IL13RA2 PPI subnetwork	0.36	>=0.20
ENSG00000164136	IL15 PPI subnetwork	0.09	>=0.20
ENSG00000134470	IL15RA PPI subnetwork	0.36	>=0.20
ENSG00000142224	IL19 PPI subnetwork	0.09	>=0.20
ENSG00000109471	IL2 PPI subnetwork	0.08	>=0.20
ENSG00000162891	IL20 PPI subnetwork	0.09	>=0.20
ENSG00000016402	IL20RA PPI subnetwork	0.39	>=0.20
ENSG00000138684	IL21 PPI subnetwork	0.09	>=0.20
ENSG00000103522	IL21R PPI subnetwork	0.36	>=0.20
ENSG00000127318	IL22 PPI subnetwork	0.08	>=0.20
ENSG00000142677	IL22RA1 PPI subnetwork	0.39	>=0.20
ENSG00000164485	IL22RA2 PPI subnetwork	0.36	>=0.20
ENSG00000110944	IL23A PPI subnetwork	0.13	>=0.20
ENSG00000162594	IL23R PPI subnetwork	0.33	>=0.20
ENSG00000162892	IL24 PPI subnetwork	0.09	>=0.20
ENSG00000111536	IL26 PPI subnetwork	0.09	>=0.20
ENSG00000183709	IL28A PPI subnetwork	0.09	>=0.20
ENSG00000197110	IL28B PPI subnetwork	0.09	>=0.20
ENSG00000185436	IL28RA PPI subnetwork	0.36	>=0.20
ENSG00000182393	IL29 PPI subnetwork	0.09	>=0.20
ENSG00000134460	IL2RA PPI subnetwork	0.25	>=0.20
ENSG00000100385	IL2RB PPI subnetwork	0.13	>=0.20
ENSG00000147168	IL2RG PPI subnetwork	0.16	>=0.20
ENSG00000164399	IL3 PPI subnetwork	0.12	>=0.20
ENSG00000185291	IL3RA PPI subnetwork	0.12	>=0.20
ENSG00000113520	IL4 PPI subnetwork	0.09	>=0.20
ENSG00000077238	IL4R PPI subnetwork	0.17	>=0.20
ENSG00000113525	IL5 PPI subnetwork	0.08	>=0.20
ENSG00000091181	IL5RA PPI subnetwork	0.29	>=0.20
ENSG00000136244	IL6 PPI subnetwork	0.05	>=0.20
ENSG00000160712	IL6R PPI subnetwork	0.25	>=0.20
ENSG00000134352	IL6ST PPI subnetwork	0.08	>=0.20
ENSG00000104432	IL7 PPI subnetwork	0.09	>=0.20
ENSG00000168685	IL7R PPI subnetwork	0.21	>=0.20
ENSG00000145839	IL9 PPI subnetwork	0.09	>=0.20
ENSG00000124334	IL9R PPI subnetwork	0.36	>=0.20
ENSG00000143621	ILF2 PPI subnetwork	0.37	>=0.20
ENSG00000129351	ILF3 PPI subnetwork	0.07	>=0.20
ENSG00000105135	ILVBL PPI subnetwork	0.17	>=0.20
ENSG00000132305	IMMT PPI subnetwork	0.87	>=0.20
GO:0002429	immune response-activating cell surface receptor signaling p	0.84	>=0.20
GO:0002757	immune response-activating signal transduction	0.33	>=0.20
GO:0002768	immune response-regulating cell surface receptor signaling p	0.83	>=0.20
GO:0002764	immune response-regulating signaling pathway	0.33	>=0.20
GO:0002377	immunoglobulin production	0.6	>=0.20
GO:0002381	immunoglobulin production involved in immunoglobulin me	1	>=0.20
GO:0048305	immunoglobulin secretion	0.55	>=0.20

GO:0001772	immunological synapse	0.2	>=0.20
MP:0002578	impaired ability to fire action potentials	0.99	>=0.20
MP:0004542	impaired acrosome reaction	0.93	>=0.20
MP:0011049	impaired adaptive thermogenesis	0.06	>=0.20
MP:0001525	impaired balance	1	>=0.20
MP:0003044	impaired basement membrane formation	0.13	>=0.20
MP:0009750	impaired behavioral response to addictive substance	0.25	>=0.20
MP:0009757	impaired behavioral response to morphine	1	>=0.20
MP:0009747	impaired behavioral response to xenobiotic	1	>=0.20
MP:0004936	impaired branching involved in ureteric bud morphogenesis	0.88	>=0.20
MP:0009712	impaired conditioned place preference behavior	1	>=0.20
MP:0009454	impaired contextual conditioning behavior	0.99	>=0.20
MP:0001405	impaired coordination	0.99	>=0.20
MP:0009456	impaired cued conditioning behavior	0.99	>=0.20
MP:0008723	impaired eosinophil recruitment	0.35	>=0.20
MP:0000242	impaired fertilization	0.72	>=0.20
MP:0006325	impaired hearing	0.86	>=0.20
MP:0001606	impaired hematopoiesis	0.03	>=0.20
MP:0001524	impaired limb coordination	1	>=0.20
MP:0006027	impaired lung alveolus development	0.69	>=0.20
MP:0003799	impaired macrophage chemotaxis	0.08	>=0.20
MP:0008719	impaired neutrophil recruitment	0.05	>=0.20
MP:0005070	impaired NK cell cytolysis	0.49	>=0.20
MP:0001129	impaired ovarian folliculogenesis	0.23	>=0.20
MP:0001523	impaired righting response	0.98	>=0.20
MP:0002841	impaired skeletal muscle contractility	0.47	>=0.20
MP:0002796	impaired skin barrier function	0.1	>=0.20
MP:0000740	impaired smooth muscle contractility	0.78	>=0.20
MP:0001522	impaired swimming	0.99	>=0.20
MP:0001900	impaired synaptic plasticity	1	>=0.20
MP:0001792	impaired wound healing	0.04	>=0.20
ENSG00000148798	INA PPI subnetwork	0.91	>=0.20
GO:0000188	inactivation of MAPK activity	0.58	>=0.20
ENSG00000132849	INADL PPI subnetwork	0.99	>=0.20
ENSG00000149503	INCENP PPI subnetwork	0.58	>=0.20
MP:0001701	incomplete embryo turning	0.16	>=0.20
MP:0001689	incomplete somite formation	0.29	>=0.20
MP:0001829	increased activated T cell number	0.56	>=0.20
MP:0001353	increased aggression towards mice	0.87	>=0.20
MP:0004794	increased anti-nuclear antigen antibody level	0.04	>=0.20
MP:0004771	increased anti-single stranded DNA antibody level	0.43	>=0.20
MP:0001363	increased anxiety-related response	1	>=0.20
MP:0008782	increased B cell apoptosis	0.06	>=0.20
MP:0005154	increased B cell proliferation	0.32	>=0.20
MP:0008965	increased basal metabolism	0.58	>=0.20
MP:0001257	increased body length	0.11	>=0.20
MP:0000321	increased bone marrow cell number	0.03	>=0.20

MP:0000062	increased bone mineral density	0.13	>=0.20
MP:0010868	increased bone trabecula number	0.23	>=0.20
MP:0002176	increased brain weight	0.46	>=0.20
MP:0000005	increased brown adipose tissue amount	0.09	>=0.20
MP:0003222	increased cardiomyocyte apoptosis	0.1	>=0.20
MP:0008074	increased CD4-positive T cell number	0.13	>=0.20
MP:0008078	increased CD8-positive T cell number	0.14	>=0.20
MP:0000351	increased cell proliferation	0.7	>=0.20
MP:0002007	increased cellular sensitivity to gamma-irradiation	0.9	>=0.20
MP:0008410	increased cellular sensitivity to ultraviolet irradiation	0.89	>=0.20
MP:0008531	increased chemical nociceptive threshold	1	>=0.20
MP:0002666	increased circulating aldosterone level	0.98	>=0.20
MP:0005344	increased circulating bilirubin level	0.07	>=0.20
MP:0001745	increased circulating corticosterone level	0.63	>=0.20
MP:0010090	increased circulating creatine kinase level	0.38	>=0.20
MP:0005553	increased circulating creatinine level	0.04	>=0.20
MP:0001750	increased circulating follicle stimulating hormone level	0.08	>=0.20
MP:0008593	increased circulating interleukin-10 level	0.06	>=0.20
MP:0005669	increased circulating leptin level	0.04	>=0.20
MP:0001751	increased circulating luteinizing hormone level	0.22	>=0.20
MP:0002904	increased circulating parathyroid hormone level	0.37	>=0.20
MP:0005627	increased circulating potassium level	0.85	>=0.20
MP:0005122	increased circulating thyroid-stimulating hormone level	0.08	>=0.20
MP:0005480	increased circulating triiodothyronine level	0.22	>=0.20
MP:0004395	increased cochlear inner hair cell number	1	>=0.20
MP:0004401	increased cochlear outer hair cell number	0.99	>=0.20
MP:0004148	increased compact bone thickness	0.11	>=0.20
MP:0003063	increased coping response	1	>=0.20
MP:0008126	increased dendritic cell number	0.24	>=0.20
MP:0008151	increased diameter of long bones	0.28	>=0.20
MP:0001906	increased dopamine level	0.98	>=0.20
MP:0005090	increased double-negative T cell number	0.08	>=0.20
MP:0005091	increased double-positive T cell number	0.71	>=0.20
MP:0005011	increased eosinophil cell number	0.07	>=0.20
MP:0003135	increased erythroid progenitor cell number	0.15	>=0.20
MP:0001415	increased exploration in new environment	0.99	>=0.20
MP:0008173	increased follicular B cell number	0.4	>=0.20
MP:0011501	increased glomerular capsule space	0.89	>=0.20
MP:0002626	increased heart rate	0.16	>=0.20
MP:0002608	increased hematocrit	0.49	>=0.20
MP:0010264	increased hepatoma incidence	0.16	>=0.20
MP:0002495	increased IgA level	0.11	>=0.20
MP:0002497	increased IgE level	0.39	>=0.20
MP:0008499	increased IgG1 level	0.22	>=0.20
MP:0008500	increased IgG2a level	0.27	>=0.20
MP:0008501	increased IgG2b level	0.41	>=0.20
MP:0002494	increased IgM level	0.08	>=0.20

MP:0008214	increased immature B cell number	0.41	>=0.20
MP:0002461	increased immunoglobulin level	0.28	>=0.20
MP:0008566	increased interferon-gamma secretion	0.05	>=0.20
MP:0008687	increased interleukin-2 secretion	0.09	>=0.20
MP:0008699	increased interleukin-4 secretion	0.05	>=0.20
MP:0009583	increased keratinocyte proliferation	0.72	>=0.20
MP:0004751	increased length of allograft survival	0.52	>=0.20
MP:0003324	increased liver adenoma incidence	0.92	>=0.20
MP:0006398	increased long bone epiphyseal plate size	0.36	>=0.20
MP:0005630	increased lung weight	0.46	>=0.20
MP:0005013	increased lymphocyte cell number	0.05	>=0.20
MP:0002022	increased lymphoma incidence	0.77	>=0.20
MP:0005425	increased macrophage cell number	0.04	>=0.20
MP:0008210	increased mature B cell number	0.14	>=0.20
MP:0004875	increased mean systemic arterial blood pressure	0.27	>=0.20
MP:0008254	increased megakaryocyte cell number	0.06	>=0.20
MP:0008049	increased memory T cell number	0.04	>=0.20
MP:0011386	increased metanephric mesenchyme apoptosis	0.99	>=0.20
MP:0001272	increased metastatic potential	0.42	>=0.20
MP:0003992	increased mortality induced by ionizing radiation	0.99	>=0.20
MP:0005192	increased motor neuron number	0.96	>=0.20
MP:0008947	increased neuron number	0.99	>=0.20
MP:0008044	increased NK cell number	0.5	>=0.20
MP:0009395	increased nucleated erythrocyte cell number	0.05	>=0.20
MP:0003645	increased pancreatic beta cell number	0.09	>=0.20
MP:0005458	increased percent body fat	0.24	>=0.20
MP:0008097	increased plasma cell number	0.67	>=0.20
MP:0003132	increased pre-B cell number	0.13	>=0.20
MP:0004485	increased response of heart to induced stress	0.47	>=0.20
MP:0000480	increased rib number	0.72	>=0.20
MP:0008082	increased single-positive T cell number	0.14	>=0.20
MP:0009399	increased skeletal muscle fiber size	0.07	>=0.20
MP:0010300	increased skin tumor incidence	0.55	>=0.20
MP:0008481	increased spleen germinal center number	0.36	>=0.20
MP:0008476	increased spleen red pulp amount	0.21	>=0.20
MP:0001488	increased startle reflex	1	>=0.20
MP:0008006	increased stomach pH	0.41	>=0.20
MP:0004803	increased susceptibility to autoimmune diabetes	0.19	>=0.20
MP:0005350	increased susceptibility to autoimmune disorder	0.72	>=0.20
MP:0009788	increased susceptibility to bacterial infection induced morbic	0.04	>=0.20
MP:0004799	increased susceptibility to experimental autoimmune encepl	0.61	>=0.20
MP:0005165	increased susceptibility to injury	0.11	>=0.20
MP:0002906	increased susceptibility to pharmacologically induced seizure	1	>=0.20
MP:0005617	increased susceptibility to type IV hypersensitivity reaction	0.08	>=0.20
MP:0002916	increased synaptic depression	1	>=0.20
MP:0002842	increased systemic arterial blood pressure	0.05	>=0.20
MP:0006144	increased systemic arterial systolic blood pressure	0.19	>=0.20

MP:0006413	increased T cell apoptosis	0.04	>=0.20
MP:0005348	increased T cell proliferation	0.49	>=0.20
MP:0001973	increased thermal nociceptive threshold	0.97	>=0.20
MP:0002797	increased thigmotaxis	0.95	>=0.20
MP:0000714	increased thymocyte number	0.07	>=0.20
MP:0010024	increased total body fat amount	0.06	>=0.20
MP:0008189	increased transitional stage B cell number	0.1	>=0.20
MP:0003721	increased tumor growth/size	0.18	>=0.20
MP:0002020	increased tumor incidence	0.3	>=0.20
MP:0005441	increased urine calcium level	0.19	>=0.20
MP:0005619	increased urine potassium level	0.66	>=0.20
MP:0006316	increased urine sodium level	0.75	>=0.20
MP:0009403	increased variability of skeletal muscle fiber size	0.48	>=0.20
MP:0003070	increased vascular permeability	0.03	>=0.20
MP:0005590	increased vasodilation	0.1	>=0.20
MP:0002574	increased vertical activity	0.77	>=0.20
MP:0003408	increased width of hypertrophic chondrocyte zone	0.36	>=0.20
GO:0006917	induction of apoptosis	0.03	>=0.20
GO:0008624	induction of apoptosis by extracellular signals	0.5	>=0.20
GO:0012502	induction of programmed cell death	0.04	>=0.20
MP:0001924	infertility	0.87	>=0.20
GO:0002437	inflammatory response to antigenic stimulus	0.98	>=0.20
ENSG00000153487	ING1 PPI subnetwork	0.15	>=0.20
ENSG00000168556	ING2 PPI subnetwork	0.77	>=0.20
ENSG00000071243	ING3 PPI subnetwork	0.16	>=0.20
ENSG00000111653	ING4 PPI subnetwork	0.05	>=0.20
ENSG00000122641	INHBA PPI subnetwork	0.19	>=0.20
ENSG00000163083	INHBB PPI subnetwork	0.24	>=0.20
ENSG00000175189	INHBC PPI subnetwork	0.75	>=0.20
ENSG00000139269	INHBE PPI subnetwork	0.83	>=0.20
GO:0002758	innate immune response-activating signal transduction	0.22	>=0.20
MP:0004965	inner cell mass degeneration	0.28	>=0.20
GO:0048839	inner ear development	1	>=0.20
GO:0042472	inner ear morphogenesis	1	>=0.20
GO:0060113	inner ear receptor cell differentiation	1	>=0.20
GO:0031011	Ino80 complex	0.22	>=0.20
ENSG00000128908	INO80 PPI subnetwork	0.53	>=0.20
ENSG00000153391	INO80C PPI subnetwork	0.35	>=0.20
ENSG00000169592	INO80E PPI subnetwork	0.55	>=0.20
GO:0015103	inorganic anion transmembrane transporter activity	0.83	>=0.20
GO:0015698	inorganic anion transport	1	>=0.20
GO:0022890	inorganic cation transmembrane transporter activity	1	>=0.20
GO:0048017	inositol lipid-mediated signaling	0.51	>=0.20
GO:0004437	inositol or phosphatidylinositol phosphatase activity	0.72	>=0.20
GO:0048016	inositol phosphate-mediated signaling	0.73	>=0.20
ENSG00000165458	INPPL1 PPI subnetwork	0.13	>=0.20
GO:0005520	insulin-like growth factor binding	0.14	>=0.20

GO:0048009	insulin-like growth factor receptor signaling pathway	0.87	>=0.20
GO:0043560	insulin receptor substrate binding	0.03	>=0.20
GO:0030073	insulin secretion	0.48	>=0.20
MP:0004031	insulitis	0.05	>=0.20
GO:0030176	integral to endoplasmic reticulum membrane	0.4	>=0.20
GO:0030173	integral to Golgi membrane	0.15	>=0.20
GO:0031301	integral to organelle membrane	0.08	>=0.20
GO:0005779	integral to peroxisomal membrane	0.7	>=0.20
GO:0032039	integrator complex	0.46	>=0.20
GO:0007229	integrin-mediated signaling pathway	0.64	>=0.20
GO:0005178	integrin binding	0.3	>=0.20
GO:0008305	integrin complex	0.06	>=0.20
GO:0014704	intercalated disc	0.92	>=0.20
GO:0032607	interferon-alpha production	0.9	>=0.20
GO:0032608	interferon-beta production	0.91	>=0.20
GO:0060333	interferon-gamma-mediated signaling pathway	0.74	>=0.20
GO:0032609	interferon-gamma production	0.77	>=0.20
GO:0032613	interleukin-10 production	0.95	>=0.20
GO:0032615	interleukin-12 production	0.77	>=0.20
GO:0032620	interleukin-17 production	1	>=0.20
GO:0042094	interleukin-2 biosynthetic process	0.53	>=0.20
GO:0032623	interleukin-2 production	0.23	>=0.20
GO:0032633	interleukin-4 production	0.67	>=0.20
GO:0032635	interleukin-6 production	0.1	>=0.20
GO:0005882	intermediate filament	0.91	>=0.20
GO:0045103	intermediate filament-based process	1	>=0.20
GO:0045111	intermediate filament cytoskeleton	0.93	>=0.20
GO:0045104	intermediate filament cytoskeleton organization	0.99	>=0.20
MP:0008475	intermingled spleen red and white pulp	0.2	>=0.20
GO:0018393	internal peptidyl-lysine acetylation	0.56	>=0.20
GO:0006475	internal protein amino acid acetylation	0.36	>=0.20
GO:0009898	internal side of plasma membrane	0.73	>=0.20
GO:0051325	interphase	0.65	>=0.20
GO:0051329	interphase of mitotic cell cycle	0.7	>=0.20
MP:0004157	interrupted aortic arch	0.8	>=0.20
GO:0005614	interstitial matrix	0.94	>=0.20
MP:0003290	intestinal hypoperistalsis	0.71	>=0.20
MP:0001858	intestinal inflammation	0.24	>=0.20
MP:0003270	intestinal obstruction	0.97	>=0.20
GO:0006891	intra-Golgi vesicle-mediated transport	0.69	>=0.20
GO:0032365	intracellular lipid transport	0.08	>=0.20
GO:0030522	intracellular receptor mediated signaling pathway	0.09	>=0.20
GO:0030518	intracellular steroid hormone receptor signaling pathway	0.67	>=0.20
GO:0016861	intramolecular oxidoreductase activity, interconverting aldos	0.77	>=0.20
GO:0031228	intrinsic to Golgi membrane	0.15	>=0.20
GO:0031231	intrinsic to peroxisomal membrane	0.7	>=0.20
ENSG00000104613	INTS10 PPI subnetwork	0.21	>=0.20

GO:0005242	inward rectifier potassium channel activity	0.98	>=0.20
GO:0005216	ion channel activity	1	>=0.20
GO:0034702	ion channel complex	1	>=0.20
GO:0034220	ion transmembrane transport	1	>=0.20
GO:0004970	ionotropic glutamate receptor activity	1	>=0.20
GO:0008328	ionotropic glutamate receptor complex	1	>=0.20
ENSG00000117408	IPO13 PPI subnetwork	0.49	>=0.20
ENSG00000065150	IPO5 PPI subnetwork	0.26	>=0.20
ENSG00000205339	IPO7 PPI subnetwork	0.05	>=0.20
ENSG00000198700	IPO9 PPI subnetwork	0.04	>=0.20
ENSG00000140575	IQGAP1 PPI subnetwork	0.15	>=0.20
ENSG00000183856	IQGAP3 PPI subnetwork	0.42	>=0.20
ENSG00000184216	IRAK1 PPI subnetwork	0.03	>=0.20
ENSG00000126456	IRF3 PPI subnetwork	0.43	>=0.20
GO:0016226	iron-sulfur cluster assembly	1	>=0.20
GO:0006826	iron ion transport	0.56	>=0.20
MP:0000372	irregular coat pigmentation	0.4	>=0.20
MP:0001636	irregular heartbeat	0.36	>=0.20
GO:0045190	isotype switching	1	>=0.20
GO:0048291	isotype switching to IgG isotypes	1	>=0.20
ENSG00000078747	ITCH PPI subnetwork	0.43	>=0.20
ENSG00000167930	ITFG3 PPI subnetwork	0.12	>=0.20
ENSG00000213949	ITGA1 PPI subnetwork	0.04	>=0.20
ENSG00000164171	ITGA2 PPI subnetwork	0.88	>=0.20
ENSG00000005884	ITGA3 PPI subnetwork	0.19	>=0.20
ENSG00000005844	ITGAL PPI subnetwork	0.31	>=0.20
ENSG00000138448	ITGAV PPI subnetwork	0.03	>=0.20
ENSG00000142856	ITGB3BP PPI subnetwork	0.42	>=0.20
ENSG00000132470	ITGB4 PPI subnetwork	0.14	>=0.20
ENSG00000115221	ITGB6 PPI subnetwork	0.21	>=0.20
ENSG00000139626	ITGB7 PPI subnetwork	0.27	>=0.20
ENSG00000105855	ITGB8 PPI subnetwork	0.07	>=0.20
ENSG00000113263	ITK PPI subnetwork	0.14	>=0.20
ENSG00000136156	ITM2B PPI subnetwork	0.2	>=0.20
ENSG00000137825	ITPKA PPI subnetwork	0.67	>=0.20
ENSG00000150995	ITPR1 PPI subnetwork	0.99	>=0.20
ENSG00000096433	ITPR3 PPI subnetwork	0.95	>=0.20
ENSG00000205726	ITSN1 PPI subnetwork	0.56	>=0.20
ENSG00000163166	IWS1 PPI subnetwork	0.24	>=0.20
GO:0007259	JAK-STAT cascade	0.17	>=0.20
ENSG00000008083	JARID2 PPI subnetwork	0.71	>=0.20
MP:0000611	jaundice	0.53	>=0.20
GO:0007254	JNK cascade	0.41	>=0.20
ENSG00000177606	JUN PPI subnetwork	0.06	>=0.20
ENSG00000171223	JUNB PPI subnetwork	0.11	>=0.20
ENSG00000130522	JUND PPI subnetwork	0.15	>=0.20
ENSG00000173801	JUP PPI subnetwork	0.21	>=0.20

ENSG00000114982	KANSL3 PPI subnetwork	0.46	>=0.20
ENSG00000065427	KARS PPI subnetwork	0.5	>=0.20
ENSG00000108773	KAT2A PPI subnetwork	0.07	>=0.20
ENSG00000114166	KAT2B PPI subnetwork	0.33	>=0.20
ENSG00000172977	KAT5 PPI subnetwork	0.54	>=0.20
ENSG00000136504	KAT7 PPI subnetwork	0.92	>=0.20
ENSG00000103510	KAT8 PPI subnetwork	0.4	>=0.20
ENSG00000120696	KBTBD7 PPI subnetwork	0.73	>=0.20
ENSG00000111262	KCNA1 PPI subnetwork	1	>=0.20
ENSG00000177301	KCNA2 PPI subnetwork	1	>=0.20
ENSG00000182255	KCNA4 PPI subnetwork	0.99	>=0.20
ENSG00000169282	KCNAB1 PPI subnetwork	1	>=0.20
ENSG00000069424	KCNAB2 PPI subnetwork	1	>=0.20
ENSG00000184408	KCND2 PPI subnetwork	1	>=0.20
ENSG00000184185	KCNJ12 PPI subnetwork	0.83	>=0.20
ENSG00000112078	KCTD20 PPI subnetwork	0.88	>=0.20
ENSG00000167977	KCTD5 PPI subnetwork	0.77	>=0.20
ENSG00000004487	KDM1A PPI subnetwork	0.06	>=0.20
ENSG00000173120	KDM2A PPI subnetwork	0.39	>=0.20
ENSG00000089094	KDM2B PPI subnetwork	0.57	>=0.20
KEGG_ALDOSTERONE_REGUL	KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTIOI	0.67	>=0.20
KEGG_ALLOGRAFT_REJECTIOI	KEGG_ALLOGRAFT_REJECTION	0.99	>=0.20
KEGG_ALZHEIMERS_DISEASE	KEGG_ALZHEIMERS_DISEASE	0.98	>=0.20
KEGG_AMINO_SUGAR_AND_I	KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOI	0.09	>=0.20
KEGG_AMINOACYL_TRNA_BIC	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	0.59	>=0.20
KEGG_AMYOTROPHIC_LATER/	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	0.89	>=0.20
KEGG_ANTIGEN_PROCESSING	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	0.95	>=0.20
KEGG_APOPTOSIS	KEGG_APOPTOSIS	0.25	>=0.20
KEGG_ARRHYTHMOGENIC_RI	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMY	0.85	>=0.20
KEGG_ASCORBATE_AND_ALD	KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	0.28	>=0.20
KEGG_ASTHMA	KEGG_ASTHMA	0.88	>=0.20
KEGG_AUTOIMMUNE_THYRO	KEGG_AUTOIMMUNE_THYROID_DISEASE	0.97	>=0.20
KEGG_AXON_GUIDANCE	KEGG_AXON_GUIDANCE	0.68	>=0.20
KEGG_B_CELL_RECEPTOR_SIG	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.13	>=0.20
KEGG_BASAL_CELL_CARCINOI	KEGG_BASAL_CELL_CARCINOMA	0.98	>=0.20
KEGG_BASAL_TRANSCRIPTIOI	KEGG_BASAL_TRANSCRIPTION_FACTORS	0.77	>=0.20
KEGG_CALCIUM_SIGNALING_	KEGG_CALCIUM_SIGNALING_PATHWAY	0.93	>=0.20
KEGG_CARDIAC_MUSCLE_COI	KEGG_CARDIAC_MUSCLE_CONTRACTION	1	>=0.20
KEGG_CELL_ADHESION_MOLI	KEGG_CELL_ADHESION_MOLECULES_CAMS	0.99	>=0.20
KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	0.4	>=0.20
KEGG_CHEMOKINE_SIGNALIN	KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.03	>=0.20
KEGG_CHRONIC_MYELOID_LE	KEGG_CHRONIC_MYELOID_LEUKEMIA	0.05	>=0.20
KEGG_CIRCADIAN_RHYTHM_I	KEGG_CIRCADIAN_RHYTHM_MAMMAL	0.11	>=0.20
KEGG_CITRATE_CYCLE_TCA_C	KEGG_CITRATE_CYCLE_TCA_CYCLE	0.07	>=0.20
KEGG_COLORECTAL_CANCER	KEGG_COLORECTAL_CANCER	0.75	>=0.20
KEGG_CYTOKINE_CYTOKINE_I	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0.07	>=0.20
KEGG_CYTOSOLIC_DNA_SENS	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	0.61	>=0.20

KEGG_DILATED_CARDIOMYOI	KEGG_DILATED_CARDIOMYOPATHY	0.92	>=0.20
KEGG_DNA_REPLICATION	KEGG_DNA_REPLICATION	0.94	>=0.20
KEGG_DORSO_VENTRAL_AXIS	KEGG_DORSO_VENTRAL_AXIS_FORMATION	0.15	>=0.20
KEGG_ECM_RECEPTOR_INTER	KEGG_ECM_RECEPTOR_INTERACTION	0.08	>=0.20
KEGG_ENDOCYTOSIS	KEGG_ENDOCYTOSIS	0.39	>=0.20
KEGG_ENDOMETRIAL_CANCE	KEGG_ENDOMETRIAL_CANCER	0.05	>=0.20
KEGG_EPITHELIAL_CELL_SIGN	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYL(	0.42	>=0.20
KEGG_ERBB_SIGNALING_PATI	KEGG_ERBB_SIGNALING_PATHWAY	0.05	>=0.20
KEGG_ETHER_LIPID_METABO	KEGG_ETHER_LIPID_METABOLISM	0.23	>=0.20
KEGG_FC_EPSILON_RI_SIGNA	KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	0.28	>=0.20
KEGG_FC_GAMMA_R_MEDIA	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.18	>=0.20
KEGG_FOCAL_ADHESION	KEGG_FOCAL_ADHESION	0.09	>=0.20
KEGG_GAP_JUNCTION	KEGG_GAP_JUNCTION	0.63	>=0.20
KEGG_GLIOMA	KEGG_GLIOMA	0.27	>=0.20
KEGG_GLUTATHIONE_METAB	KEGG_GLUTATHIONE_METABOLISM	0.07	>=0.20
KEGG_GLYCOSAMINOGLYCAN	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN	0.06	>=0.20
KEGG_GLYCOSAMINOGLYCAN	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SUL	0.45	>=0.20
KEGG_GLYCOSPHINGOLIPID_E	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIE	0.43	>=0.20
KEGG_GLYCOSPHINGOLIPID_E	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	0.28	>=0.20
KEGG_GLYCOSPHINGOLIPID_E	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NE	0.42	>=0.20
KEGG_GLYCOSYLPHOSPHATID	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIC	0.84	>=0.20
KEGG_GNRH_SIGNALING_PAT	KEGG_GNRH_SIGNALING_PATHWAY	0.89	>=0.20
KEGG_GRAFT_VERSUS_HOST_	KEGG_GRAFT_VERSUS_HOST_DISEASE	0.96	>=0.20
KEGG_HEDGEHOG_SIGNALIN(	KEGG_HEDGEHOG_SIGNALING_PATHWAY	0.99	>=0.20
KEGG_HEMATOPOIETIC_CELL_	KEGG_HEMATOPOIETIC_CELL_LINEAGE	0.03	>=0.20
KEGG_HOMOLOGOUS_RECOI	KEGG_HOMOLOGOUS_RECOMBINATION	0.92	>=0.20
KEGG_HUNTINGTONS_DISEAS	KEGG_HUNTINGTONS_DISEASE	0.94	>=0.20
KEGG_HYPERTROPHIC_CARDI	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	0.81	>=0.20
KEGG_INOSITOL_PHOSPHATE_	KEGG_INOSITOL_PHOSPHATE_METABOLISM	0.88	>=0.20
KEGG_INTESTINAL_IMMUNE_	KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCT	0.89	>=0.20
KEGG_JAK_STAT_SIGNALING_	KEGG_JAK_STAT_SIGNALING_PATHWAY	0.04	>=0.20
KEGG_LEISHMANIA_INFECTIO	KEGG_LEISHMANIA_INFECTION	0.15	>=0.20
KEGG_LEUKOCYTE_TRANSENI	KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	0.3	>=0.20
KEGG_LONG_TERM_DEPRESS	KEGG_LONG_TERM_DEPRESSION	0.2	>=0.20
KEGG_LONG_TERM_POTENTI	KEGG_LONG_TERM_POTENTIATION	0.93	>=0.20
KEGG_MAPK_SIGNALING_PAT	KEGG_MAPK_SIGNALING_PATHWAY	0.5	>=0.20
KEGG_MELANOGENESIS	KEGG_MELANOGENESIS	0.93	>=0.20
KEGG_MELANOMA	KEGG_MELANOMA	0.58	>=0.20
KEGG_MISMATCH_REPAIR	KEGG_MISMATCH_REPAIR	0.92	>=0.20
KEGG_NATURAL_KILLER_CELL	KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.46	>=0.20
KEGG_NEUROACTIVE_LIGAND	KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	0.99	>=0.20
KEGG_NEUROTROPHIN_SIGN/	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	0.22	>=0.20
KEGG_NITROGEN_METABOLIS	KEGG_NITROGEN_METABOLISM	0.11	>=0.20
KEGG_NOD_LIKE_RECEPTOR_	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.09	>=0.20
KEGG_NON_SMALL_CELL_LUI	KEGG_NON_SMALL_CELL_LUNG_CANCER	0.04	>=0.20
KEGG_NUCLEOTIDE_EXCISION	KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.99	>=0.20
KEGG_O_GLYCAN_BIOSYNTHE	KEGG_O_GLYCAN_BIOSYNTHESIS	0.99	>=0.20

KEGG_OLFACTORY_TRANSDU	KEGG_OLFACTORY_TRANSDUCTION	1	>=0.20
KEGG_OOCYTE_MEIOSIS	KEGG_OOCYTE_MEIOSIS	0.71	>=0.20
KEGG_OXIDATIVE_PHOSPHOF	KEGG_OXIDATIVE_PHOSPHORYLATION	0.97	>=0.20
KEGG_P53_SIGNALING_PATH	KEGG_P53_SIGNALING_PATHWAY	0.92	>=0.20
KEGG_PANCREATIC_CANCER	KEGG_PANCREATIC_CANCER	0.28	>=0.20
KEGG_PARKINSONS_DISEASE	KEGG_PARKINSONS_DISEASE	1	>=0.20
KEGG_PATHOGENIC_ESCHERI	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	0.19	>=0.20
KEGG_PATHWAYS_IN_CANCE	KEGG_PATHWAYS_IN_CANCER	0.14	>=0.20
KEGG_PENTOSE_AND_GLUCU	KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	0.28	>=0.20
KEGG_PHOSPHATIDYLINOSITC	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	0.99	>=0.20
KEGG_PRIMARY_IMMUNODE	KEGG_PRIMARY_IMMUNODEFICIENCY	0.46	>=0.20
KEGG_PROGESTERONE_MEDI	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	0.17	>=0.20
KEGG_PROTEASOME	KEGG_PROTEASOME	0.59	>=0.20
KEGG_PROTEIN_EXPORT	KEGG_PROTEIN_EXPORT	0.23	>=0.20
KEGG_PROXIMAL_TUBULE_BI	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	0.34	>=0.20
KEGG_PURINE_METABOLISM	KEGG_PURINE_METABOLISM	0.87	>=0.20
KEGG_PYRIMIDINE_METABOL	KEGG_PYRIMIDINE_METABOLISM	0.88	>=0.20
KEGG_REGULATION_OF_ACTI	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	0.23	>=0.20
KEGG_REGULATION_OF_AUT	KEGG_REGULATION_OF_AUTOPHAGY	0.65	>=0.20
KEGG_RENAL_CELL_CARCINO	KEGG_RENAL_CELL_CARCINOMA	0.05	>=0.20
KEGG_RENIN_ANGIOTENSIN_	KEGG_RENIN_ANGIOTENSIN_SYSTEM	0.09	>=0.20
KEGG_RIBOSOME	KEGG_RIBOSOME	0.97	>=0.20
KEGG_RIG_I_LIKE_RECEPTOR_	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.59	>=0.20
KEGG_RNA_DEGRADATION	KEGG_RNA_DEGRADATION	0.87	>=0.20
KEGG_RNA_POLYMERASE	KEGG_RNA_POLYMERASE	0.95	>=0.20
KEGG_SELENOAMINO_ACID_I	KEGG_SELENOAMINO_ACID_METABOLISM	0.71	>=0.20
KEGG_SMALL_CELL_LUNG_CA	KEGG_SMALL_CELL_LUNG_CANCER	0.05	>=0.20
KEGG_SNARE_INTERACTIONS_	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	0.93	>=0.20
KEGG_SPLICEOSOME	KEGG_SPLICEOSOME	0.38	>=0.20
KEGG_SYSTEMIC_LUPUS_ERY	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	0.12	>=0.20
KEGG_T_CELL_RECEPTOR_SIG	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.6	>=0.20
KEGG_TASTE_TRANSDUCTION	KEGG_TASTE_TRANSDUCTION	0.93	>=0.20
KEGG_TGF_BETA_SIGNALING_	KEGG_TGF_BETA_SIGNALING_PATHWAY	0.13	>=0.20
KEGG_THYROID_CANCER	KEGG_THYROID_CANCER	0.06	>=0.20
KEGG_TIGHT_JUNCTION	KEGG_TIGHT_JUNCTION	0.9	>=0.20
KEGG_TOLL_LIKE_RECEPTOR_	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	0.14	>=0.20
KEGG_TYPE_I_DIABETES_MEL	KEGG_TYPE_I_DIABETES_MELLITUS	1	>=0.20
KEGG_TYPE_II_DIABETES_MEI	KEGG_TYPE_II_DIABETES_MELLITUS	0.05	>=0.20
KEGG_UBIQUITIN_MEDIATED_	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	0.55	>=0.20
KEGG_VALINE_LEUCINE_AND_	KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_BIOSYNTHESIS	0.77	>=0.20
KEGG_VASCULAR_SMOOTH_M	KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	0.2	>=0.20
KEGG_VASOPRESSIN_REGULA	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	0.64	>=0.20
KEGG_VIBRIO_CHOLERAE_INF	KEGG_VIBRIO_CHOLERAE_INFECTION	0.39	>=0.20
KEGG_VIRAL_MYOCARDITIS	KEGG_VIRAL_MYOCARDITIS	0.98	>=0.20
KEGG_WNT_SIGNALING_PATH	KEGG_WNT_SIGNALING_PATHWAY	0.7	>=0.20
GO:0045095	keratin filament	0.92	>=0.20
GO:0031424	keratinization	0.94	>=0.20

GO:0030216	keratinocyte differentiation	0.93	>=0.20
GO:0043616	keratinocyte proliferation	0.98	>=0.20
ENSG00000121774	KHDRBS1 PPI subnetwork	0.35	>=0.20
ENSG00000080608	KIAA0020 PPI subnetwork	0.6	>=0.20
ENSG00000131149	KIAA0182 PPI subnetwork	0.04	>=0.20
ENSG00000177728	KIAA0195 PPI subnetwork	0.19	>=0.20
ENSG00000111731	KIAA0528 PPI subnetwork	0.34	>=0.20
ENSG00000100364	KIAA0930 PPI subnetwork	0.16	>=0.20
ENSG00000112379	KIAA1244 PPI subnetwork	1	>=0.20
ENSG00000120071	KIAA1267 PPI subnetwork	0.67	>=0.20
ENSG00000134444	KIAA1468 PPI subnetwork	1	>=0.20
MP:0004970	kidney atrophy	0.67	>=0.20
MP:0000522	kidney cortex cysts	0.91	>=0.20
MP:0003675	kidney cysts	0.92	>=0.20
GO:0001822	kidney development	0.98	>=0.20
GO:0072073	kidney epithelium development	1	>=0.20
MP:0003606	kidney failure	0.11	>=0.20
GO:0072074	kidney mesenchyme development	1	>=0.20
GO:0060993	kidney morphogenesis	1	>=0.20
ENSG00000197892	KIF13B PPI subnetwork	0.35	>=0.20
ENSG00000121621	KIF18A PPI subnetwork	0.7	>=0.20
ENSG00000130294	KIF1A PPI subnetwork	0.13	>=0.20
ENSG00000054523	KIF1B PPI subnetwork	0.23	>=0.20
ENSG00000129250	KIF1C PPI subnetwork	0.05	>=0.20
ENSG00000139116	KIF21A PPI subnetwork	1	>=0.20
ENSG00000116852	KIF21B PPI subnetwork	1	>=0.20
ENSG00000137807	KIF23 PPI subnetwork	0.19	>=0.20
ENSG00000068796	KIF2A PPI subnetwork	0.67	>=0.20
ENSG00000141200	KIF2B PPI subnetwork	0.76	>=0.20
ENSG00000142945	KIF2C PPI subnetwork	0.78	>=0.20
ENSG00000131437	KIF3A PPI subnetwork	0.81	>=0.20
ENSG00000155980	KIF5A PPI subnetwork	0.99	>=0.20
ENSG00000170759	KIF5B PPI subnetwork	0.03	>=0.20
ENSG00000075945	KIFAP3 PPI subnetwork	0.95	>=0.20
ENSG00000204197	KIFC1 PPI subnetwork	0.72	>=0.20
GO:0031640	killing of cells of other organism	0.74	>=0.20
GO:0019207	kinase regulator activity	0.05	>=0.20
GO:0019894	kinesin binding	0.93	>=0.20
GO:0005871	kinesin complex	0.83	>=0.20
GO:0000776	kinetochore	0.58	>=0.20
MP:0003400	kinked neural tube	0.13	>=0.20
MP:0000585	kinked tail	0.56	>=0.20
ENSG00000157404	KIT PPI subnetwork	0.1	>=0.20
ENSG00000133116	KL PPI subnetwork	0.8	>=0.20
ENSG00000174996	KLC2 PPI subnetwork	0.33	>=0.20
ENSG00000104892	KLC3 PPI subnetwork	0.3	>=0.20
ENSG00000137171	KLC4 PPI subnetwork	0.08	>=0.20

ENSG00000119138	KLF9 PPI subnetwork	0.39	>=0.20
ENSG00000165516	KLHDC2 PPI subnetwork	0.04	>=0.20
ENSG00000124702	KLHDC3 PPI subnetwork	0.95	>=0.20
ENSG00000117153	KLHL12 PPI subnetwork	0.53	>=0.20
ENSG00000003096	KLHL13 PPI subnetwork	0.97	>=0.20
ENSG00000184445	KNTC1 PPI subnetwork	0.82	>=0.20
ENSG00000114030	KPNA1 PPI subnetwork	0.78	>=0.20
ENSG00000182481	KPNA2 PPI subnetwork	0.17	>=0.20
ENSG00000108424	KPNB1 PPI subnetwork	0.31	>=0.20
ENSG00000133703	KRAS PPI subnetwork	0.73	>=0.20
ENSG00000129347	KRI1 PPI subnetwork	0.7	>=0.20
ENSG00000171346	KRT15 PPI subnetwork	0.91	>=0.20
ENSG00000186081	KRT5 PPI subnetwork	0.11	>=0.20
ENSG00000170421	KRT8 PPI subnetwork	0.3	>=0.20
ENSG00000171403	KRT9 PPI subnetwork	0.33	>=0.20
ENSG00000141068	KSR1 PPI subnetwork	0.23	>=0.20
MP:0000069	kyphoscoliosis	0.07	>=0.20
MP:0000160	kyphosis	0.78	>=0.20
GO:0015179	L-amino acid transmembrane transporter activity	0.85	>=0.20
GO:0015807	L-amino acid transport	0.95	>=0.20
GO:0042354	L-fucose metabolic process	0.98	>=0.20
GO:0005313	L-glutamate transmembrane transporter activity	1	>=0.20
GO:0015813	L-glutamate transport	1	>=0.20
ENSG00000198910	L1CAM PPI subnetwork	0.59	>=0.20
ENSG00000185513	L3MBTL1 PPI subnetwork	0.24	>=0.20
ENSG00000100395	L3MBTL2 PPI subnetwork	0.31	>=0.20
MP:0010249	lactation failure	0.25	>=0.20
ENSG00000159166	LAD1 PPI subnetwork	0.49	>=0.20
ENSG00000130702	LAMA5 PPI subnetwork	0.42	>=0.20
ENSG00000091136	LAMB1 PPI subnetwork	0.1	>=0.20
ENSG00000135862	LAMC1 PPI subnetwork	0.17	>=0.20
GO:0030027	lamellipodium	0.03	>=0.20
GO:0030032	lamellipodium assembly	0.94	>=0.20
GO:0031258	lamellipodium membrane	0.62	>=0.20
GO:0043236	laminin binding	0.12	>=0.20
GO:0043256	laminin complex	0.39	>=0.20
ENSG00000162511	LAPTM5 PPI subnetwork	1	>=0.20
MP:0003304	large intestinal inflammation	0.04	>=0.20
GO:0015934	large ribosomal subunit	0.6	>=0.20
ENSG00000155506	LARP1 PPI subnetwork	0.27	>=0.20
ENSG00000138709	LARP1B PPI subnetwork	0.5	>=0.20
ENSG00000133706	LARS PPI subnetwork	0.36	>=0.20
ENSG00000001497	LAS1L PPI subnetwork	0.35	>=0.20
ENSG00000213658	LAT PPI subnetwork	0.42	>=0.20
GO:0031902	late endosome membrane	0.43	>=0.20
GO:0048368	lateral mesoderm development	0.94	>=0.20
GO:0016328	lateral plasma membrane	0.94	>=0.20

GO:0060601	lateral sprouting from an epithelium	1	>=0.20
ENSG00000131023	LATS1 PPI subnetwork	0.08	>=0.20
ENSG00000143815	LBR PPI subnetwork	0.05	>=0.20
ENSG00000135338	LCA5 PPI subnetwork	0.98	>=0.20
ENSG00000182866	LCK PPI subnetwork	0.08	>=0.20
ENSG00000043462	LCP2 PPI subnetwork	0.12	>=0.20
ENSG00000198728	LDB1 PPI subnetwork	0.99	>=0.20
ENSG00000134333	LDHA PPI subnetwork	0.52	>=0.20
ENSG00000111716	LDHB PPI subnetwork	0.82	>=0.20
ENSG00000182195	LDOC1 PPI subnetwork	0.29	>=0.20
GO:0031256	leading edge membrane	0.91	>=0.20
GO:0007612	learning	1	>=0.20
GO:0007611	learning or memory	1	>=0.20
ENSG00000138795	LEF1 PPI subnetwork	0.46	>=0.20
ENSG00000143768	LEFTY2 PPI subnetwork	0.77	>=0.20
GO:0002088	lens development in camera-type eye	1	>=0.20
GO:0070307	lens fiber cell development	1	>=0.20
GO:0070306	lens fiber cell differentiation	1	>=0.20
GO:0002089	lens morphogenesis in camera-type eye	0.98	>=0.20
ENSG00000166477	LEO1 PPI subnetwork	0.25	>=0.20
ENSG00000116678	LEPR PPI subnetwork	0.12	>=0.20
ENSG00000117385	LEPRE1 PPI subnetwork	0.8	>=0.20
MP:0005202	lethargy	0.4	>=0.20
ENSG00000168924	LETM1 PPI subnetwork	0.9	>=0.20
MP:0002026	leukemia	0.22	>=0.20
GO:0045321	leukocyte activation	0.08	>=0.20
GO:0002366	leukocyte activation involved in immune response	0.83	>=0.20
GO:0071887	leukocyte apoptotic process	0.48	>=0.20
GO:0007159	leukocyte cell-cell adhesion	0.47	>=0.20
GO:0030595	leukocyte chemotaxis	0.36	>=0.20
GO:0043299	leukocyte degranulation	0.72	>=0.20
GO:0002521	leukocyte differentiation	0.06	>=0.20
GO:0001776	leukocyte homeostasis	0.41	>=0.20
GO:0001909	leukocyte mediated cytotoxicity	0.99	>=0.20
GO:0050900	leukocyte migration	0.04	>=0.20
GO:0070661	leukocyte proliferation	0.37	>=0.20
GO:0019370	leukotriene biosynthetic process	0.93	>=0.20
GO:0006691	leukotriene metabolic process	0.92	>=0.20
ENSG00000100097	LGALS1 PPI subnetwork	0.65	>=0.20
ENSG00000108679	LGALS3BP PPI subnetwork	0.71	>=0.20
ENSG00000171747	LGALS4 PPI subnetwork	0.57	>=0.20
ENSG00000108231	LGI1 PPI subnetwork	0.98	>=0.20
ENSG00000128342	LIF PPI subnetwork	0.09	>=0.20
ENSG00000113594	LIFR PPI subnetwork	0.26	>=0.20
ENSG00000105486	LIG1 PPI subnetwork	0.86	>=0.20
ENSG00000005156	LIG3 PPI subnetwork	0.73	>=0.20
ENSG00000174405	LIG4 PPI subnetwork	0.5	>=0.20

GO:0016922	ligand-dependent nuclear receptor binding	0.07	>=0.20
GO:0030374	ligand-dependent nuclear receptor transcription coactivator	0.8	>=0.20
GO:0022834	ligand-gated channel activity	1	>=0.20
GO:0015276	ligand-gated ion channel activity	1	>=0.20
GO:0016874	ligase activity	0.35	>=0.20
GO:0016876	ligase activity, forming aminoacyl-tRNA and related compour	0.51	>=0.20
GO:0016879	ligase activity, forming carbon-nitrogen bonds	0.64	>=0.20
GO:0016875	ligase activity, forming carbon-oxygen bonds	0.51	>=0.20
ENSG00000050405	LIMA1 PPI subnetwork	0.31	>=0.20
GO:0060174	limb bud formation	1	>=0.20
GO:0060173	limb development	1	>=0.20
MP:0001513	limb grasping	0.98	>=0.20
GO:0035108	limb morphogenesis	1	>=0.20
GO:0021761	limbic system development	0.84	>=0.20
ENSG00000106683	LIMK1 PPI subnetwork	0.04	>=0.20
ENSG00000182541	LIMK2 PPI subnetwork	0.22	>=0.20
ENSG00000188223	LIN37 PPI subnetwork	0.68	>=0.20
ENSG00000205659	LIN52 PPI subnetwork	0.43	>=0.20
ENSG00000189308	LIN54 PPI subnetwork	0.54	>=0.20
ENSG00000111052	LIN7A PPI subnetwork	0.91	>=0.20
ENSG00000104863	LIN7B PPI subnetwork	1	>=0.20
ENSG00000148943	LIN7C PPI subnetwork	0.98	>=0.20
ENSG00000183814	LIN9 PPI subnetwork	0.37	>=0.20
ENSG00000169783	LINGO1 PPI subnetwork	0.86	>=0.20
GO:0030259	lipid glycosylation	1	>=0.20
GO:0001727	lipid kinase activity	0.64	>=0.20
GO:0009103	lipopolysaccharide biosynthetic process	0.21	>=0.20
GO:0008653	lipopolysaccharide metabolic process	0.19	>=0.20
MP:0010019	liver vascular congestion	0.91	>=0.20
ENSG00000160789	LMNA PPI subnetwork	0.04	>=0.20
ENSG00000113368	LMNB1 PPI subnetwork	0.98	>=0.20
ENSG00000166407	LMO1 PPI subnetwork	0.52	>=0.20
ENSG00000135363	LMO2 PPI subnetwork	0.58	>=0.20
ENSG00000136153	LMO7 PPI subnetwork	0.21	>=0.20
GO:0007626	locomotory behavior	1	>=0.20
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	0.26	>=0.20
GO:0035336	long-chain fatty-acyl-CoA metabolic process	0.26	>=0.20
GO:0001676	long-chain fatty acid metabolic process	0.85	>=0.20
GO:0007616	long-term memory	1	>=0.20
MP:0005421	loose skin	0.5	>=0.20
MP:0000162	lordosis	0.48	>=0.20
MP:0000024	lowered ear position	0.95	>=0.20
ENSG00000064547	LPAR2 PPI subnetwork	0.34	>=0.20
ENSG00000147145	LPAR4 PPI subnetwork	0.29	>=0.20
ENSG00000153395	LPCAT1 PPI subnetwork	0.13	>=0.20
ENSG00000077454	LRCH4 PPI subnetwork	0.12	>=0.20
ENSG00000121931	LRIF1 PPI subnetwork	0.22	>=0.20

ENSG00000162337	LRP5 PPI subnetwork	0.58	>=0.20
ENSG00000070018	LRP6 PPI subnetwork	0.77	>=0.20
ENSG00000157193	LRP8 PPI subnetwork	0.33	>=0.20
ENSG00000033122	LRRC7 PPI subnetwork	1	>=0.20
ENSG00000093167	LRRFIP2 PPI subnetwork	0.5	>=0.20
ENSG00000175324	LSM1 PPI subnetwork	0.18	>=0.20
ENSG00000181817	LSM10 PPI subnetwork	0.95	>=0.20
ENSG00000130332	LSM7 PPI subnetwork	0.53	>=0.20
ENSG00000105699	LSR PPI subnetwork	0.06	>=0.20
ENSG00000049323	LTBP1 PPI subnetwork	0.1	>=0.20
ENSG00000012223	LTF PPI subnetwork	0.08	>=0.20
ENSG00000146963	LUC7L2 PPI subnetwork	0.03	>=0.20
ENSG00000108848	LUC7L3 PPI subnetwork	0.91	>=0.20
MP:0004616	lumbar vertebral transformation	0.08	>=0.20
MP:0002027	lung adenocarcinoma	0.24	>=0.20
GO:0048286	lung alveolus development	0.9	>=0.20
GO:0060479	lung cell differentiation	0.69	>=0.20
GO:0030324	lung development	0.68	>=0.20
GO:0060487	lung epithelial cell differentiation	0.67	>=0.20
GO:0060428	lung epithelium development	0.85	>=0.20
MP:0001182	lung hemorrhage	0.37	>=0.20
GO:0060425	lung morphogenesis	1	>=0.20
ENSG00000169641	LUZP1 PPI subnetwork	0.34	>=0.20
ENSG00000145220	LYAR PPI subnetwork	0.58	>=0.20
MP:0008101	lymph node hypoplasia	0.28	>=0.20
GO:0001945	lymph vessel development	0.97	>=0.20
GO:0046649	lymphocyte activation	0.14	>=0.20
GO:0002285	lymphocyte activation involved in immune response	0.96	>=0.20
GO:0070227	lymphocyte apoptotic process	0.82	>=0.20
GO:0031294	lymphocyte costimulation	0.8	>=0.20
GO:0030098	lymphocyte differentiation	0.3	>=0.20
GO:0002260	lymphocyte homeostasis	0.41	>=0.20
GO:0046651	lymphocyte proliferation	0.41	>=0.20
MP:0000688	lymphoid hyperplasia	0.48	>=0.20
GO:0016278	lysine N-methyltransferase activity	0.11	>=0.20
GO:0007041	lysosomal transport	0.36	>=0.20
GO:0007040	lysosome organization	0.51	>=0.20
GO:0001619	lysosphingolipid and lysophosphatidic acid receptor activity	0.91	>=0.20
ENSG00000061337	LZTS1 PPI subnetwork	0.91	>=0.20
GO:0000279	M phase	0.98	>=0.20
GO:0051327	M phase of meiotic cell cycle	1	>=0.20
GO:0000087	M phase of mitotic cell cycle	0.75	>=0.20
GO:0000216	M/G1 transition of mitotic cell cycle	0.96	>=0.20
GO:0016236	macroautophagy	0.76	>=0.20
MP:0000248	macrocytosis	0.13	>=0.20
GO:0032984	macromolecular complex disassembly	0.81	>=0.20
GO:0043413	macromolecule glycosylation	0.91	>=0.20

GO:0043414	macromolecule methylation	0.61	>=0.20
GO:0048246	macrophage chemotaxis	0.65	>=0.20
GO:0010742	macrophage derived foam cell differentiation	0.04	>=0.20
ENSG00000002822	MAD1L1 PPI subnetwork	0.8	>=0.20
ENSG00000164109	MAD2L1 PPI subnetwork	0.52	>=0.20
ENSG00000179632	MAF1 PPI subnetwork	0.88	>=0.20
ENSG00000197063	MAFG PPI subnetwork	0.27	>=0.20
ENSG00000198517	MAFK PPI subnetwork	0.03	>=0.20
ENSG00000105695	MAG PPI subnetwork	0.91	>=0.20
ENSG00000183305	MAGEA2B PPI subnetwork	0.12	>=0.20
ENSG00000099399	MAGEB2 PPI subnetwork	0.85	>=0.20
ENSG00000179222	MAGED1 PPI subnetwork	0.48	>=0.20
ENSG00000151276	MAGI1 PPI subnetwork	0.21	>=0.20
ENSG00000187391	MAGI2 PPI subnetwork	0.97	>=0.20
ENSG00000162385	MAGOH PPI subnetwork	0.07	>=0.20
ENSG00000102158	MAGT1 PPI subnetwork	0.65	>=0.20
GO:0044304	main axon	1	>=0.20
GO:0045005	maintenance of fidelity involved in DNA-dependent DNA repl	0.99	>=0.20
ENSG00000198042	MAK16 PPI subnetwork	0.7	>=0.20
GO:0048232	male gamete generation	0.96	>=0.20
MP:0008280	male germ cell apoptosis	0.46	>=0.20
GO:0001673	male germ cell nucleus	1	>=0.20
GO:0008584	male gonad development	0.69	>=0.20
MP:0001925	male infertility	0.8	>=0.20
GO:0007140	male meiosis	1	>=0.20
GO:0007141	male meiosis I	0.99	>=0.20
GO:0046661	male sex differentiation	0.75	>=0.20
MP:0000120	malocclusion	0.59	>=0.20
ENSG00000172175	MALT1 PPI subnetwork	0.79	>=0.20
MP:0001883	mammary adenocarcinoma	0.32	>=0.20
GO:0030879	mammary gland development	0.37	>=0.20
GO:0060603	mammary gland duct morphogenesis	0.97	>=0.20
GO:0061180	mammary gland epithelium development	0.82	>=0.20
GO:0060443	mammary gland morphogenesis	0.74	>=0.20
ENSG00000140400	MAN2C1 PPI subnetwork	1	>=0.20
MP:0000460	mandible hypoplasia	0.47	>=0.20
GO:0006013	mannose metabolic process	0.81	>=0.20
GO:0033549	MAP kinase phosphatase activity	0.08	>=0.20
GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	0.1	>=0.20
ENSG00000166963	MAP1A PPI subnetwork	0.99	>=0.20
ENSG00000131711	MAP1B PPI subnetwork	0.95	>=0.20
ENSG00000130479	MAP1S PPI subnetwork	0.09	>=0.20
ENSG00000078018	MAP2 PPI subnetwork	0.68	>=0.20
ENSG00000169032	MAP2K1 PPI subnetwork	0.09	>=0.20
ENSG00000034152	MAP2K3 PPI subnetwork	0.05	>=0.20
ENSG00000065559	MAP2K4 PPI subnetwork	0.16	>=0.20
ENSG00000095015	MAP3K1 PPI subnetwork	0.17	>=0.20

ENSG00000130758	MAP3K10 PPI subnetwork	0.93	>=0.20
ENSG00000173327	MAP3K11 PPI subnetwork	0.75	>=0.20
ENSG00000006062	MAP3K14 PPI subnetwork	0.06	>=0.20
ENSG00000085511	MAP3K4 PPI subnetwork	0.4	>=0.20
ENSG00000197442	MAP3K5 PPI subnetwork	0.52	>=0.20
ENSG00000107968	MAP3K8 PPI subnetwork	0.09	>=0.20
ENSG00000104814	MAP4K1 PPI subnetwork	0.04	>=0.20
ENSG00000168067	MAP4K2 PPI subnetwork	0.39	>=0.20
ENSG00000012983	MAP4K5 PPI subnetwork	0.16	>=0.20
ENSG00000171533	MAP6 PPI subnetwork	1	>=0.20
GO:0000165	MAPK cascade	0.19	>=0.20
ENSG00000109339	MAPK10 PPI subnetwork	0.11	>=0.20
ENSG00000185386	MAPK11 PPI subnetwork	0.07	>=0.20
ENSG00000188130	MAPK12 PPI subnetwork	0.16	>=0.20
ENSG00000156711	MAPK13 PPI subnetwork	0.43	>=0.20
ENSG00000112062	MAPK14 PPI subnetwork	0.04	>=0.20
ENSG00000069956	MAPK6 PPI subnetwork	0.26	>=0.20
ENSG00000121653	MAPK8IP1 PPI subnetwork	0.29	>=0.20
ENSG00000008735	MAPK8IP2 PPI subnetwork	0.79	>=0.20
ENSG00000050748	MAPK9 PPI subnetwork	0.04	>=0.20
ENSG00000162889	MAPKAPK2 PPI subnetwork	0.09	>=0.20
ENSG00000101367	MAPRE1 PPI subnetwork	0.85	>=0.20
ENSG00000155130	MARCKS PPI subnetwork	1	>=0.20
ENSG00000116141	MARK1 PPI subnetwork	0.43	>=0.20
ENSG00000007047	MARK4 PPI subnetwork	0.88	>=0.20
ENSG00000166986	MARS PPI subnetwork	0.27	>=0.20
GO:0045576	mast cell activation	0.82	>=0.20
GO:0002279	mast cell activation involved in immune response	0.88	>=0.20
GO:0043303	mast cell degranulation	0.82	>=0.20
GO:0002448	mast cell mediated immunity	0.92	>=0.20
ENSG00000099308	MAST3 PPI subnetwork	0.12	>=0.20
ENSG00000038274	MAT2B PPI subnetwork	1	>=0.20
MP:0003718	maternal effect	0.79	>=0.20
MP:0003122	maternal imprinting	0.48	>=0.20
GO:0001893	maternal placenta development	0.22	>=0.20
GO:0007618	mating	0.96	>=0.20
GO:0007617	mating behavior	0.91	>=0.20
ENSG00000132561	MATN2 PPI subnetwork	0.75	>=0.20
ENSG00000015479	MATR3 PPI subnetwork	0.2	>=0.20
GO:0000460	maturation of 5.8S rRNA	1	>=0.20
ENSG00000125952	MAX PPI subnetwork	0.05	>=0.20
ENSG00000134046	MBD2 PPI subnetwork	0.11	>=0.20
ENSG00000071655	MBD3 PPI subnetwork	0.51	>=0.20
ENSG00000197971	MBP PPI subnetwork	0.05	>=0.20
ENSG00000166603	MC4R PPI subnetwork	0.96	>=0.20
ENSG00000100294	MCAT PPI subnetwork	0.09	>=0.20
ENSG00000143384	MCL1 PPI subnetwork	0.82	>=0.20

ENSG00000065328	MCM10 PPI subnetwork	0.87	>=0.20
ENSG00000073111	MCM2 PPI subnetwork	0.92	>=0.20
ENSG00000112118	MCM3 PPI subnetwork	0.82	>=0.20
ENSG00000104738	MCM4 PPI subnetwork	0.97	>=0.20
ENSG00000100297	MCM5 PPI subnetwork	0.73	>=0.20
ENSG00000076003	MCM6 PPI subnetwork	0.85	>=0.20
ENSG00000166508	MCM7 PPI subnetwork	0.51	>=0.20
ENSG00000125885	MCM8 PPI subnetwork	0.95	>=0.20
ENSG00000055732	MCOLN3 PPI subnetwork	0.49	>=0.20
ENSG00000187778	MCRS1 PPI subnetwork	0.72	>=0.20
ENSG00000137337	MDC1 PPI subnetwork	0.92	>=0.20
ENSG00000112559	MDFI PPI subnetwork	0.38	>=0.20
ENSG00000110492	MDK PPI subnetwork	0.32	>=0.20
ENSG00000135679	MDM2 PPI subnetwork	0.1	>=0.20
ENSG00000198625	MDM4 PPI subnetwork	0.38	>=0.20
ENSG00000163875	MEAF6 PPI subnetwork	0.86	>=0.20
GO:0042490	mechanoreceptor differentiation	1	>=0.20
ENSG00000085276	MECOM PPI subnetwork	0.85	>=0.20
ENSG00000169057	MECP2 PPI subnetwork	0.43	>=0.20
ENSG00000133398	MED10 PPI subnetwork	0.68	>=0.20
ENSG00000161920	MED11 PPI subnetwork	0.68	>=0.20
ENSG00000184634	MED12 PPI subnetwork	0.72	>=0.20
ENSG00000108510	MED13 PPI subnetwork	0.66	>=0.20
ENSG00000123066	MED13L PPI subnetwork	0.96	>=0.20
ENSG00000180182	MED14 PPI subnetwork	0.16	>=0.20
ENSG00000099917	MED15 PPI subnetwork	0.45	>=0.20
ENSG00000175221	MED16 PPI subnetwork	0.5	>=0.20
ENSG00000042429	MED17 PPI subnetwork	0.41	>=0.20
ENSG00000130772	MED18 PPI subnetwork	0.88	>=0.20
ENSG00000156603	MED19 PPI subnetwork	0.63	>=0.20
ENSG00000124641	MED20 PPI subnetwork	0.9	>=0.20
ENSG00000152944	MED21 PPI subnetwork	0.17	>=0.20
ENSG00000148297	MED22 PPI subnetwork	0.98	>=0.20
ENSG00000112282	MED23 PPI subnetwork	0.64	>=0.20
ENSG00000008838	MED24 PPI subnetwork	0.06	>=0.20
ENSG00000104973	MED25 PPI subnetwork	0.33	>=0.20
ENSG00000105085	MED26 PPI subnetwork	0.4	>=0.20
ENSG00000160563	MED27 PPI subnetwork	0.83	>=0.20
ENSG00000118579	MED28 PPI subnetwork	0.52	>=0.20
ENSG00000063322	MED29 PPI subnetwork	0.43	>=0.20
ENSG00000164758	MED30 PPI subnetwork	0.7	>=0.20
ENSG00000108590	MED31 PPI subnetwork	0.88	>=0.20
ENSG00000136146	MED4 PPI subnetwork	0.51	>=0.20
ENSG00000133997	MED6 PPI subnetwork	0.24	>=0.20
ENSG00000155868	MED7 PPI subnetwork	0.62	>=0.20
ENSG00000159479	MED8 PPI subnetwork	0.61	>=0.20
ENSG00000141026	MED9 PPI subnetwork	0.64	>=0.20

GO:0016592	mediator complex	0.83	>=0.20
ENSG00000068305	MEF2A PPI subnetwork	0.45	>=0.20
ENSG00000081189	MEF2C PPI subnetwork	0.27	>=0.20
MP:0002731	megacolon	0.25	>=0.20
GO:0030219	megakaryocyte differentiation	0.47	>=0.20
ENSG00000145794	MEGF10 PPI subnetwork	0.17	>=0.20
GO:0007126	meiosis	1	>=0.20
GO:0007127	meiosis I	1	>=0.20
GO:0051321	meiotic cell cycle	1	>=0.20
GO:0045132	meiotic chromosome segregation	1	>=0.20
GO:0007128	meiotic prophase I	1	>=0.20
ENSG00000143995	MEIS1 PPI subnetwork	0.81	>=0.20
GO:0006582	melanin metabolic process	1	>=0.20
GO:0030318	melanocyte differentiation	0.99	>=0.20
GO:0032400	melanosome localization	1	>=0.20
GO:0006900	membrane budding	0.26	>=0.20
GO:0030117	membrane coat	0.12	>=0.20
GO:0051899	membrane depolarization	1	>=0.20
GO:0022406	membrane docking	0.64	>=0.20
GO:0061025	membrane fusion	0.49	>=0.20
GO:0046467	membrane lipid biosynthetic process	0.91	>=0.20
GO:0046466	membrane lipid catabolic process	0.47	>=0.20
GO:0006643	membrane lipid metabolic process	0.54	>=0.20
GO:0006509	membrane protein ectodomain proteolysis	0.18	>=0.20
GO:0031293	membrane protein intracellular domain proteolysis	0.92	>=0.20
GO:0033619	membrane protein proteolysis	0.26	>=0.20
GO:0045121	membrane raft	0.04	>=0.20
GO:0007613	memory	1	>=0.20
ENSG00000133895	MEN1 PPI subnetwork	0.74	>=0.20
ENSG00000112818	MEP1A PPI subnetwork	0.23	>=0.20
GO:0014031	mesenchymal cell development	1	>=0.20
GO:0048762	mesenchymal cell differentiation	1	>=0.20
GO:0010463	mesenchymal cell proliferation	1	>=0.20
GO:0060485	mesenchyme development	1	>=0.20
GO:0072132	mesenchyme morphogenesis	1	>=0.20
GO:0007498	mesoderm development	0.87	>=0.20
GO:0001707	mesoderm formation	0.99	>=0.20
GO:0048332	mesoderm morphogenesis	0.98	>=0.20
GO:0048333	mesodermal cell differentiation	1	>=0.20
GO:0001710	mesodermal cell fate commitment	1	>=0.20
GO:0007501	mesodermal cell fate specification	1	>=0.20
GO:0072163	mesonephric epithelium development	0.98	>=0.20
GO:0072164	mesonephric tubule development	0.98	>=0.20
GO:0001823	mesonephros development	1	>=0.20
GO:0055065	metal ion homeostasis	0.13	>=0.20
GO:0046873	metal ion transmembrane transporter activity	1	>=0.20
GO:0031163	metallo-sulfur cluster assembly	1	>=0.20

GO:0004181	metallocarboxypeptidase activity	0.06	>=0.20
GO:0004222	metalloendopeptidase activity	0.93	>=0.20
GO:0008191	metalloendopeptidase inhibitor activity	0.14	>=0.20
GO:0048551	metalloenzyme inhibitor activity	0.14	>=0.20
GO:0010576	metalloenzyme regulator activity	0.1	>=0.20
GO:0008235	metalloexopeptidase activity	0.07	>=0.20
GO:0008237	metallopeptidase activity	0.47	>=0.20
GO:0072207	metanephric epithelium development	0.96	>=0.20
GO:0072075	metanephric mesenchyme development	0.99	>=0.20
GO:0072210	metanephric nephron development	1	>=0.20
GO:0072243	metanephric nephron epithelium development	1	>=0.20
GO:0072273	metanephric nephron morphogenesis	1	>=0.20
GO:0072234	metanephric nephron tubule development	1	>=0.20
GO:0072283	metanephric renal vesicle morphogenesis	0.99	>=0.20
GO:0072170	metanephric tubule development	1	>=0.20
GO:0001656	metanephros development	1	>=0.20
GO:0003338	metanephros morphogenesis	1	>=0.20
GO:0051310	metaphase plate congression	0.95	>=0.20
GO:0022037	metencephalon development	0.76	>=0.20
GO:0009086	methionine biosynthetic process	0.75	>=0.20
GO:0006555	methionine metabolic process	0.46	>=0.20
GO:0035064	methylated histone residue binding	0.4	>=0.20
ENSG00000174197	MGA PPI subnetwork	0.1	>=0.20
GO:0042288	MHC class I protein binding	0.92	>=0.20
GO:0042612	MHC class I protein complex	0.52	>=0.20
GO:0032393	MHC class I receptor activity	0.96	>=0.20
GO:0042613	MHC class II protein complex	0.99	>=0.20
GO:0042287	MHC protein binding	0.72	>=0.20
GO:0042611	MHC protein complex	0.92	>=0.20
MP:0000433	microcephaly	0.46	>=0.20
MP:0002813	microcytosis	0.07	>=0.20
GO:0000146	microfilament motor activity	0.83	>=0.20
GO:0001774	microglial cell activation	0.99	>=0.20
MP:0002639	micrognathia	0.95	>=0.20
MP:0001297	microphthalmia	0.49	>=0.20
GO:0005874	microtubule	0.91	>=0.20
GO:0009434	microtubule-based flagellum	0.82	>=0.20
GO:0044442	microtubule-based flagellum part	0.69	>=0.20
GO:0007018	microtubule-based movement	1	>=0.20
GO:0007017	microtubule-based process	1	>=0.20
GO:0010970	microtubule-based transport	1	>=0.20
GO:0034453	microtubule anchoring	0.99	>=0.20
GO:0005875	microtubule associated complex	0.86	>=0.20
GO:0005932	microtubule basal body	0.85	>=0.20
GO:0008017	microtubule binding	0.77	>=0.20
GO:0001578	microtubule bundle formation	0.94	>=0.20
GO:0000226	microtubule cytoskeleton organization	0.98	>=0.20

GO:0007019	microtubule depolymerization	0.99	>=0.20
GO:0003777	microtubule motor activity	0.99	>=0.20
GO:0005815	microtubule organizing center	0.28	>=0.20
GO:0031023	microtubule organizing center organization	0.95	>=0.20
GO:0044450	microtubule organizing center part	0.34	>=0.20
GO:0031109	microtubule polymerization or depolymerization	1	>=0.20
GO:0005902	microvillus	0.15	>=0.20
GO:0030496	midbody	0.72	>=0.20
GO:0030917	midbrain-hindbrain boundary development	0.99	>=0.20
GO:0030901	midbrain development	0.99	>=0.20
GO:0042474	middle ear morphogenesis	1	>=0.20
GO:0007494	midgut development	0.91	>=0.20
ENSG00000141503	MINK1 PPI subnetwork	0.95	>=0.20
ENSG00000167842	MIS12 PPI subnetwork	0.79	>=0.20
GO:0006298	mismatch repair	1	>=0.20
GO:0030983	mismatched DNA binding	0.69	>=0.20
GO:0042775	mitochondrial ATP synthesis coupled electron transport	1	>=0.20
GO:0042776	mitochondrial ATP synthesis coupled proton transport	1	>=0.20
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1	>=0.20
GO:0005743	mitochondrial inner membrane	0.15	>=0.20
GO:0005758	mitochondrial intermembrane space	0.26	>=0.20
GO:0005762	mitochondrial large ribosomal subunit	0.07	>=0.20
GO:0031966	mitochondrial membrane	0.05	>=0.20
GO:0007006	mitochondrial membrane organization	0.98	>=0.20
GO:0044455	mitochondrial membrane part	0.85	>=0.20
GO:0005753	mitochondrial proton-transporting ATP synthase complex	0.93	>=0.20
GO:0005746	mitochondrial respiratory chain	0.98	>=0.20
GO:0033108	mitochondrial respiratory chain complex assembly	1	>=0.20
GO:0005747	mitochondrial respiratory chain complex I	0.98	>=0.20
GO:0032981	mitochondrial respiratory chain complex I assembly	1	>=0.20
GO:0097031	mitochondrial respiratory chain complex I biogenesis	1	>=0.20
GO:0005761	mitochondrial ribosome	0.72	>=0.20
GO:0000959	mitochondrial RNA metabolic process	0.92	>=0.20
GO:0005763	mitochondrial small ribosomal subunit	0.9	>=0.20
GO:0032543	mitochondrial translation	0.98	>=0.20
GO:0006839	mitochondrial transport	0.83	>=0.20
GO:0007005	mitochondrion organization	0.49	>=0.20
GO:0051019	mitogen-activated protein kinase binding	0.46	>=0.20
GO:0007067	mitosis	0.8	>=0.20
GO:0007093	mitotic cell cycle checkpoint	0.9	>=0.20
GO:0031575	mitotic cell cycle G1/S transition checkpoint	0.96	>=0.20
GO:0031571	mitotic cell cycle G1/S transition DNA damage checkpoint	0.94	>=0.20
GO:0007094	mitotic cell cycle spindle assembly checkpoint	0.92	>=0.20
GO:0071174	mitotic cell cycle spindle checkpoint	0.93	>=0.20
GO:0007076	mitotic chromosome condensation	0.83	>=0.20
GO:0007091	mitotic metaphase/anaphase transition	0.93	>=0.20
GO:0000236	mitotic prometaphase	0.91	>=0.20

GO:0006312	mitotic recombination	0.97	>=0.20
GO:0000070	mitotic sister chromatid segregation	0.95	>=0.20
GO:0007052	mitotic spindle organization	0.79	>=0.20
ENSG00000148773	MKI67 PPI subnetwork	0.09	>=0.20
ENSG00000155438	MKI67IP PPI subnetwork	0.82	>=0.20
ENSG00000151725	MLF1IP PPI subnetwork	0.84	>=0.20
ENSG00000089693	MLF2 PPI subnetwork	0.36	>=0.20
ENSG00000076242	MLH1 PPI subnetwork	0.93	>=0.20
ENSG00000118058	MLL PPI subnetwork	0.6	>=0.20
GO:0071339	MLL1 complex	0.27	>=0.20
ENSG00000130382	MLLT1 PPI subnetwork	0.14	>=0.20
ENSG00000130396	MLLT4 PPI subnetwork	0.5	>=0.20
ENSG00000196611	MMP1 PPI subnetwork	0.17	>=0.20
ENSG00000157227	MMP14 PPI subnetwork	0.19	>=0.20
ENSG00000149968	MMP3 PPI subnetwork	0.43	>=0.20
ENSG00000137673	MMP7 PPI subnetwork	0.68	>=0.20
ENSG00000100985	MMP9 PPI subnetwork	0.2	>=0.20
ENSG00000138722	MMRN1 PPI subnetwork	0.04	>=0.20
ENSG00000155229	MMS19 PPI subnetwork	0.41	>=0.20
ENSG00000114978	MOB1A PPI subnetwork	0.26	>=0.20
ENSG00000115540	MOB4 PPI subnetwork	1	>=0.20
ENSG00000124217	MOCS3 PPI subnetwork	0.99	>=0.20
GO:0043632	modification-dependent macromolecule catabolic process	0.85	>=0.20
GO:0019941	modification-dependent protein catabolic process	0.83	>=0.20
GO:0044144	modulation of growth of symbiont involved in interaction wit	0.93	>=0.20
ENSG00000137345	MOG PPI subnetwork	0.83	>=0.20
ENSG00000204655	MOG PPI subnetwork	0.83	>=0.20
GO:0042303	molting cycle	0.98	>=0.20
GO:0022404	molting cycle process	0.98	>=0.20
GO:0015844	monoamine transport	0.91	>=0.20
GO:0032943	mononuclear cell proliferation	0.42	>=0.20
GO:0015145	monosaccharide transmembrane transporter activity	0.08	>=0.20
GO:0015749	monosaccharide transport	0.16	>=0.20
GO:0055067	monovalent inorganic cation homeostasis	0.98	>=0.20
GO:0015077	monovalent inorganic cation transmembrane transporter act	1	>=0.20
GO:0015672	monovalent inorganic cation transport	1	>=0.20
ENSG00000185787	MORF4L1 PPI subnetwork	0.21	>=0.20
ENSG00000123562	MORF4L2 PPI subnetwork	0.57	>=0.20
GO:0061138	morphogenesis of a branching epithelium	0.86	>=0.20
GO:0001763	morphogenesis of a branching structure	0.95	>=0.20
GO:0001738	morphogenesis of a polarized epithelium	1	>=0.20
GO:0060572	morphogenesis of an epithelial bud	1	>=0.20
GO:0060571	morphogenesis of an epithelial fold	1	>=0.20
GO:0002011	morphogenesis of an epithelial sheet	0.98	>=0.20
GO:0002009	morphogenesis of an epithelium	0.98	>=0.20
GO:0016331	morphogenesis of embryonic epithelium	1	>=0.20
ENSG00000172680	MOS PPI subnetwork	0.6	>=0.20

GO:0031514	motile cilium	0.47	>=0.20
GO:0003774	motor activity	0.99	>=0.20
GO:0008045	motor axon guidance	1	>=0.20
ENSG00000129255	MPDU1 PPI subnetwork	0.54	>=0.20
ENSG00000107186	MPDZ PPI subnetwork	0.93	>=0.20
ENSG00000117400	MPL PPI subnetwork	0.21	>=0.20
ENSG00000108852	MPP2 PPI subnetwork	0.98	>=0.20
ENSG00000161647	MPP3 PPI subnetwork	0.92	>=0.20
ENSG00000072415	MPP5 PPI subnetwork	0.99	>=0.20
ENSG00000105926	MPP6 PPI subnetwork	0.65	>=0.20
ENSG00000133030	MPRIP PPI subnetwork	0.2	>=0.20
ENSG00000158186	MRAS PPI subnetwork	0.13	>=0.20
ENSG00000020922	MRE11A PPI subnetwork	0.91	>=0.20
ENSG00000129282	MRM1 PPI subnetwork	0.32	>=0.20
GO:0031124	mRNA 3'-end processing	0.31	>=0.20
GO:0003730	mRNA 3'-UTR binding	0.19	>=0.20
GO:0003729	mRNA binding	0.46	>=0.20
GO:0006370	mRNA capping	0.93	>=0.20
GO:0006402	mRNA catabolic process	0.83	>=0.20
GO:0006406	mRNA export from nucleus	0.59	>=0.20
GO:0006378	mRNA polyadenylation	0.78	>=0.20
GO:0006397	mRNA processing	0.49	>=0.20
GO:0006376	mRNA splice site selection	0.77	>=0.20
ENSG00000174547	MRPL11 PPI subnetwork	0.66	>=0.20
ENSG00000137547	MRPL15 PPI subnetwork	0.61	>=0.20
ENSG00000214026	MRPL23 PPI subnetwork	0.66	>=0.20
ENSG00000114686	MRPL3 PPI subnetwork	0.55	>=0.20
ENSG00000130312	MRPL34 PPI subnetwork	0.88	>=0.20
ENSG00000171421	MRPL36 PPI subnetwork	0.5	>=0.20
ENSG00000105364	MRPL4 PPI subnetwork	0.62	>=0.20
ENSG00000182180	MRPS16 PPI subnetwork	0.99	>=0.20
ENSG00000122140	MRPS2 PPI subnetwork	0.88	>=0.20
ENSG00000181610	MRPS23 PPI subnetwork	0.81	>=0.20
ENSG00000074071	MRPS34 PPI subnetwork	0.07	>=0.20
ENSG00000144029	MRPS5 PPI subnetwork	0.17	>=0.20
ENSG00000135972	MRPS9 PPI subnetwork	1	>=0.20
ENSG00000053372	MRTO4 PPI subnetwork	0.36	>=0.20
ENSG00000095002	MSH2 PPI subnetwork	0.39	>=0.20
ENSG00000113318	MSH3 PPI subnetwork	0.62	>=0.20
ENSG00000057468	MSH4 PPI subnetwork	0.57	>=0.20
ENSG00000116062	MSH6 PPI subnetwork	0.4	>=0.20
ENSG00000135097	MSI1 PPI subnetwork	0.75	>=0.20
ENSG00000147065	MSN PPI subnetwork	0.17	>=0.20
ENSG00000163132	MSX1 PPI subnetwork	0.99	>=0.20
ENSG00000120149	MSX2 PPI subnetwork	0.99	>=0.20
ENSG00000198899	MT-ATP6 PPI subnetwork	0.74	>=0.20
ENSG00000198804	MT-CO1 PPI subnetwork	0.97	>=0.20

ENSG00000198712	MT-CO2 PPI subnetwork	0.99	>=0.20
ENSG00000198938	MT-CO3 PPI subnetwork	0.99	>=0.20
ENSG00000198727	MT-CYB PPI subnetwork	0.99	>=0.20
ENSG00000198888	MT-ND1 PPI subnetwork	0.91	>=0.20
ENSG00000198763	MT-ND2 PPI subnetwork	0.99	>=0.20
ENSG00000198840	MT-ND3 PPI subnetwork	0.98	>=0.20
ENSG00000198886	MT-ND4 PPI subnetwork	0.95	>=0.20
ENSG00000198786	MT-ND5 PPI subnetwork	0.96	>=0.20
ENSG00000198695	MT-ND6 PPI subnetwork	0.98	>=0.20
ENSG00000087250	MT3 PPI subnetwork	0.61	>=0.20
ENSG00000182979	MTA1 PPI subnetwork	0.11	>=0.20
ENSG00000149480	MTA2 PPI subnetwork	0.11	>=0.20
ENSG00000120254	MTHFD1L PPI subnetwork	1	>=0.20
ENSG00000063601	MTMR1 PPI subnetwork	1	>=0.20
ENSG00000139505	MTMR6 PPI subnetwork	0.37	>=0.20
ENSG00000168412	MTNR1A PPI subnetwork	0.46	>=0.20
ENSG00000134640	MTNR1B PPI subnetwork	0.26	>=0.20
ENSG00000185499	MUC1 PPI subnetwork	0.43	>=0.20
ENSG00000173702	MUC13 PPI subnetwork	0.03	>=0.20
ENSG00000198788	MUC2 PPI subnetwork	0.14	>=0.20
ENSG00000171195	MUC7 PPI subnetwork	0.98	>=0.20
GO:0044243	multicellular organismal catabolic process	0.97	>=0.20
GO:0048871	multicellular organismal homeostasis	0.57	>=0.20
GO:0044259	multicellular organismal macromolecule metabolic process	0.55	>=0.20
GO:0044236	multicellular organismal metabolic process	0.42	>=0.20
GO:0050879	multicellular organismal movement	1	>=0.20
GO:0033555	multicellular organismal response to stress	1	>=0.20
MP:0001655	multifocal hepatic necrosis	0.14	>=0.20
ENSG00000172732	MUS81 PPI subnetwork	0.7	>=0.20
GO:0043500	muscle adaptation	0.55	>=0.20
GO:0055001	muscle cell development	0.93	>=0.20
GO:0042692	muscle cell differentiation	0.98	>=0.20
GO:0042693	muscle cell fate commitment	0.92	>=0.20
GO:0014812	muscle cell migration	0.71	>=0.20
GO:0033002	muscle cell proliferation	0.15	>=0.20
GO:0006936	muscle contraction	0.98	>=0.20
MP:0000749	muscle degeneration	0.98	>=0.20
GO:0048747	muscle fiber development	0.99	>=0.20
GO:0030049	muscle filament sliding	1	>=0.20
GO:0005859	muscle myosin complex	0.97	>=0.20
GO:0007517	muscle organ development	0.98	>=0.20
GO:0048644	muscle organ morphogenesis	0.99	>=0.20
MP:0000743	muscle spasm	1	>=0.20
GO:0061061	muscle structure development	0.98	>=0.20
GO:0003012	muscle system process	0.96	>=0.20
GO:0060537	muscle tissue development	0.98	>=0.20
GO:0060415	muscle tissue morphogenesis	0.99	>=0.20

MP:0000747	muscle weakness	0.46	>=0.20
GO:0050881	musculoskeletal movement	1	>=0.20
ENSG00000030304	MUSK PPI subnetwork	0.86	>=0.20
ENSG00000157601	MX1 PPI subnetwork	1	>=0.20
ENSG00000118513	MYB PPI subnetwork	0.09	>=0.20
ENSG00000132382	MYBBP1A PPI subnetwork	0.06	>=0.20
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	0.39	>=0.20
GO:0002756	MyD88-independent toll-like receptor signaling pathway	0.63	>=0.20
ENSG00000172936	MYD88 PPI subnetwork	0.24	>=0.20
MP:0002546	mydriasis	0.98	>=0.20
ENSG00000104177	MYEF2 PPI subnetwork	0.08	>=0.20
GO:0043209	myelin sheath	0.98	>=0.20
GO:0042552	myelination	1	>=0.20
GO:0002275	myeloid cell activation involved in immune response	0.75	>=0.20
MP:0010373	myeloid hyperplasia	0.12	>=0.20
GO:0002274	myeloid leukocyte activation	0.38	>=0.20
GO:0002573	myeloid leukocyte differentiation	0.08	>=0.20
GO:0002444	myeloid leukocyte mediated immunity	0.73	>=0.20
ENSG00000133026	MYH10 PPI subnetwork	0.25	>=0.20
ENSG00000105357	MYH14 PPI subnetwork	0.47	>=0.20
ENSG00000197616	MYH6 PPI subnetwork	0.24	>=0.20
ENSG00000092054	MYH7 PPI subnetwork	0.88	>=0.20
ENSG00000100345	MYH9 PPI subnetwork	0.08	>=0.20
ENSG00000168530	MYL1 PPI subnetwork	0.3	>=0.20
ENSG00000101608	MYL12A PPI subnetwork	0.52	>=0.20
ENSG00000118680	MYL12B PPI subnetwork	0.72	>=0.20
ENSG00000111245	MYL2 PPI subnetwork	0.54	>=0.20
ENSG00000092841	MYL6 PPI subnetwork	0.05	>=0.20
ENSG00000065534	MYLK PPI subnetwork	0.31	>=0.20
ENSG00000101306	MYLK2 PPI subnetwork	0.5	>=0.20
ENSG00000180209	MYLPF PPI subnetwork	0.24	>=0.20
ENSG00000145555	MYO10 PPI subnetwork	0.89	>=0.20
ENSG00000196535	MYO18A PPI subnetwork	0.47	>=0.20
ENSG00000166866	MYO1A PPI subnetwork	0.31	>=0.20
ENSG00000197879	MYO1C PPI subnetwork	0.26	>=0.20
ENSG00000157483	MYO1E PPI subnetwork	0.81	>=0.20
ENSG00000136286	MYO1G PPI subnetwork	0.07	>=0.20
ENSG00000071909	MYO3B PPI subnetwork	0.86	>=0.20
ENSG00000197535	MYO5A PPI subnetwork	0.9	>=0.20
ENSG00000167306	MYO5B PPI subnetwork	0.53	>=0.20
ENSG00000128833	MYO5C PPI subnetwork	0.11	>=0.20
ENSG00000196586	MYO6 PPI subnetwork	0.2	>=0.20
ENSG00000099331	MYO9B PPI subnetwork	0.07	>=0.20
GO:0045445	myoblast differentiation	0.93	>=0.20
MP:0004566	myocardial fiber degeneration	0.36	>=0.20
MP:0000243	myoclonus	0.98	>=0.20
ENSG00000129152	MYOD1 PPI subnetwork	0.08	>=0.20

GO:0030016	myofibril	0.71	>=0.20
GO:0030239	myofibril assembly	0.93	>=0.20
ENSG00000122180	MYOG PPI subnetwork	0.03	>=0.20
MP:0000751	myopathy	0.65	>=0.20
GO:0017022	myosin binding	0.95	>=0.20
GO:0016459	myosin complex	0.98	>=0.20
GO:0032982	myosin filament	0.97	>=0.20
GO:0016460	myosin II complex	0.95	>=0.20
GO:0014902	myotube differentiation	0.86	>=0.20
ENSG00000177791	MYOZ1 PPI subnetwork	0.72	>=0.20
ENSG00000172399	MYOZ2 PPI subnetwork	0.26	>=0.20
GO:0006044	N-acetylglucosamine metabolic process	0.96	>=0.20
GO:0008080	N-acetyltransferase activity	0.45	>=0.20
ENSG00000164134	NAA15 PPI subnetwork	0.71	>=0.20
ENSG00000128534	NAA38 PPI subnetwork	0.9	>=0.20
ENSG00000196531	NACA PPI subnetwork	0.85	>=0.20
GO:0017136	NAD-dependent histone deacetylase activity	0.87	>=0.20
GO:0032041	NAD-dependent histone deacetylase activity (H3-K14 specific	0.95	>=0.20
GO:0046969	NAD-dependent histone deacetylase activity (H3-K9 specific)	0.92	>=0.20
GO:0046970	NAD-dependent histone deacetylase activity (H4-K16 specific	0.95	>=0.20
GO:0034979	NAD-dependent protein deacetylase activity	0.87	>=0.20
GO:0019674	NAD metabolic process	0.42	>=0.20
GO:0003950	NAD+ ADP-ribosyltransferase activity	0.71	>=0.20
GO:0050136	NADH dehydrogenase (quinone) activity	0.99	>=0.20
GO:0008137	NADH dehydrogenase (ubiquinone) activity	0.99	>=0.20
GO:0003954	NADH dehydrogenase activity	0.99	>=0.20
GO:0030964	NADH dehydrogenase complex	0.98	>=0.20
GO:0010257	NADH dehydrogenase complex assembly	1	>=0.20
GO:0006740	NADPH regeneration	0.67	>=0.20
ENSG00000145414	NAF1 PPI subnetwork	0.97	>=0.20
ENSG00000095380	NANS PPI subnetwork	0.14	>=0.20
ENSG00000187109	NAP1L1 PPI subnetwork	0.03	>=0.20
ENSG00000205531	NAP1L4 PPI subnetwork	0.08	>=0.20
ENSG00000105402	NAPA PPI subnetwork	0.44	>=0.20
ENSG00000125814	NAPB PPI subnetwork	1	>=0.20
GO:0030101	natural killer cell activation	0.97	>=0.20
GO:0042267	natural killer cell mediated cytotoxicity	0.87	>=0.20
GO:0002228	natural killer cell mediated immunity	0.87	>=0.20
GO:0071565	nBAF complex	0.45	>=0.20
ENSG00000104320	NBN PPI subnetwork	0.88	>=0.20
ENSG00000149294	NCAM1 PPI subnetwork	0.99	>=0.20
ENSG00000121152	NCAPH PPI subnetwork	0.82	>=0.20
ENSG00000025770	NCAPH2 PPI subnetwork	0.94	>=0.20
ENSG00000158517	NCF1 PPI subnetwork	0.19	>=0.20
ENSG00000158092	NCK1 PPI subnetwork	0.06	>=0.20
ENSG00000071051	NCK2 PPI subnetwork	0.86	>=0.20
ENSG00000061676	NCKAP1 PPI subnetwork	0.99	>=0.20

ENSG00000123338	NCKAP1L PPI subnetwork	0.08	>=0.20
ENSG00000213672	NCKIPSD PPI subnetwork	0.3	>=0.20
ENSG00000115053	NCL PPI subnetwork	0.23	>=0.20
ENSG00000140396	NCOA2 PPI subnetwork	0.05	>=0.20
ENSG00000141027	NCOR1 PPI subnetwork	0.09	>=0.20
ENSG00000196498	NCOR2 PPI subnetwork	0.03	>=0.20
ENSG00000162736	NCSTN PPI subnetwork	0.45	>=0.20
ENSG00000080986	NDC80 PPI subnetwork	0.81	>=0.20
ENSG00000072864	NDE1 PPI subnetwork	0.71	>=0.20
ENSG00000166579	NDEL1 PPI subnetwork	0.7	>=0.20
ENSG00000104419	NDRG1 PPI subnetwork	0.25	>=0.20
ENSG00000125356	NDUFA1 PPI subnetwork	0.98	>=0.20
ENSG00000130414	NDUFA10 PPI subnetwork	0.75	>=0.20
ENSG00000184752	NDUFA12 PPI subnetwork	0.98	>=0.20
ENSG00000131495	NDUFA2 PPI subnetwork	0.97	>=0.20
ENSG00000170906	NDUFA3 PPI subnetwork	0.98	>=0.20
ENSG00000189043	NDUFA4 PPI subnetwork	0.96	>=0.20
ENSG00000128609	NDUFA5 PPI subnetwork	0.36	>=0.20
ENSG00000184983	NDUFA6 PPI subnetwork	0.97	>=0.20
ENSG00000167774	NDUFA7 PPI subnetwork	0.96	>=0.20
ENSG00000119421	NDUFA8 PPI subnetwork	0.36	>=0.20
ENSG00000139180	NDUFA9 PPI subnetwork	0.92	>=0.20
ENSG00000004779	NDUFAB1 PPI subnetwork	1	>=0.20
ENSG00000183648	NDUFB1 PPI subnetwork	0.96	>=0.20
ENSG00000140990	NDUFB10 PPI subnetwork	0.98	>=0.20
ENSG00000147123	NDUFB11 PPI subnetwork	0.99	>=0.20
ENSG00000090266	NDUFB2 PPI subnetwork	0.97	>=0.20
ENSG00000119013	NDUFB3 PPI subnetwork	0.98	>=0.20
ENSG00000065518	NDUFB4 PPI subnetwork	0.48	>=0.20
ENSG00000136521	NDUFB5 PPI subnetwork	0.97	>=0.20
ENSG00000165264	NDUFB6 PPI subnetwork	0.98	>=0.20
ENSG00000099795	NDUFB7 PPI subnetwork	0.97	>=0.20
ENSG00000166136	NDUFB8 PPI subnetwork	0.98	>=0.20
ENSG00000147684	NDUFB9 PPI subnetwork	0.96	>=0.20
ENSG00000109390	NDUFC1 PPI subnetwork	0.98	>=0.20
ENSG00000151366	NDUFC2 PPI subnetwork	0.99	>=0.20
ENSG00000023228	NDUFS1 PPI subnetwork	0.96	>=0.20
ENSG00000158864	NDUFS2 PPI subnetwork	0.52	>=0.20
ENSG00000213619	NDUFS3 PPI subnetwork	0.69	>=0.20
ENSG00000164258	NDUFS4 PPI subnetwork	0.95	>=0.20
ENSG00000168653	NDUFS5 PPI subnetwork	0.98	>=0.20
ENSG00000145494	NDUFS6 PPI subnetwork	0.93	>=0.20
ENSG00000115286	NDUFS7 PPI subnetwork	0.96	>=0.20
ENSG00000110717	NDUFS8 PPI subnetwork	0.98	>=0.20
ENSG00000167792	NDUFV1 PPI subnetwork	0.96	>=0.20
ENSG00000178127	NDUFV2 PPI subnetwork	0.99	>=0.20
ENSG00000160194	NDUFV3 PPI subnetwork	0.98	>=0.20

ENSG00000183091	NEB PPI subnetwork	0.82	>=0.20
ENSG00000089818	NECAP1 PPI subnetwork	0.13	>=0.20
ENSG00000069869	NEDD4 PPI subnetwork	0.75	>=0.20
ENSG00000129559	NEDD8 PPI subnetwork	0.95	>=0.20
ENSG00000111859	NEDD9 PPI subnetwork	0.09	>=0.20
ENSG00000100285	NEFH PPI subnetwork	0.06	>=0.20
ENSG00000104722	NEFM PPI subnetwork	0.4	>=0.20
GO:0050919	negative chemotaxis	1	>=0.20
GO:0030835	negative regulation of actin filament depolymerization	0.4	>=0.20
GO:0030837	negative regulation of actin filament polymerization	0.49	>=0.20
GO:0007194	negative regulation of adenylate cyclase activity	1	>=0.20
GO:0051953	negative regulation of amine transport	0.88	>=0.20
GO:0050858	negative regulation of antigen receptor-mediated signaling p	0.61	>=0.20
GO:0050771	negative regulation of axonogenesis	0.97	>=0.20
GO:0045776	negative regulation of blood pressure	0.99	>=0.20
GO:0030514	negative regulation of BMP signaling pathway	0.87	>=0.20
GO:0030818	negative regulation of cAMP biosynthetic process	1	>=0.20
GO:0030815	negative regulation of cAMP metabolic process	1	>=0.20
GO:0090090	negative regulation of canonical Wnt receptor signaling path	1	>=0.20
GO:0022408	negative regulation of cell-cell adhesion	0.14	>=0.20
GO:0050866	negative regulation of cell activation	0.33	>=0.20
GO:0045786	negative regulation of cell cycle	0.72	>=0.20
GO:0010948	negative regulation of cell cycle process	0.93	>=0.20
GO:0010721	negative regulation of cell development	0.65	>=0.20
GO:0045596	negative regulation of cell differentiation	0.26	>=0.20
GO:0031345	negative regulation of cell projection organization	0.99	>=0.20
GO:0008285	negative regulation of cell proliferation	0.07	>=0.20
GO:0051129	negative regulation of cellular component organization	0.29	>=0.20
GO:0050922	negative regulation of chemotaxis	1	>=0.20
GO:0032331	negative regulation of chondrocyte differentiation	0.97	>=0.20
GO:0031280	negative regulation of cyclase activity	1	>=0.20
GO:0030803	negative regulation of cyclic nucleotide biosynthetic process	1	>=0.20
GO:0030800	negative regulation of cyclic nucleotide metabolic process	1	>=0.20
GO:0001818	negative regulation of cytokine production	0.05	>=0.20
GO:0051494	negative regulation of cytoskeleton organization	0.94	>=0.20
GO:0051093	negative regulation of developmental process	0.09	>=0.20
GO:2000104	negative regulation of DNA-dependent DNA replication	0.99	>=0.20
GO:0043392	negative regulation of DNA binding	0.3	>=0.20
GO:0051053	negative regulation of DNA metabolic process	0.59	>=0.20
GO:0008156	negative regulation of DNA replication	0.95	>=0.20
GO:0042059	negative regulation of epidermal growth factor receptor sign	0.77	>=0.20
GO:0050680	negative regulation of epithelial cell proliferation	0.81	>=0.20
GO:0051918	negative regulation of fibrinolysis	0.07	>=0.20
GO:0045744	negative regulation of G-protein coupled receptor protein sig	1	>=0.20
GO:0010972	negative regulation of G2/M transition of mitotic cell cycle	1	>=0.20
GO:0045686	negative regulation of glial cell differentiation	0.93	>=0.20
GO:0014014	negative regulation of gliogenesis	0.84	>=0.20

GO:0045926	negative regulation of growth	0.03	>=0.20
GO:0044130	negative regulation of growth of symbiont in host	0.93	>=0.20
GO:0044146	negative regulation of growth of symbiont involved in interac	0.93	>=0.20
GO:0046888	negative regulation of hormone secretion	0.03	>=0.20
GO:0050777	negative regulation of immune response	0.41	>=0.20
GO:0002683	negative regulation of immune system process	0.29	>=0.20
GO:0046676	negative regulation of insulin secretion	0.14	>=0.20
GO:0032715	negative regulation of interleukin-6 production	0.5	>=0.20
GO:0010741	negative regulation of intracellular protein kinase cascade	0.25	>=0.20
GO:0033673	negative regulation of kinase activity	0.07	>=0.20
GO:0002695	negative regulation of leukocyte activation	0.53	>=0.20
GO:0051352	negative regulation of ligase activity	0.85	>=0.20
GO:0010888	negative regulation of lipid storage	0.11	>=0.20
GO:0040013	negative regulation of locomotion	0.19	>=0.20
GO:0051350	negative regulation of lyase activity	1	>=0.20
GO:0051250	negative regulation of lymphocyte activation	0.66	>=0.20
GO:0045620	negative regulation of lymphocyte differentiation	0.75	>=0.20
GO:0043407	negative regulation of MAP kinase activity	0.23	>=0.20
GO:0043409	negative regulation of MAPK cascade	0.31	>=0.20
GO:0007026	negative regulation of microtubule depolymerization	1	>=0.20
GO:0031111	negative regulation of microtubule polymerization or depoly	1	>=0.20
GO:0045839	negative regulation of mitosis	0.95	>=0.20
GO:0045841	negative regulation of mitotic metaphase/anaphase transitio	0.95	>=0.20
GO:0050686	negative regulation of mRNA processing	0.88	>=0.20
GO:0043901	negative regulation of multi-organism process	0.78	>=0.20
GO:0048635	negative regulation of muscle organ development	0.99	>=0.20
GO:0045638	negative regulation of myeloid cell differentiation	0.04	>=0.20
GO:0050768	negative regulation of neurogenesis	0.87	>=0.20
GO:0043524	negative regulation of neuron apoptotic process	0.99	>=0.20
GO:0045665	negative regulation of neuron differentiation	1	>=0.20
GO:0045746	negative regulation of Notch signaling pathway	0.97	>=0.20
GO:0051784	negative regulation of nuclear division	0.95	>=0.20
GO:0030809	negative regulation of nucleotide biosynthetic process	1	>=0.20
GO:0045980	negative regulation of nucleotide metabolic process	1	>=0.20
GO:0048715	negative regulation of oligodendrocyte differentiation	1	>=0.20
GO:0010639	negative regulation of organelle organization	0.95	>=0.20
GO:0030279	negative regulation of ossification	0.8	>=0.20
GO:0045668	negative regulation of osteoblast differentiation	0.67	>=0.20
GO:0090278	negative regulation of peptide hormone secretion	0.07	>=0.20
GO:0002792	negative regulation of peptide secretion	0.07	>=0.20
GO:0031333	negative regulation of protein complex assembly	0.3	>=0.20
GO:0043242	negative regulation of protein complex disassembly	0.81	>=0.20
GO:0006469	negative regulation of protein kinase activity	0.13	>=0.20
GO:0031400	negative regulation of protein modification process	0.15	>=0.20
GO:0032272	negative regulation of protein polymerization	0.73	>=0.20
GO:0071901	negative regulation of protein serine/threonine kinase activit	0.17	>=0.20
GO:0031397	negative regulation of protein ubiquitination	0.7	>=0.20

GO:0046580	negative regulation of Ras protein signal transduction	0.87	>=0.20
GO:2000242	negative regulation of reproductive process	0.99	>=0.20
GO:0032102	negative regulation of response to external stimulus	0.59	>=0.20
GO:0033119	negative regulation of RNA splicing	0.27	>=0.20
GO:0009968	negative regulation of signal transduction	0.43	>=0.20
GO:0051058	negative regulation of small GTPase mediated signal transdu	0.94	>=0.20
GO:0045843	negative regulation of striated muscle tissue development	0.99	>=0.20
GO:0050868	negative regulation of T cell activation	0.72	>=0.20
GO:0050860	negative regulation of T cell receptor signaling pathway	0.61	>=0.20
GO:0000122	negative regulation of transcription from RNA polymerase II p	0.31	>=0.20
GO:0051348	negative regulation of transferase activity	0.05	>=0.20
GO:0030512	negative regulation of transforming growth factor beta recep	0.93	>=0.20
GO:0017148	negative regulation of translation	0.26	>=0.20
GO:0090101	negative regulation of transmembrane receptor protein serir	0.86	>=0.20
GO:0032480	negative regulation of type I interferon production	0.86	>=0.20
GO:0051444	negative regulation of ubiquitin-protein ligase activity	0.85	>=0.20
GO:0051436	negative regulation of ubiquitin-protein ligase activity involve	0.9	>=0.20
GO:0045071	negative regulation of viral genome replication	0.95	>=0.20
GO:0048525	negative regulation of viral reproduction	0.95	>=0.20
GO:0030178	negative regulation of Wnt receptor signaling pathway	0.99	>=0.20
GO:0043383	negative T cell selection	1	>=0.20
GO:0045060	negative thymic T cell selection	0.99	>=0.20
ENSG00000114670	NEK11 PPI subnetwork	0.35	>=0.20
ENSG00000117650	NEK2 PPI subnetwork	0.57	>=0.20
MP:0002058	neonatal lethality	0.99	>=0.20
GO:0072006	nephron development	0.99	>=0.20
GO:0072009	nephron epithelium development	1	>=0.20
GO:0072088	nephron epithelium morphogenesis	1	>=0.20
GO:0072028	nephron morphogenesis	1	>=0.20
GO:0072080	nephron tubule development	1	>=0.20
GO:0072079	nephron tubule formation	1	>=0.20
GO:0072078	nephron tubule morphogenesis	1	>=0.20
GO:0021675	nerve development	1	>=0.20
GO:0048011	nerve growth factor receptor signaling pathway	0.09	>=0.20
ENSG00000173848	NET1 PPI subnetwork	0.35	>=0.20
ENSG00000171208	NETO2 PPI subnetwork	0.92	>=0.20
GO:0014032	neural crest cell development	1	>=0.20
GO:0014033	neural crest cell differentiation	1	>=0.20
GO:0001755	neural crest cell migration	1	>=0.20
GO:0001840	neural plate development	1	>=0.20
GO:0061351	neural precursor cell proliferation	1	>=0.20
GO:0003407	neural retina development	1	>=0.20
GO:0001843	neural tube closure	1	>=0.20
GO:0021915	neural tube development	0.99	>=0.20
GO:0001841	neural tube formation	0.99	>=0.20
GO:0021532	neural tube patterning	1	>=0.20
GO:0007405	neuroblast proliferation	1	>=0.20

MP:0002229	neurodegeneration	0.76	>=0.20
GO:0060053	neurofilament cytoskeleton	0.68	>=0.20
GO:0031594	neuromuscular junction	0.97	>=0.20
GO:0050905	neuromuscular process	1	>=0.20
GO:0050885	neuromuscular process controlling balance	1	>=0.20
GO:0007274	neuromuscular synaptic transmission	1	>=0.20
GO:0007270	neuron-neuron synaptic transmission	1	>=0.20
GO:0051402	neuron apoptotic process	1	>=0.20
GO:0007158	neuron cell-cell adhesion	1	>=0.20
GO:0070997	neuron death	1	>=0.20
GO:0048663	neuron fate commitment	1	>=0.20
GO:0048665	neuron fate specification	1	>=0.20
GO:0001764	neuron migration	1	>=0.20
GO:0032589	neuron projection membrane	0.99	>=0.20
GO:0044306	neuron projection terminus	1	>=0.20
GO:0008038	neuron recognition	1	>=0.20
GO:0044309	neuron spine	1	>=0.20
GO:0043025	neuronal cell body	1	>=0.20
GO:0005184	neuropeptide hormone activity	1	>=0.20
GO:0008188	neuropeptide receptor activity	0.99	>=0.20
GO:0071855	neuropeptide receptor binding	1	>=0.20
GO:0007218	neuropeptide signaling pathway	1	>=0.20
GO:0042165	neurotransmitter binding	0.99	>=0.20
GO:0042136	neurotransmitter biosynthetic process	0.83	>=0.20
GO:0042133	neurotransmitter metabolic process	0.76	>=0.20
GO:0030594	neurotransmitter receptor activity	1	>=0.20
GO:0007269	neurotransmitter secretion	1	>=0.20
GO:0006836	neurotransmitter transport	1	>=0.20
GO:0001504	neurotransmitter uptake	1	>=0.20
GO:0005328	neurotransmitter:sodium symporter activity	0.29	>=0.20
GO:0015175	neutral amino acid transmembrane transporter activity	0.54	>=0.20
GO:0015804	neutral amino acid transport	0.91	>=0.20
GO:0042119	neutrophil activation	0.81	>=0.20
GO:0030593	neutrophil chemotaxis	0.63	>=0.20
ENSG00000162614	NEXN PPI subnetwork	0.53	>=0.20
ENSG00000196712	NF1 PPI subnetwork	0.79	>=0.20
ENSG00000163531	NFASC PPI subnetwork	0.96	>=0.20
ENSG00000101096	NFATC2 PPI subnetwork	0.82	>=0.20
ENSG00000100968	NFATC4 PPI subnetwork	0.92	>=0.20
ENSG00000082641	NFE2L1 PPI subnetwork	0.07	>=0.20
ENSG00000165030	NFIL3 PPI subnetwork	0.15	>=0.20
ENSG00000077150	NFKB2 PPI subnetwork	0.07	>=0.20
ENSG00000100906	NFKBIA PPI subnetwork	0.16	>=0.20
ENSG00000104825	NFKBIB PPI subnetwork	0.26	>=0.20
ENSG00000146232	NFKBIE PPI subnetwork	0.51	>=0.20
ENSG00000206440	NFKBIL1 PPI subnetwork	0.91	>=0.20
ENSG00000086102	NFX1 PPI subnetwork	0.09	>=0.20

ENSG00000120837	NFYB PPI subnetwork	0.72	>=0.20
ENSG00000066248	NGEF PPI subnetwork	1	>=0.20
ENSG00000134259	NGF PPI subnetwork	0.15	>=0.20
ENSG00000064300	NGFR PPI subnetwork	0.88	>=0.20
ENSG00000087303	NID2 PPI subnetwork	0.85	>=0.20
ENSG00000100503	NIN PPI subnetwork	1	>=0.20
ENSG00000101004	NINL PPI subnetwork	0.73	>=0.20
ENSG00000132603	NIP7 PPI subnetwork	0.72	>=0.20
ENSG00000184117	NIPSNAP1 PPI subnetwork	1	>=0.20
GO:0006809	nitric oxide biosynthetic process	0.2	>=0.20
GO:0071705	nitrogen compound transport	0.62	>=0.20
ENSG00000186416	NKRF PPI subnetwork	0.37	>=0.20
ENSG00000183072	NKX2-5 PPI subnetwork	0.15	>=0.20
ENSG00000073536	NLE1 PPI subnetwork	0.49	>=0.20
ENSG00000169992	NLGN2 PPI subnetwork	0.99	>=0.20
ENSG00000091106	NLRC4 PPI subnetwork	0.95	>=0.20
GO:0006607	NLS-bearing substrate import into nucleus	0.95	>=0.20
ENSG00000169251	NMD3 PPI subnetwork	0.57	>=0.20
ENSG00000011052	NME2 PPI subnetwork	0.75	>=0.20
ENSG00000112992	NNT PPI subnetwork	0.11	>=0.20
MP:0001404	no spontaneous movement	0.95	>=0.20
ENSG00000188976	NOC2L PPI subnetwork	0.73	>=0.20
ENSG00000184967	NOC4L PPI subnetwork	0.94	>=0.20
ENSG00000106100	NOD1 PPI subnetwork	0.74	>=0.20
ENSG00000183691	NOG PPI subnetwork	0.75	>=0.20
ENSG00000198000	NOL8 PPI subnetwork	0.91	>=0.20
GO:0035567	non-canonical Wnt receptor signaling pathway	1	>=0.20
GO:0004715	non-membrane spanning protein tyrosine kinase activity	0.06	>=0.20
GO:0000726	non-recombinational repair	0.96	>=0.20
GO:0031513	nonmotile primary cilium	0.99	>=0.20
ENSG00000182117	NOP10 PPI subnetwork	0.94	>=0.20
ENSG00000111641	NOP2 PPI subnetwork	0.46	>=0.20
ENSG00000089250	NOS1 PPI subnetwork	0.47	>=0.20
ENSG00000007171	NOS2 PPI subnetwork	0.1	>=0.20
GO:0043584	nose development	1	>=0.20
GO:0005112	Notch binding	0.78	>=0.20
GO:0007220	Notch receptor processing	0.73	>=0.20
GO:0007219	Notch signaling pathway	0.98	>=0.20
ENSG00000148400	NOTCH1 PPI subnetwork	0.52	>=0.20
ENSG00000134250	NOTCH2 PPI subnetwork	0.56	>=0.20
ENSG00000074181	NOTCH3 PPI subnetwork	0.64	>=0.20
ENSG00000204301	NOTCH4 PPI subnetwork	0.57	>=0.20
GO:0030903	notochord development	1	>=0.20
ENSG00000136999	NOV PPI subnetwork	0.13	>=0.20
GO:0071564	npBAF complex	0.62	>=0.20
ENSG00000144061	NPHP1 PPI subnetwork	0.35	>=0.20
ENSG00000161270	NPHS1 PPI subnetwork	1	>=0.20

ENSG00000181163	NPM1 PPI subnetwork	0.05	>=0.20
ENSG00000122585	NPY PPI subnetwork	0.94	>=0.20
ENSG00000124588	NQO2 PPI subnetwork	0.38	>=0.20
ENSG00000123358	NR4A1 PPI subnetwork	0.25	>=0.20
ENSG00000153234	NR4A2 PPI subnetwork	0.56	>=0.20
ENSG00000136931	NR5A1 PPI subnetwork	0.52	>=0.20
ENSG00000091129	NRCAM PPI subnetwork	0.99	>=0.20
ENSG00000157168	NRG1 PPI subnetwork	0.97	>=0.20
ENSG00000099250	NRP1 PPI subnetwork	0.38	>=0.20
ENSG00000179915	NRXN1 PPI subnetwork	1	>=0.20
ENSG00000164346	NSA2 PPI subnetwork	0.68	>=0.20
ENSG00000073969	NSF PPI subnetwork	0.35	>=0.20
ENSG00000117697	NSL1 PPI subnetwork	0.77	>=0.20
ENSG00000169189	NSMCE1 PPI subnetwork	1	>=0.20
ENSG00000065057	NTHL1 PPI subnetwork	0.97	>=0.20
ENSG00000148053	NTRK2 PPI subnetwork	0.73	>=0.20
GO:0035267	NuA4 histone acetyltransferase complex	0.32	>=0.20
ENSG00000069275	NUCKS1 PPI subnetwork	0.41	>=0.20
GO:0000956	nuclear-transcribed mRNA catabolic process	0.88	>=0.20
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-	0.65	>=0.20
GO:0000291	nuclear-transcribed mRNA catabolic process, exonucleolytic	0.99	>=0.20
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	0.47	>=0.20
GO:0016604	nuclear body	0.5	>=0.20
MP:0010254	nuclear cataracts	0.95	>=0.20
GO:0000228	nuclear chromosome	0.16	>=0.20
GO:0044454	nuclear chromosome part	0.06	>=0.20
GO:0000784	nuclear chromosome, telomeric region	0.5	>=0.20
GO:0000280	nuclear division	0.8	>=0.20
GO:0055029	nuclear DNA-directed RNA polymerase complex	0.96	>=0.20
GO:0051168	nuclear export	0.14	>=0.20
GO:0005720	nuclear heterochromatin	0.03	>=0.20
GO:0005637	nuclear inner membrane	0.48	>=0.20
GO:0016363	nuclear matrix	0.39	>=0.20
GO:0000398	nuclear mRNA splicing, via spliceosome	0.53	>=0.20
GO:0034399	nuclear periphery	0.48	>=0.20
GO:0043596	nuclear replication fork	0.93	>=0.20
GO:0043601	nuclear replisome	0.99	>=0.20
GO:0016607	nuclear speck	0.48	>=0.20
GO:0000783	nuclear telomere cap complex	0.77	>=0.20
GO:0000152	nuclear ubiquitin ligase complex	0.45	>=0.20
GO:0050657	nucleic acid transport	0.51	>=0.20
GO:0034654	nucleobase-containing compound biosynthetic process	0.83	>=0.20
GO:0015949	nucleobase-containing small molecule interconversion	0.99	>=0.20
GO:0046112	nucleobase biosynthetic process	0.9	>=0.20
GO:0009112	nucleobase metabolic process	0.51	>=0.20
GO:0005487	nucleocytoplasmic transporter activity	0.87	>=0.20
GO:0005730	nucleolus	0.65	>=0.20

GO:0060589	nucleoside-triphosphatase regulator activity	0.36	>=0.20
GO:0009163	nucleoside biosynthetic process	0.54	>=0.20
GO:0009164	nucleoside catabolic process	0.81	>=0.20
GO:0009124	nucleoside monophosphate biosynthetic process	0.99	>=0.20
GO:0009123	nucleoside monophosphate metabolic process	0.99	>=0.20
GO:0043174	nucleoside salvage	0.42	>=0.20
GO:0009142	nucleoside triphosphate biosynthetic process	0.68	>=0.20
GO:0000786	nucleosome	0.3	>=0.20
GO:0006334	nucleosome assembly	0.99	>=0.20
GO:0006337	nucleosome disassembly	0.66	>=0.20
GO:0034728	nucleosome organization	0.92	>=0.20
GO:0035872	nucleotide-binding domain, leucine rich repeat containing re	0.66	>=0.20
GO:0070423	nucleotide-binding oligomerization domain containing signal	0.66	>=0.20
GO:0006289	nucleotide-excision repair	0.89	>=0.20
GO:0000718	nucleotide-excision repair, DNA damage removal	1	>=0.20
GO:0006297	nucleotide-excision repair, DNA gap filling	0.97	>=0.20
GO:0009225	nucleotide-sugar metabolic process	0.6	>=0.20
GO:0009165	nucleotide biosynthetic process	0.92	>=0.20
GO:0016502	nucleotide receptor activity	0.85	>=0.20
GO:0006997	nucleus organization	0.32	>=0.20
ENSG00000090273	NUDC PPI subnetwork	0.99	>=0.20
ENSG00000167005	NUDT21 PPI subnetwork	0.22	>=0.20
ENSG00000173598	NUDT4 PPI subnetwork	0.64	>=0.20
ENSG00000143228	NUF2 PPI subnetwork	0.77	>=0.20
ENSG00000108256	NUFIP2 PPI subnetwork	0.07	>=0.20
ENSG00000137497	NUMA1 PPI subnetwork	0.24	>=0.20
ENSG00000133961	NUMB PPI subnetwork	0.12	>=0.20
ENSG00000105245	NUMBL PPI subnetwork	0.76	>=0.20
ENSG00000111581	NUP107 PPI subnetwork	0.77	>=0.20
ENSG00000069248	NUP133 PPI subnetwork	0.53	>=0.20
ENSG00000030066	NUP160 PPI subnetwork	0.8	>=0.20
ENSG00000095319	NUP188 PPI subnetwork	0.64	>=0.20
ENSG00000155561	NUP205 PPI subnetwork	0.52	>=0.20
ENSG00000126883	NUP214 PPI subnetwork	0.49	>=0.20
ENSG00000075188	NUP37 PPI subnetwork	0.72	>=0.20
ENSG00000120253	NUP43 PPI subnetwork	0.71	>=0.20
ENSG00000093000	NUP50 PPI subnetwork	0.28	>=0.20
ENSG00000125450	NUP85 PPI subnetwork	0.6	>=0.20
ENSG00000110713	NUP98 PPI subnetwork	0.53	>=0.20
GO:0016581	NuRD complex	0.78	>=0.20
ENSG00000102898	NUTF2 PPI subnetwork	0.07	>=0.20
ENSG00000143748	NVL PPI subnetwork	0.7	>=0.20
ENSG00000162231	NXF1 PPI subnetwork	0.32	>=0.20
MP:0001261	obese	0.23	>=0.20
GO:0070160	occluding junction	0.89	>=0.20
ENSG00000197822	OCLN PPI subnetwork	0.45	>=0.20
ENSG00000122126	OCRL PPI subnetwork	0.05	>=0.20

GO:0042476	odontogenesis	1	>=0.20
GO:0042475	odontogenesis of dentin-containing tooth	1	>=0.20
ENSG00000105953	OGDH PPI subnetwork	0.89	>=0.20
ENSG00000087263	OGFOD1 PPI subnetwork	0.82	>=0.20
ENSG00000114026	OGG1 PPI subnetwork	0.92	>=0.20
ENSG00000147162	OGT PPI subnetwork	0.06	>=0.20
GO:0021772	olfactory bulb development	1	>=0.20
GO:0021889	olfactory bulb interneuron differentiation	1	>=0.20
GO:0021988	olfactory lobe development	1	>=0.20
GO:0004984	olfactory receptor activity	0.98	>=0.20
MP:0000565	oligodactyly	0.88	>=0.20
GO:0014003	oligodendrocyte development	0.93	>=0.20
GO:0048709	oligodendrocyte differentiation	0.97	>=0.20
GO:0009312	oligosaccharide biosynthetic process	0.98	>=0.20
GO:0009311	oligosaccharide metabolic process	0.92	>=0.20
GO:0004576	oligosaccharyl transferase activity	0.92	>=0.20
GO:0008250	oligosaccharyltransferase complex	0.95	>=0.20
MP:0002687	oligozoospermia	0.48	>=0.20
MP:0003052	omphalocele	0.93	>=0.20
ENSG00000198836	OPA1 PPI subnetwork	0.36	>=0.20
MP:0000929	open neural tube	0.81	>=0.20
ENSG00000116329	OPRD1 PPI subnetwork	0.48	>=0.20
ENSG00000085840	ORC1 PPI subnetwork	0.91	>=0.20
ENSG00000115942	ORC2 PPI subnetwork	0.97	>=0.20
ENSG00000135336	ORC3 PPI subnetwork	0.96	>=0.20
ENSG00000115947	ORC4 PPI subnetwork	0.97	>=0.20
ENSG00000164815	ORC5 PPI subnetwork	0.91	>=0.20
ENSG00000091651	ORC6 PPI subnetwork	0.98	>=0.20
GO:0048645	organ formation	0.99	>=0.20
GO:0035265	organ growth	0.97	>=0.20
GO:0001759	organ induction	1	>=0.20
MP:0000043	organ of Corti degeneration	0.45	>=0.20
GO:0000315	organellar large ribosomal subunit	0.07	>=0.20
GO:0000313	organellar ribosome	0.72	>=0.20
GO:0000314	organellar small ribosomal subunit	0.9	>=0.20
GO:0070925	organelle assembly	0.95	>=0.20
GO:0031970	organelle envelope lumen	0.27	>=0.20
GO:0048285	organelle fission	0.77	>=0.20
GO:0048284	organelle fusion	0.33	>=0.20
GO:0019866	organelle inner membrane	0.14	>=0.20
GO:0051640	organelle localization	0.52	>=0.20
GO:0031984	organelle subcompartment	0.18	>=0.20
GO:0072384	organelle transport along microtubule	0.99	>=0.20
GO:0005342	organic acid transmembrane transporter activity	0.24	>=0.20
GO:0005343	organic acid:sodium symporter activity	0.73	>=0.20
GO:0015850	organic alcohol transport	0.69	>=0.20
GO:0008514	organic anion transmembrane transporter activity	0.37	>=0.20

GO:0015711	organic anion transport	0.98	>=0.20
GO:0015101	organic cation transmembrane transporter activity	0.14	>=0.20
GO:0015695	organic cation transport	0.38	>=0.20
ENSG00000141447	OSBPL1A PPI subnetwork	0.37	>=0.20
ENSG00000099985	OSM PPI subnetwork	0.06	>=0.20
ENSG00000145623	OSMR PPI subnetwork	0.33	>=0.20
ENSG00000143867	OSR1 PPI subnetwork	0.37	>=0.20
GO:0001503	ossification	0.65	>=0.20
MP:0003560	osteoarthritis	0.6	>=0.20
GO:0001649	osteoblast differentiation	0.72	>=0.20
MP:0000067	osteopetrosis	0.03	>=0.20
MP:0010404	ostium primum atrial septal defect	0.99	>=0.20
MP:0002168	other aberrant phenotype	0.5	>=0.20
GO:0030288	outer membrane-bounded periplasmic space	1	>=0.20
GO:0003151	outflow tract morphogenesis	0.87	>=0.20
MP:0002016	ovary cysts	0.82	>=0.20
MP:0001183	overexpanded pulmonary alveoli	0.25	>=0.20
GO:0042698	ovulation cycle	0.8	>=0.20
GO:0022602	ovulation cycle process	0.72	>=0.20
GO:0061039	ovum-producing ovary development	0.58	>=0.20
GO:0006107	oxaloacetate metabolic process	0.07	>=0.20
GO:0006119	oxidative phosphorylation	1	>=0.20
GO:0016675	oxidoreductase activity, acting on a heme group of donors	0.84	>=0.20
GO:0016676	oxidoreductase activity, acting on a heme group of donors, o	0.99	>=0.20
GO:0016667	oxidoreductase activity, acting on a sulfur group of donors	0.1	>=0.20
GO:0016651	oxidoreductase activity, acting on NADH or NADPH	0.77	>=0.20
GO:0050664	oxidoreductase activity, acting on NADH or NADPH, oxygen a	0.49	>=0.20
GO:0016655	oxidoreductase activity, acting on NADH or NADPH, quinone	0.98	>=0.20
GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	0.07	>=0.20
GO:0016624	oxidoreductase activity, acting on the aldehyde or oxo group	0.62	>=0.20
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group	0.13	>=0.20
GO:0016646	oxidoreductase activity, acting on the CH-NH group of donors	0.62	>=0.20
GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transpor	0.26	>=0.20
GO:0015405	P-P-bond-hydrolysis-driven transmembrane transporter activ	0.16	>=0.20
GO:0043186	P granule	0.95	>=0.20
ENSG00000122884	P4HA1 PPI subnetwork	0.07	>=0.20
ENSG00000072682	P4HA2 PPI subnetwork	0.11	>=0.20
GO:0002039	p53 binding	0.72	>=0.20
ENSG00000070756	PABPC1 PPI subnetwork	0.08	>=0.20
ENSG00000151846	PABPC3 PPI subnetwork	0.75	>=0.20
ENSG00000205022	PABPN1L PPI subnetwork	0.82	>=0.20
ENSG00000175115	PACS1 PPI subnetwork	0.98	>=0.20
ENSG00000179364	PACS2 PPI subnetwork	0.49	>=0.20
ENSG00000124507	PACSIN1 PPI subnetwork	0.78	>=0.20
ENSG00000165912	PACSIN3 PPI subnetwork	0.14	>=0.20
ENSG00000006712	PAF1 PPI subnetwork	0.41	>=0.20
ENSG00000007168	PAFAH1B1 PPI subnetwork	0.76	>=0.20

ENSG00000079462	PAFAH1B3 PPI subnetwork	0.76	>=0.20
ENSG00000076641	PAG1 PPI subnetwork	0.04	>=0.20
ENSG00000128050	PAICS PPI subnetwork	1	>=0.20
ENSG00000149269	PAK1 PPI subnetwork	0.05	>=0.20
ENSG00000180370	PAK2 PPI subnetwork	0.07	>=0.20
ENSG00000130669	PAK4 PPI subnetwork	0.17	>=0.20
MP:0009888	palatal shelves fail to meet at midline	1	>=0.20
GO:0060021	palate development	0.99	>=0.20
GO:0021543	pallium development	0.96	>=0.20
GO:0016409	palmitoyltransferase activity	0.89	>=0.20
GO:0031016	pancreas development	0.71	>=0.20
ENSG00000154143	PANX3 PPI subnetwork	0.39	>=0.20
ENSG00000164329	PAPD4 PPI subnetwork	0.22	>=0.20
ENSG00000100767	PAPLN PPI subnetwork	0.55	>=0.20
ENSG00000090060	PAPOLA PPI subnetwork	0.04	>=0.20
MP:0003427	parakeratosis	0.14	>=0.20
MP:0000753	paralysis	0.93	>=0.20
MP:0009434	paraparesis	0.85	>=0.20
GO:0048486	parasympathetic nervous system development	0.98	>=0.20
ENSG00000148498	PARD3 PPI subnetwork	0.18	>=0.20
ENSG00000102981	PARD6A PPI subnetwork	0.94	>=0.20
ENSG00000178184	PARD6G PPI subnetwork	0.48	>=0.20
ENSG00000185345	PARK2 PPI subnetwork	0.59	>=0.20
ENSG00000116288	PARK7 PPI subnetwork	0.58	>=0.20
ENSG00000140694	PARN PPI subnetwork	0.97	>=0.20
ENSG00000143799	PARP1 PPI subnetwork	0.48	>=0.20
ENSG00000059378	PARP12 PPI subnetwork	0.12	>=0.20
MP:0011104	partial embryonic lethality before implantation	0.54	>=0.20
MP:0011088	partial neonatal lethality	0.03	>=0.20
MP:0011090	partial perinatal lethality	0.11	>=0.20
MP:0011110	partial preweaning lethality	0.91	>=0.20
GO:0022803	passive transmembrane transporter activity	1	>=0.20
MP:0003139	patent ductus arteriosus	0.16	>=0.20
MP:0003123	paternal imprinting	0.13	>=0.20
GO:0060389	pathway-restricted SMAD protein phosphorylation	0.81	>=0.20
ENSG00000166889	PATL1 PPI subnetwork	0.51	>=0.20
GO:0002221	pattern recognition receptor signaling pathway	0.2	>=0.20
GO:0007389	pattern specification process	1	>=0.20
GO:0001569	patterning of blood vessels	0.4	>=0.20
ENSG00000135903	PAX3 PPI subnetwork	0.39	>=0.20
ENSG00000196092	PAX5 PPI subnetwork	0.04	>=0.20
ENSG00000168078	PBK PPI subnetwork	0.91	>=0.20
ENSG00000163939	PBRM1 PPI subnetwork	0.86	>=0.20
ENSG00000185630	PBX1 PPI subnetwork	0.93	>=0.20
ENSG00000163346	PBXIP1 PPI subnetwork	0.05	>=0.20
ENSG00000169564	PCBP1 PPI subnetwork	0.03	>=0.20
ENSG00000113555	PCDH12 PPI subnetwork	0.3	>=0.20

ENSG00000184226	PCDH9 PPI subnetwork	0.34	>=0.20
ENSG00000165494	PCF11 PPI subnetwork	0.05	>=0.20
GO:0031519	PcG protein complex	0.39	>=0.20
ENSG00000115289	PCGF1 PPI subnetwork	0.48	>=0.20
ENSG00000056661	PCGF2 PPI subnetwork	0.61	>=0.20
ENSG00000185619	PCGF3 PPI subnetwork	0.4	>=0.20
ENSG00000180628	PCGF5 PPI subnetwork	0.45	>=0.20
ENSG00000156374	PCGF6 PPI subnetwork	0.24	>=0.20
ENSG00000126226	PCID2 PPI subnetwork	0.35	>=0.20
ENSG00000120265	PCMT1 PPI subnetwork	0.9	>=0.20
ENSG00000102109	PCSK1N PPI subnetwork	1	>=0.20
ENSG00000114209	PDCD10 PPI subnetwork	0.65	>=0.20
ENSG00000170248	PDCD6IP PPI subnetwork	0.99	>=0.20
ENSG00000090470	PDCD7 PPI subnetwork	0.95	>=0.20
ENSG00000163440	PDCL2 PPI subnetwork	0.13	>=0.20
ENSG00000115252	PDE1A PPI subnetwork	0.99	>=0.20
ENSG00000123360	PDE1B PPI subnetwork	1	>=0.20
ENSG00000172572	PDE3A PPI subnetwork	0.14	>=0.20
ENSG00000152270	PDE3B PPI subnetwork	0.07	>=0.20
ENSG00000065989	PDE4A PPI subnetwork	0.11	>=0.20
ENSG00000156973	PDE6D PPI subnetwork	0.75	>=0.20
ENSG00000134853	PDGFRA PPI subnetwork	0.2	>=0.20
ENSG00000131828	PDHA1 PPI subnetwork	0.06	>=0.20
ENSG00000168291	PDHB PPI subnetwork	0.12	>=0.20
ENSG00000065485	PDIA5 PPI subnetwork	0.39	>=0.20
ENSG00000143870	PDIA6 PPI subnetwork	0.75	>=0.20
ENSG00000152256	PDK1 PPI subnetwork	0.35	>=0.20
ENSG00000088356	PDRG1 PPI subnetwork	0.73	>=0.20
ENSG00000121892	PDS5A PPI subnetwork	0.67	>=0.20
ENSG00000083642	PDS5B PPI subnetwork	0.98	>=0.20
ENSG00000164494	PDSS2 PPI subnetwork	1	>=0.20
ENSG00000139515	PDX1 PPI subnetwork	0.19	>=0.20
GO:0030165	PDZ domain binding	0.95	>=0.20
ENSG00000120509	PDZD11 PPI subnetwork	0.28	>=0.20
ENSG00000174827	PDZK1 PPI subnetwork	0.59	>=0.20
ENSG00000152684	PELO PPI subnetwork	0.43	>=0.20
GO:0006098	pentose-phosphate shunt	0.81	>=0.20
GO:0019321	pentose metabolic process	0.5	>=0.20
ENSG00000124299	PEPD PPI subnetwork	0.87	>=0.20
GO:0042605	peptide antigen binding	0.19	>=0.20
GO:0018149	peptide cross-linking	0.91	>=0.20
GO:0016486	peptide hormone processing	1	>=0.20
GO:0051428	peptide hormone receptor binding	0.06	>=0.20
GO:0030072	peptide hormone secretion	0.46	>=0.20
GO:0006518	peptide metabolic process	0.44	>=0.20
GO:0001653	peptide receptor activity	0.42	>=0.20
GO:0002790	peptide secretion	0.41	>=0.20

GO:0015833	peptide transport	0.34	>=0.20
GO:0018195	peptidyl-arginine modification	0.98	>=0.20
GO:0018196	peptidyl-asparagine modification	0.81	>=0.20
GO:0018394	peptidyl-lysine acetylation	0.59	>=0.20
GO:0018205	peptidyl-lysine modification	0.4	>=0.20
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	0.07	>=0.20
GO:0018209	peptidyl-serine modification	0.34	>=0.20
GO:0018105	peptidyl-serine phosphorylation	0.09	>=0.20
GO:0018212	peptidyl-tyrosine modification	0.05	>=0.20
GO:0018108	peptidyl-tyrosine phosphorylation	0.07	>=0.20
MP:0005312	pericardial effusion	0.08	>=0.20
GO:0000242	pericentriolar material	0.18	>=0.20
GO:0043204	perikaryon	0.37	>=0.20
MP:0010418	perimembraneous ventricular septal defect	0.67	>=0.20
GO:0048471	perinuclear region of cytoplasm	0.05	>=0.20
GO:0007422	peripheral nervous system development	0.97	>=0.20
GO:0048935	peripheral nervous system neuron development	1	>=0.20
GO:0048934	peripheral nervous system neuron differentiation	1	>=0.20
GO:0042597	periplasmic space	1	>=0.20
GO:0004601	peroxidase activity	0.07	>=0.20
GO:0007031	peroxisome organization	0.62	>=0.20
MP:0002633	persistent truncus arteriosis	0.06	>=0.20
ENSG00000100029	PES1 PPI subnetwork	0.62	>=0.20
ENSG00000162928	PEX13 PPI subnetwork	0.35	>=0.20
ENSG00000142655	PEX14 PPI subnetwork	0.21	>=0.20
ENSG00000162735	PEX19 PPI subnetwork	0.48	>=0.20
ENSG00000139197	PEX5 PPI subnetwork	0.23	>=0.20
ENSG00000163737	PF4 PPI subnetwork	0.05	>=0.20
ENSG00000143256	PFDN2 PPI subnetwork	0.82	>=0.20
ENSG00000101132	PFDN4 PPI subnetwork	0.65	>=0.20
ENSG00000123349	PFDN5 PPI subnetwork	0.94	>=0.20
ENSG00000204220	PFDN6 PPI subnetwork	0.83	>=0.20
ENSG00000206283	PFDN6 PPI subnetwork	0.83	>=0.20
ENSG00000141959	PFKL PPI subnetwork	0.94	>=0.20
ENSG00000152556	PFKM PPI subnetwork	0.91	>=0.20
ENSG00000067057	PFKP PPI subnetwork	0.21	>=0.20
ENSG00000108518	PFN1 PPI subnetwork	0.11	>=0.20
ENSG00000171314	PGAM1 PPI subnetwork	0.84	>=0.20
ENSG00000164708	PGAM2 PPI subnetwork	0.71	>=0.20
ENSG00000102144	PGK1 PPI subnetwork	0.06	>=0.20
ENSG00000079739	PGM1 PPI subnetwork	0.11	>=0.20
ENSG00000082175	PGR PPI subnetwork	0.07	>=0.20
ENSG00000101856	PGRMC1 PPI subnetwork	0.66	>=0.20
GO:0045851	pH reduction	0.99	>=0.20
GO:0045335	phagocytic vesicle	0.15	>=0.20
GO:0030670	phagocytic vesicle membrane	0.1	>=0.20
GO:0006909	phagocytosis	0.12	>=0.20

ENSG00000167085	PHB PPI subnetwork	0.04	>=0.20
ENSG00000215021	PHB2 PPI subnetwork	0.34	>=0.20
ENSG00000111752	PHC1 PPI subnetwork	0.15	>=0.20
GO:0018958	phenol-containing compound metabolic process	0.98	>=0.20
ENSG00000130024	PHF10 PPI subnetwork	0.11	>=0.20
ENSG00000025293	PHF20 PPI subnetwork	0.25	>=0.20
ENSG00000135365	PHF21A PPI subnetwork	0.18	>=0.20
ENSG00000172943	PHF8 PPI subnetwork	0.19	>=0.20
ENSG00000067177	PHKA1 PPI subnetwork	0.09	>=0.20
ENSG00000102893	PHKB PPI subnetwork	0.97	>=0.20
ENSG00000164776	PHKG1 PPI subnetwork	0.27	>=0.20
ENSG00000174307	PHLDA3 PPI subnetwork	0.63	>=0.20
ENSG00000040199	PHLPP2 PPI subnetwork	0.4	>=0.20
GO:0016791	phosphatase activity	0.04	>=0.20
GO:0019212	phosphatase inhibitor activity	0.94	>=0.20
GO:0019208	phosphatase regulator activity	0.23	>=0.20
GO:0015114	phosphate ion transmembrane transporter activity	0.26	>=0.20
GO:0005547	phosphatidylinositol-3,4,5-trisphosphate binding	0.2	>=0.20
GO:0048015	phosphatidylinositol-mediated signaling	0.51	>=0.20
GO:0005942	phosphatidylinositol 3-kinase complex	0.59	>=0.20
GO:0035091	phosphatidylinositol binding	0.03	>=0.20
GO:0006661	phosphatidylinositol biosynthetic process	0.99	>=0.20
GO:0046488	phosphatidylinositol metabolic process	0.99	>=0.20
GO:0004435	phosphatidylinositol phospholipase C activity	0.97	>=0.20
GO:0007200	phospholipase C-activating G-protein coupled receptor signa	0.71	>=0.20
GO:0004629	phospholipase C activity	0.97	>=0.20
GO:0004859	phospholipase inhibitor activity	0.69	>=0.20
GO:0004012	phospholipid-translocating ATPase activity	0.99	>=0.20
GO:0005548	phospholipid transporter activity	0.95	>=0.20
GO:0004721	phosphoprotein phosphatase activity	0.46	>=0.20
GO:0008081	phosphoric diester hydrolase activity	0.66	>=0.20
GO:0042578	phosphoric ester hydrolase activity	0.09	>=0.20
GO:0016849	phosphorus-oxygen lyase activity	0.75	>=0.20
GO:0016780	phosphotransferase activity, for other substituted phosphate	0.52	>=0.20
GO:0016775	phosphotransferase activity, nitrogenous group as acceptor	0.04	>=0.20
GO:0016776	phosphotransferase activity, phosphate group as acceptor	1	>=0.20
GO:0009881	photoreceptor activity	0.93	>=0.20
GO:0042461	photoreceptor cell development	1	>=0.20
GO:0046530	photoreceptor cell differentiation	1	>=0.20
GO:0045494	photoreceptor cell maintenance	1	>=0.20
GO:0032391	photoreceptor connecting cilium	0.96	>=0.20
GO:0001917	photoreceptor inner segment	0.96	>=0.20
GO:0001750	photoreceptor outer segment	0.98	>=0.20
MP:0008584	photoreceptor outer segment degeneration	0.29	>=0.20
GO:0007602	phototransduction	1	>=0.20
GO:0007603	phototransduction, visible light	1	>=0.20
ENSG00000143393	PI4KB PPI subnetwork	0.11	>=0.20

ENSG00000033800	PIAS1 PPI subnetwork	0.46	>=0.20
ENSG00000078043	PIAS2 PPI subnetwork	0.79	>=0.20
ENSG00000131788	PIAS3 PPI subnetwork	0.55	>=0.20
ENSG00000105229	PIAS4 PPI subnetwork	0.62	>=0.20
ENSG00000100151	PICK1 PPI subnetwork	1	>=0.20
ENSG00000135845	PIGC PPI subnetwork	0.08	>=0.20
ENSG00000174227	PIGG PPI subnetwork	0.74	>=0.20
GO:0046148	pigment biosynthetic process	0.93	>=0.20
GO:0050931	pigment cell differentiation	1	>=0.20
GO:0051875	pigment granule localization	0.99	>=0.20
GO:0051904	pigment granule transport	1	>=0.20
GO:0043473	pigmentation	0.99	>=0.20
ENSG00000087111	PIGS PPI subnetwork	0.19	>=0.20
ENSG00000184886	PIGW PPI subnetwork	0.85	>=0.20
ENSG00000011405	PIK3C2A PPI subnetwork	0.12	>=0.20
ENSG00000133056	PIK3C2B PPI subnetwork	0.11	>=0.20
ENSG00000139144	PIK3C2G PPI subnetwork	0.38	>=0.20
ENSG00000078142	PIK3C3 PPI subnetwork	0.38	>=0.20
ENSG00000121879	PIK3CA PPI subnetwork	0.03	>=0.20
ENSG00000171608	PIK3CD PPI subnetwork	0.04	>=0.20
ENSG00000105647	PIK3R2 PPI subnetwork	0.03	>=0.20
ENSG00000117461	PIK3R3 PPI subnetwork	0.03	>=0.20
ENSG00000102096	PIM2 PPI subnetwork	0.64	>=0.20
ENSG00000150867	PIP4K2A PPI subnetwork	0.26	>=0.20
ENSG00000166908	PIP4K2C PPI subnetwork	0.11	>=0.20
ENSG00000143398	PIP5K1A PPI subnetwork	0.63	>=0.20
ENSG00000107242	PIP5K1B PPI subnetwork	0.09	>=0.20
ENSG00000186111	PIP5K1C PPI subnetwork	0.03	>=0.20
GO:0021983	pituitary gland development	1	>=0.20
ENSG00000181191	PJA1 PPI subnetwork	0.97	>=0.20
ENSG00000198961	PJA2 PPI subnetwork	0.73	>=0.20
ENSG00000008710	PKD1 PPI subnetwork	0.3	>=0.20
ENSG00000127564	PKMYT1 PPI subnetwork	0.66	>=0.20
ENSG00000160447	PKN3 PPI subnetwork	0.25	>=0.20
ENSG00000160199	PKNOX1 PPI subnetwork	0.76	>=0.20
ENSG00000184363	PKP3 PPI subnetwork	0.06	>=0.20
ENSG00000144283	PKP4 PPI subnetwork	0.89	>=0.20
ENSG00000138308	PLA2G12B PPI subnetwork	1	>=0.20
ENSG00000116711	PLA2G4A PPI subnetwork	0.04	>=0.20
ENSG00000137055	PLAA PPI subnetwork	0.95	>=0.20
ENSG00000118495	PLAGL1 PPI subnetwork	0.24	>=0.20
GO:0090179	planar cell polarity pathway involved in neural tube closure	0.99	>=0.20
GO:0048407	platelet-derived growth factor binding	0.9	>=0.20
GO:0005161	platelet-derived growth factor receptor binding	0.07	>=0.20
GO:0048008	platelet-derived growth factor receptor signaling pathway	0.21	>=0.20
GO:0030168	platelet activation	0.03	>=0.20
ENSG00000011422	PLAUR PPI subnetwork	0.05	>=0.20

ENSG00000182621	PLCB1 PPI subnetwork	0.83	>=0.20
ENSG00000137841	PLCB2 PPI subnetwork	0.57	>=0.20
ENSG00000149782	PLCB3 PPI subnetwork	0.97	>=0.20
ENSG00000101333	PLCB4 PPI subnetwork	0.99	>=0.20
ENSG00000124181	PLCG1 PPI subnetwork	0.08	>=0.20
ENSG00000075651	PLD1 PPI subnetwork	0.18	>=0.20
ENSG00000129219	PLD2 PPI subnetwork	0.04	>=0.20
ENSG00000104164	PLDN PPI subnetwork	0.81	>=0.20
ENSG00000178209	PLEC PPI subnetwork	0.35	>=0.20
ENSG00000116095	PLEKHA3 PPI subnetwork	0.54	>=0.20
ENSG00000143850	PLEKHA6 PPI subnetwork	0.08	>=0.20
ENSG00000175895	PLEKHF2 PPI subnetwork	0.4	>=0.20
ENSG00000166851	PLK1 PPI subnetwork	0.55	>=0.20
ENSG00000198523	PLN PPI subnetwork	0.45	>=0.20
ENSG00000106397	PLOD3 PPI subnetwork	0.05	>=0.20
ENSG00000114698	PLSCR4 PPI subnetwork	0.57	>=0.20
ENSG00000114554	PLXNA1 PPI subnetwork	1	>=0.20
ENSG00000164050	PLXNB1 PPI subnetwork	0.3	>=0.20
ENSG00000183395	PMCH PPI subnetwork	0.32	>=0.20
ENSG00000160783	PMF1 PPI subnetwork	0.74	>=0.20
GO:0016605	PML body	0.72	>=0.20
ENSG00000140650	PMM2 PPI subnetwork	0.04	>=0.20
ENSG00000122512	PMS2 PPI subnetwork	0.65	>=0.20
ENSG00000132424	PNISR PPI subnetwork	0.03	>=0.20
ENSG00000039650	PNKP PPI subnetwork	0.58	>=0.20
ENSG00000115946	PNO1 PPI subnetwork	0.9	>=0.20
MP:0008140	podocyte foot process effacement	0.33	>=0.20
ENSG00000101868	POLA1 PPI subnetwork	0.9	>=0.20
ENSG00000014138	POLA2 PPI subnetwork	0.63	>=0.20
ENSG00000070501	POLB PPI subnetwork	0.95	>=0.20
ENSG00000062822	POLD1 PPI subnetwork	0.94	>=0.20
ENSG00000106628	POLD2 PPI subnetwork	0.65	>=0.20
ENSG00000077514	POLD3 PPI subnetwork	0.93	>=0.20
ENSG00000175482	POLD4 PPI subnetwork	0.97	>=0.20
ENSG00000100227	POLDIP3 PPI subnetwork	0.03	>=0.20
GO:0045495	pole plasm	0.95	>=0.20
ENSG00000177084	POLE PPI subnetwork	0.87	>=0.20
ENSG00000100479	POLE2 PPI subnetwork	0.97	>=0.20
ENSG00000148229	POLE3 PPI subnetwork	0.94	>=0.20
ENSG00000170734	POLH PPI subnetwork	0.98	>=0.20
ENSG00000068654	POLR1A PPI subnetwork	0.94	>=0.20
ENSG00000125630	POLR1B PPI subnetwork	0.6	>=0.20
ENSG00000171453	POLR1C PPI subnetwork	1	>=0.20
ENSG00000186184	POLR1D PPI subnetwork	0.93	>=0.20
ENSG00000137054	POLR1E PPI subnetwork	0.95	>=0.20
ENSG00000181222	POLR2A PPI subnetwork	0.1	>=0.20
ENSG00000168255	POLR2J3 PPI subnetwork	0.74	>=0.20

ENSG00000148606	POLR3A PPI subnetwork	0.99	>=0.20
ENSG00000013503	POLR3B PPI subnetwork	0.98	>=0.20
ENSG00000186141	POLR3C PPI subnetwork	1	>=0.20
ENSG00000168495	POLR3D PPI subnetwork	0.99	>=0.20
ENSG00000058600	POLR3E PPI subnetwork	0.81	>=0.20
ENSG00000132664	POLR3F PPI subnetwork	0.98	>=0.20
ENSG00000113356	POLR3G PPI subnetwork	1	>=0.20
ENSG00000100413	POLR3H PPI subnetwork	0.99	>=0.20
ENSG00000161980	POLR3K PPI subnetwork	0.98	>=0.20
GO:0070717	poly-purine tract binding	1	>=0.20
MP:0008528	polycystic kidney	0.83	>=0.20
MP:0000562	polydactyly	0.97	>=0.20
MP:0001426	polydipsia	0.34	>=0.20
GO:0004653	polypeptide N-acetylgalactosaminyltransferase activity	1	>=0.20
MP:0001433	polyphagia	0.38	>=0.20
MP:0004025	polyploidy	0.33	>=0.20
GO:0031593	polyubiquitin binding	0.69	>=0.20
MP:0001762	polyuria	0.07	>=0.20
ENSG00000135213	POM121C PPI subnetwork	0.4	>=0.20
ENSG00000132963	POMP PPI subnetwork	0.81	>=0.20
ENSG00000009830	POMT2 PPI subnetwork	0.9	>=0.20
ENSG00000102312	PORCN PPI subnetwork	1	>=0.20
GO:0006779	porphyrin-containing compound biosynthetic process	0.75	>=0.20
GO:0030838	positive regulation of actin filament polymerization	0.79	>=0.20
GO:0042104	positive regulation of activated T cell proliferation	0.64	>=0.20
GO:0002675	positive regulation of acute inflammatory response	0.88	>=0.20
GO:0002821	positive regulation of adaptive immune response	0.98	>=0.20
GO:0002824	positive regulation of adaptive immune response based on s	0.98	>=0.20
GO:0045762	positive regulation of adenylate cyclase activity	0.99	>=0.20
GO:0010579	positive regulation of adenylate cyclase activity involved in G	0.96	>=0.20
GO:0046635	positive regulation of alpha-beta T cell activation	0.91	>=0.20
GO:0046641	positive regulation of alpha-beta T cell proliferation	0.99	>=0.20
GO:0045766	positive regulation of angiogenesis	0.17	>=0.20
GO:0002579	positive regulation of antigen processing and presentation	0.91	>=0.20
GO:0045773	positive regulation of axon extension	0.99	>=0.20
GO:0050871	positive regulation of B cell activation	0.85	>=0.20
GO:0030890	positive regulation of B cell proliferation	0.94	>=0.20
GO:0048520	positive regulation of behavior	0.58	>=0.20
GO:0070169	positive regulation of biomineral tissue development	1	>=0.20
GO:0045777	positive regulation of blood pressure	0.76	>=0.20
GO:0030513	positive regulation of BMP signaling pathway	0.95	>=0.20
GO:0030501	positive regulation of bone mineralization	1	>=0.20
GO:0051928	positive regulation of calcium ion transport	0.83	>=0.20
GO:0030819	positive regulation of cAMP biosynthetic process	0.97	>=0.20
GO:0030816	positive regulation of cAMP metabolic process	0.97	>=0.20
GO:0090263	positive regulation of canonical Wnt receptor signaling pathv	1	>=0.20
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activatic	0.67	>=0.20

GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differen	0.67	>=0.20
GO:0050867	positive regulation of cell activation	0.42	>=0.20
GO:0045785	positive regulation of cell adhesion	0.85	>=0.20
GO:0045787	positive regulation of cell cycle	0.66	>=0.20
GO:0071158	positive regulation of cell cycle arrest	0.79	>=0.20
GO:0090068	positive regulation of cell cycle process	0.81	>=0.20
GO:0010720	positive regulation of cell development	1	>=0.20
GO:0045597	positive regulation of cell differentiation	0.72	>=0.20
GO:0031343	positive regulation of cell killing	1	>=0.20
GO:0030335	positive regulation of cell migration	0.13	>=0.20
GO:0010770	positive regulation of cell morphogenesis involved in differer	1	>=0.20
GO:2000147	positive regulation of cell motility	0.1	>=0.20
GO:0031346	positive regulation of cell projection organization	1	>=0.20
GO:0051272	positive regulation of cellular component movement	0.04	>=0.20
GO:0051130	positive regulation of cellular component organization	0.56	>=0.20
GO:0032270	positive regulation of cellular protein metabolic process	0.07	>=0.20
GO:0032722	positive regulation of chemokine production	0.6	>=0.20
GO:0050921	positive regulation of chemotaxis	0.37	>=0.20
GO:2001252	positive regulation of chromosome organization	0.77	>=0.20
GO:0031281	positive regulation of cyclase activity	0.99	>=0.20
GO:0030804	positive regulation of cyclic nucleotide biosynthetic process	0.91	>=0.20
GO:0030801	positive regulation of cyclic nucleotide metabolic process	0.92	>=0.20
GO:0045737	positive regulation of cyclin-dependent protein kinase activit	0.99	>=0.20
GO:0042108	positive regulation of cytokine biosynthetic process	0.62	>=0.20
GO:0001819	positive regulation of cytokine production	0.28	>=0.20
GO:0050715	positive regulation of cytokine secretion	0.99	>=0.20
GO:0032467	positive regulation of cytokinesis	0.97	>=0.20
GO:0051495	positive regulation of cytoskeleton organization	0.66	>=0.20
GO:0031349	positive regulation of defense response	0.04	>=0.20
GO:0002230	positive regulation of defense response to virus by host	0.99	>=0.20
GO:0051054	positive regulation of DNA metabolic process	0.93	>=0.20
GO:0045807	positive regulation of endocytosis	0.28	>=0.20
GO:0010595	positive regulation of endothelial cell migration	0.4	>=0.20
GO:0001938	positive regulation of endothelial cell proliferation	0.34	>=0.20
GO:0050679	positive regulation of epithelial cell proliferation	0.77	>=0.20
GO:0010718	positive regulation of epithelial to mesenchymal transition	1	>=0.20
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.9	>=0.20
GO:0045921	positive regulation of exocytosis	0.98	>=0.20
GO:0045745	positive regulation of G-protein coupled receptor protein sig	0.97	>=0.20
GO:0045815	positive regulation of gene expression, epigenetic	0.99	>=0.20
GO:0045687	positive regulation of glial cell differentiation	0.96	>=0.20
GO:0043547	positive regulation of GTPase activity	0.88	>=0.20
GO:0045823	positive regulation of heart contraction	0.98	>=0.20
GO:0031058	positive regulation of histone modification	0.74	>=0.20
GO:0046887	positive regulation of hormone secretion	0.8	>=0.20
GO:0002922	positive regulation of humoral immune response	0.73	>=0.20
GO:0051345	positive regulation of hydrolase activity	0.17	>=0.20

GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	0.48	>=0.20
GO:0002699	positive regulation of immune effector process	0.78	>=0.20
GO:0050778	positive regulation of immune response	0.09	>=0.20
GO:0050729	positive regulation of inflammatory response	0.21	>=0.20
GO:0045089	positive regulation of innate immune response	0.17	>=0.20
GO:0043568	positive regulation of insulin-like growth factor receptor sign	0.98	>=0.20
GO:0032024	positive regulation of insulin secretion	0.51	>=0.20
GO:0032728	positive regulation of interferon-beta production	0.98	>=0.20
GO:0032729	positive regulation of interferon-gamma production	0.95	>=0.20
GO:0032733	positive regulation of interleukin-10 production	0.99	>=0.20
GO:0032735	positive regulation of interleukin-12 production	0.99	>=0.20
GO:0045086	positive regulation of interleukin-2 biosynthetic process	0.77	>=0.20
GO:0032755	positive regulation of interleukin-6 production	0.33	>=0.20
GO:0010740	positive regulation of intracellular protein kinase cascade	0.51	>=0.20
GO:0043270	positive regulation of ion transport	0.86	>=0.20
GO:0046427	positive regulation of JAK-STAT cascade	0.93	>=0.20
GO:0033674	positive regulation of kinase activity	0.17	>=0.20
GO:0002696	positive regulation of leukocyte activation	0.6	>=0.20
GO:0002690	positive regulation of leukocyte chemotaxis	0.2	>=0.20
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	1	>=0.20
GO:0002705	positive regulation of leukocyte mediated immunity	0.94	>=0.20
GO:0002687	positive regulation of leukocyte migration	0.27	>=0.20
GO:0070665	positive regulation of leukocyte proliferation	0.9	>=0.20
GO:0051351	positive regulation of ligase activity	0.93	>=0.20
GO:0060193	positive regulation of lipase activity	0.25	>=0.20
GO:0040017	positive regulation of locomotion	0.15	>=0.20
GO:0051349	positive regulation of lyase activity	0.99	>=0.20
GO:0051251	positive regulation of lymphocyte activation	0.61	>=0.20
GO:0045621	positive regulation of lymphocyte differentiation	0.67	>=0.20
GO:0002708	positive regulation of lymphocyte mediated immunity	0.94	>=0.20
GO:0050671	positive regulation of lymphocyte proliferation	0.88	>=0.20
GO:0010744	positive regulation of macrophage derived foam cell differen	0.61	>=0.20
GO:0043406	positive regulation of MAP kinase activity	0.12	>=0.20
GO:0043410	positive regulation of MAPK cascade	0.62	>=0.20
GO:0002053	positive regulation of mesenchymal cell proliferation	0.99	>=0.20
GO:0010822	positive regulation of mitochondrion organization	1	>=0.20
GO:0032946	positive regulation of mononuclear cell proliferation	0.9	>=0.20
GO:0040018	positive regulation of multicellular organism growth	0.34	>=0.20
GO:0051240	positive regulation of multicellular organismal process	0.17	>=0.20
GO:0051149	positive regulation of muscle cell differentiation	0.98	>=0.20
GO:0045933	positive regulation of muscle contraction	0.99	>=0.20
GO:0045639	positive regulation of myeloid cell differentiation	0.75	>=0.20
GO:0002763	positive regulation of myeloid leukocyte differentiation	1	>=0.20
GO:0032816	positive regulation of natural killer cell activation	0.99	>=0.20
GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	0.93	>=0.20
GO:0002717	positive regulation of natural killer cell mediated immunity	0.93	>=0.20
GO:2000179	positive regulation of neural precursor cell proliferation	0.98	>=0.20

GO:0002052	positive regulation of neuroblast proliferation	0.99	>=0.20
GO:0050769	positive regulation of neurogenesis	1	>=0.20
GO:0031646	positive regulation of neurological system process	1	>=0.20
GO:0045666	positive regulation of neuron differentiation	1	>=0.20
GO:0051092	positive regulation of NF-kappaB transcription factor activity	0.88	>=0.20
GO:0045429	positive regulation of nitric oxide biosynthetic process	0.29	>=0.20
GO:0030810	positive regulation of nucleotide biosynthetic process	0.91	>=0.20
GO:0045981	positive regulation of nucleotide metabolic process	0.94	>=0.20
GO:0010638	positive regulation of organelle organization	0.35	>=0.20
GO:0045778	positive regulation of ossification	1	>=0.20
GO:0045669	positive regulation of osteoblast differentiation	0.88	>=0.20
GO:0045672	positive regulation of osteoclast differentiation	1	>=0.20
GO:0090277	positive regulation of peptide hormone secretion	0.7	>=0.20
GO:0002793	positive regulation of peptide secretion	0.7	>=0.20
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	0.41	>=0.20
GO:0045937	positive regulation of phosphate metabolic process	0.21	>=0.20
GO:0010518	positive regulation of phospholipase activity	0.54	>=0.20
GO:0010863	positive regulation of phospholipase C activity	0.55	>=0.20
GO:0010562	positive regulation of phosphorus metabolic process	0.21	>=0.20
GO:0042327	positive regulation of phosphorylation	0.3	>=0.20
GO:0031954	positive regulation of protein autophosphorylation	0.99	>=0.20
GO:0031334	positive regulation of protein complex assembly	0.89	>=0.20
GO:0090312	positive regulation of protein deacetylation	0.29	>=0.20
GO:0045860	positive regulation of protein kinase activity	0.29	>=0.20
GO:0031401	positive regulation of protein modification process	0.18	>=0.20
GO:0032461	positive regulation of protein oligomerization	1	>=0.20
GO:0001934	positive regulation of protein phosphorylation	0.35	>=0.20
GO:0032273	positive regulation of protein polymerization	0.85	>=0.20
GO:0050714	positive regulation of protein secretion	0.86	>=0.20
GO:0071902	positive regulation of protein serine/threonine kinase activity	0.08	>=0.20
GO:0051222	positive regulation of protein transport	0.45	>=0.20
GO:0031398	positive regulation of protein ubiquitination	0.94	>=0.20
GO:0032320	positive regulation of Ras GTPase activity	0.44	>=0.20
GO:2000243	positive regulation of reproductive process	0.61	>=0.20
GO:0032103	positive regulation of response to external stimulus	0.13	>=0.20
GO:0032321	positive regulation of Rho GTPase activity	0.53	>=0.20
GO:0051047	positive regulation of secretion	0.9	>=0.20
GO:0051091	positive regulation of sequence-specific DNA binding transcri	0.22	>=0.20
GO:0014911	positive regulation of smooth muscle cell migration	0.7	>=0.20
GO:0048661	positive regulation of smooth muscle cell proliferation	0.36	>=0.20
GO:0045987	positive regulation of smooth muscle contraction	1	>=0.20
GO:0045880	positive regulation of smoothened signaling pathway	0.64	>=0.20
GO:0070304	positive regulation of stress-activated protein kinase signalin	0.9	>=0.20
GO:0050806	positive regulation of synaptic transmission	1	>=0.20
GO:0002827	positive regulation of T-helper 1 type immune response	1	>=0.20
GO:0045624	positive regulation of T-helper cell differentiation	0.77	>=0.20
GO:0050870	positive regulation of T cell activation	0.68	>=0.20

GO:0045582	positive regulation of T cell differentiation	0.58	>=0.20
GO:0001916	positive regulation of T cell mediated cytotoxicity	1	>=0.20
GO:0002711	positive regulation of T cell mediated immunity	1	>=0.20
GO:0042102	positive regulation of T cell proliferation	0.94	>=0.20
GO:0032008	positive regulation of TOR signaling cascade	0.6	>=0.20
GO:0051347	positive regulation of transferase activity	0.1	>=0.20
GO:0090100	positive regulation of transmembrane receptor protein serin	0.74	>=0.20
GO:0051971	positive regulation of transmission of nerve impulse	1	>=0.20
GO:0051050	positive regulation of transport	0.25	>=0.20
GO:0032760	positive regulation of tumor necrosis factor production	0.4	>=0.20
GO:0032481	positive regulation of type I interferon production	0.99	>=0.20
GO:0042531	positive regulation of tyrosine phosphorylation of STAT prote	0.97	>=0.20
GO:0051443	positive regulation of ubiquitin-protein ligase activity	0.93	>=0.20
GO:0051437	positive regulation of ubiquitin-protein ligase activity involve	0.9	>=0.20
GO:0030949	positive regulation of vascular endothelial growth factor rece	0.82	>=0.20
GO:0045907	positive regulation of vasoconstriction	0.55	>=0.20
GO:0048524	positive regulation of viral reproduction	0.51	>=0.20
GO:0050434	positive regulation of viral transcription	0.54	>=0.20
GO:0030177	positive regulation of Wnt receptor signaling pathway	0.99	>=0.20
GO:0043368	positive T cell selection	0.97	>=0.20
GO:0006892	post-Golgi vesicle-mediated transport	0.78	>=0.20
MP:0002082	postnatal lethality	0.17	>=0.20
GO:0006301	postreplication repair	1	>=0.20
GO:0014069	postsynaptic density	1	>=0.20
GO:0045211	postsynaptic membrane	1	>=0.20
GO:0016441	posttranscriptional gene silencing	0.99	>=0.20
GO:0035194	posttranscriptional gene silencing by RNA	0.99	>=0.20
ENSG00000128513	POT1 PPI subnetwork	0.44	>=0.20
GO:0008556	potassium-transporting ATPase activity	0.84	>=0.20
GO:0005267	potassium channel activity	1	>=0.20
GO:0034705	potassium channel complex	1	>=0.20
GO:0015459	potassium channel regulator activity	1	>=0.20
GO:0071805	potassium ion transmembrane transport	1	>=0.20
GO:0015079	potassium ion transmembrane transporter activity	1	>=0.20
GO:0006813	potassium ion transport	1	>=0.20
ENSG00000198062	POTEH PPI subnetwork	0.08	>=0.20
ENSG00000143190	POU2F1 PPI subnetwork	0.37	>=0.20
ENSG00000137709	POU2F3 PPI subnetwork	0.3	>=0.20
ENSG00000184486	POU3F2 PPI subnetwork	0.69	>=0.20
ENSG00000180817	PPA1 PPI subnetwork	0.18	>=0.20
ENSG00000130810	PPAN PPI subnetwork	0.57	>=0.20
ENSG00000162407	PPAP2B PPI subnetwork	0.32	>=0.20
ENSG00000186951	PPARA PPI subnetwork	0.05	>=0.20
ENSG00000112033	PPARD PPI subnetwork	0.45	>=0.20
ENSG00000132170	PPARG PPI subnetwork	0.46	>=0.20
ENSG00000177380	PPFIA3 PPI subnetwork	0.96	>=0.20
ENSG00000196262	PPIA PPI subnetwork	0.03	>=0.20

ENSG00000166794	PPIB PPI subnetwork	0.64	>=0.20
ENSG00000108179	PPIF PPI subnetwork	0.18	>=0.20
ENSG00000138398	PPIG PPI subnetwork	0.84	>=0.20
ENSG00000138032	PPM1B PPI subnetwork	0.48	>=0.20
ENSG00000115241	PPM1G PPI subnetwork	0.42	>=0.20
ENSG00000172531	PPP1CA PPI subnetwork	0.16	>=0.20
ENSG00000213639	PPP1CB PPI subnetwork	0.21	>=0.20
ENSG00000186298	PPP1CC PPI subnetwork	0.17	>=0.20
ENSG00000058272	PPP1R12A PPI subnetwork	0.28	>=0.20
ENSG00000125503	PPP1R12C PPI subnetwork	0.08	>=0.20
ENSG00000167641	PPP1R14A PPI subnetwork	0.63	>=0.20
ENSG00000184203	PPP1R2 PPI subnetwork	0.68	>=0.20
ENSG00000115685	PPP1R7 PPI subnetwork	0.32	>=0.20
ENSG00000113575	PPP2CA PPI subnetwork	0.34	>=0.20
ENSG00000104695	PPP2CB PPI subnetwork	0.83	>=0.20
ENSG00000105568	PPP2R1A PPI subnetwork	0.81	>=0.20
ENSG00000137713	PPP2R1B PPI subnetwork	0.62	>=0.20
ENSG00000074211	PPP2R2C PPI subnetwork	0.43	>=0.20
ENSG00000119383	PPP2R4 PPI subnetwork	0.81	>=0.20
ENSG00000078304	PPP2R5C PPI subnetwork	0.29	>=0.20
ENSG00000112640	PPP2R5D PPI subnetwork	0.31	>=0.20
ENSG00000138814	PPP3CA PPI subnetwork	0.98	>=0.20
ENSG00000107758	PPP3CB PPI subnetwork	0.92	>=0.20
ENSG00000120910	PPP3CC PPI subnetwork	1	>=0.20
ENSG00000188386	PPP3R2 PPI subnetwork	0.99	>=0.20
ENSG00000149923	PPP4C PPI subnetwork	0.07	>=0.20
ENSG00000163605	PPP4R2 PPI subnetwork	0.72	>=0.20
ENSG00000011485	PPP5C PPI subnetwork	0.17	>=0.20
ENSG00000100239	PPP6R2 PPI subnetwork	0.79	>=0.20
GO:0035102	PRC1 complex	0.58	>=0.20
ENSG00000117450	PRDX1 PPI subnetwork	0.04	>=0.20
ENSG00000126432	PRDX5 PPI subnetwork	0.28	>=0.20
ENSG00000117592	PRDX6 PPI subnetwork	0.83	>=0.20
GO:0000407	pre-autophagosomal structure	0.35	>=0.20
GO:0016254	preassembly of GPI anchor in ER membrane	1	>=0.20
MP:0009743	preaxial polydactyly	0.96	>=0.20
GO:0016272	prefoldin complex	1	>=0.20
MP:0002080	prenatal lethality	0.06	>=0.20
GO:0004659	prenyltransferase activity	0.17	>=0.20
GO:0060134	prepulse inhibition	1	>=0.20
GO:0030684	preribosome	0.83	>=0.20
GO:0042734	presynaptic membrane	1	>=0.20
ENSG00000198056	PRIM1 PPI subnetwork	0.97	>=0.20
GO:0015399	primary active transmembrane transporter activity	0.16	>=0.20
GO:0072372	primary cilium	0.99	>=0.20
GO:0014020	primary neural tube formation	1	>=0.20
GO:0090009	primitive streak formation	0.99	>=0.20

ENSG00000131791	PRKAB2 PPI subnetwork	0.11	>=0.20
ENSG00000072062	PRKACA PPI subnetwork	0.05	>=0.20
ENSG00000142875	PRKACB PPI subnetwork	0.33	>=0.20
ENSG00000165059	PRKACG PPI subnetwork	0.58	>=0.20
ENSG00000005249	PRKAR2B PPI subnetwork	0.45	>=0.20
ENSG00000154229	PRKCA PPI subnetwork	0.9	>=0.20
ENSG00000166501	PRKCB PPI subnetwork	0.26	>=0.20
ENSG00000163932	PRKCD PPI subnetwork	0.2	>=0.20
ENSG00000171132	PRKCE PPI subnetwork	0.5	>=0.20
ENSG00000126583	PRKCG PPI subnetwork	0.84	>=0.20
ENSG00000163558	PRKCI PPI subnetwork	0.68	>=0.20
ENSG00000065675	PRKCQ PPI subnetwork	0.65	>=0.20
ENSG00000067606	PRKCZ PPI subnetwork	0.57	>=0.20
ENSG00000105287	PRKD2 PPI subnetwork	0.09	>=0.20
ENSG00000185532	PRKG1 PPI subnetwork	0.87	>=0.20
ENSG00000183943	PRKX PPI subnetwork	0.81	>=0.20
ENSG00000172179	PRL PPI subnetwork	0.06	>=0.20
ENSG00000113494	PRLR PPI subnetwork	0.19	>=0.20
ENSG00000126457	PRMT1 PPI subnetwork	0.45	>=0.20
ENSG00000100462	PRMT5 PPI subnetwork	0.09	>=0.20
ENSG00000171867	PRNP PPI subnetwork	0.8	>=0.20
GO:0002440	production of molecular mediator of immune response	0.36	>=0.20
MP:0000748	progressive muscle weakness	0.26	>=0.20
MP:0003896	prolonged PR interval	0.63	>=0.20
MP:0010392	prolonged QRS complex duration	0.84	>=0.20
MP:0003233	prolonged QT interval	0.33	>=0.20
GO:0051324	prophase	0.99	>=0.20
GO:0006693	prostaglandin metabolic process	0.99	>=0.20
GO:0006692	prostanoid metabolic process	0.93	>=0.20
GO:0004954	prostanoid receptor activity	0.04	>=0.20
GO:0030850	prostate gland development	0.95	>=0.20
GO:0060740	prostate gland epithelium morphogenesis	0.99	>=0.20
GO:0060512	prostate gland morphogenesis	0.98	>=0.20
GO:0010498	proteasomal protein catabolic process	0.8	>=0.20
GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	0.75	>=0.20
GO:0000502	proteasome complex	0.65	>=0.20
GO:0005839	proteasome core complex	0.86	>=0.20
GO:0018298	protein-chromophore linkage	0.77	>=0.20
GO:0032993	protein-DNA complex	0.31	>=0.20
GO:0065004	protein-DNA complex assembly	0.99	>=0.20
GO:0032986	protein-DNA complex disassembly	0.66	>=0.20
GO:0071824	protein-DNA complex subunit organization	0.97	>=0.20
GO:0016279	protein-lysine N-methyltransferase activity	0.11	>=0.20
GO:0006473	protein acetylation	0.45	>=0.20
GO:0043543	protein acylation	0.6	>=0.20
GO:0008213	protein alkylation	0.72	>=0.20
GO:0051865	protein autoubiquitination	1	>=0.20

GO:0000988	protein binding transcription factor activity	0.04	>=0.20
GO:0008022	protein C-terminus binding	0.18	>=0.20
GO:0030163	protein catabolic process	0.51	>=0.20
GO:0043241	protein complex disassembly	0.94	>=0.20
GO:0032947	protein complex scaffold	0.1	>=0.20
GO:0006476	protein deacetylation	0.55	>=0.20
GO:0035601	protein deacylation	0.48	>=0.20
GO:0006470	protein dephosphorylation	0.83	>=0.20
GO:0051261	protein depolymerization	0.85	>=0.20
GO:0016579	protein deubiquitination	0.93	>=0.20
GO:0015035	protein disulfide oxidoreductase activity	0.09	>=0.20
GO:0006457	protein folding	0.77	>=0.20
GO:0006486	protein glycosylation	0.91	>=0.20
GO:0016558	protein import into peroxisome matrix	0.84	>=0.20
GO:0070979	protein K11-linked ubiquitination	0.8	>=0.20
GO:0070936	protein K48-linked ubiquitination	0.95	>=0.20
GO:0051018	protein kinase A binding	0.51	>=0.20
GO:0043491	protein kinase B signaling cascade	0.44	>=0.20
GO:0070528	protein kinase C signaling cascade	1	>=0.20
GO:0019887	protein kinase regulator activity	0.08	>=0.20
GO:0006497	protein lipidation	0.98	>=0.20
GO:0070972	protein localization in endoplasmic reticulum	0.53	>=0.20
GO:0072657	protein localization in membrane	0.66	>=0.20
GO:0070585	protein localization in mitochondrion	0.94	>=0.20
GO:0072659	protein localization in plasma membrane	0.41	>=0.20
GO:0034502	protein localization to chromosome	0.86	>=0.20
GO:0006479	protein methylation	0.72	>=0.20
GO:0008276	protein methyltransferase activity	0.6	>=0.20
GO:0032446	protein modification by small protein conjugation	0.85	>=0.20
GO:0070647	protein modification by small protein conjugation or remova	0.8	>=0.20
GO:0070646	protein modification by small protein removal	0.9	>=0.20
GO:0006513	protein monoubiquitination	1	>=0.20
GO:0006487	protein N-linked glycosylation	0.81	>=0.20
GO:0018279	protein N-linked glycosylation via asparagine	0.81	>=0.20
GO:0047485	protein N-terminus binding	0.57	>=0.20
GO:0006493	protein O-linked glycosylation	1	>=0.20
GO:0018345	protein palmitoylation	1	>=0.20
GO:0019888	protein phosphatase regulator activity	0.67	>=0.20
GO:0000159	protein phosphatase type 2A complex	0.83	>=0.20
GO:0008601	protein phosphatase type 2A regulator activity	0.96	>=0.20
GO:0051258	protein polymerization	0.16	>=0.20
GO:0000209	protein polyubiquitination	0.73	>=0.20
GO:0042026	protein refolding	0.93	>=0.20
GO:0030291	protein serine/threonine kinase inhibitor activity	0.07	>=0.20
GO:0004722	protein serine/threonine phosphatase activity	0.6	>=0.20
GO:0008287	protein serine/threonine phosphatase complex	0.47	>=0.20
GO:0004712	protein serine/threonine/tyrosine kinase activity	0.13	>=0.20

GO:0006612	protein targeting to membrane	0.9	>=0.20
GO:0006626	protein targeting to mitochondrion	0.96	>=0.20
GO:0004725	protein tyrosine phosphatase activity	0.71	>=0.20
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	0.53	>=0.20
GO:0016567	protein ubiquitination	0.78	>=0.20
GO:0042787	protein ubiquitination involved in ubiquitin-dependent prote	0.95	>=0.20
GO:0005578	proteinaceous extracellular matrix	0.94	>=0.20
GO:0043394	proteoglycan binding	0.28	>=0.20
GO:0006029	proteoglycan metabolic process	0.87	>=0.20
GO:0051603	proteolysis involved in cellular protein catabolic process	0.78	>=0.20
GO:0045259	proton-transporting ATP synthase complex	0.97	>=0.20
GO:0045263	proton-transporting ATP synthase complex, coupling factor F	1	>=0.20
GO:0046961	proton-transporting ATPase activity, rotational mechanism	0.47	>=0.20
GO:0016469	proton-transporting two-sector ATPase complex	0.85	>=0.20
GO:0033178	proton-transporting two-sector ATPase complex, catalytic do	0.57	>=0.20
GO:0033177	proton-transporting two-sector ATPase complex, proton-trar	0.91	>=0.20
GO:0033176	proton-transporting V-type ATPase complex	0.75	>=0.20
GO:0033180	proton-transporting V-type ATPase, V1 domain	0.77	>=0.20
GO:0015992	proton transport	0.98	>=0.20
GO:0009954	proximal/distal pattern formation	1	>=0.20
ENSG00000105618	PRPF31 PPI subnetwork	0.26	>=0.20
ENSG00000112739	PRPF4B PPI subnetwork	0.07	>=0.20
ENSG00000164244	PRRC1 PPI subnetwork	0.08	>=0.20
ENSG00000196415	PRTN3 PPI subnetwork	0.11	>=0.20
ENSG00000135069	PSAT1 PPI subnetwork	0.08	>=0.20
ENSG00000143801	PSEN2 PPI subnetwork	0.62	>=0.20
ENSG00000205155	PSENEN PPI subnetwork	0.4	>=0.20
GO:0031143	pseudopodium	0.61	>=0.20
GO:0001522	pseudouridine synthesis	0.97	>=0.20
ENSG00000129084	PSMA1 PPI subnetwork	0.56	>=0.20
ENSG00000106588	PSMA2 PPI subnetwork	0.77	>=0.20
ENSG00000100567	PSMA3 PPI subnetwork	0.44	>=0.20
ENSG00000008018	PSMB1 PPI subnetwork	0.56	>=0.20
ENSG00000205220	PSMB10 PPI subnetwork	0.5	>=0.20
ENSG00000126067	PSMB2 PPI subnetwork	0.75	>=0.20
ENSG00000108294	PSMB3 PPI subnetwork	0.9	>=0.20
ENSG00000100804	PSMB5 PPI subnetwork	0.64	>=0.20
ENSG00000136930	PSMB7 PPI subnetwork	0.75	>=0.20
ENSG00000204264	PSMB8 PPI subnetwork	0.73	>=0.20
ENSG00000206298	PSMB8 PPI subnetwork	0.73	>=0.20
ENSG00000100764	PSMC1 PPI subnetwork	0.44	>=0.20
ENSG00000100519	PSMC6 PPI subnetwork	0.55	>=0.20
ENSG00000101843	PSMD10 PPI subnetwork	0.64	>=0.20
ENSG00000108671	PSMD11 PPI subnetwork	0.4	>=0.20
ENSG00000095261	PSMD5 PPI subnetwork	0.6	>=0.20
ENSG00000163636	PSMD6 PPI subnetwork	0.44	>=0.20
ENSG00000110801	PSMD9 PPI subnetwork	0.67	>=0.20

ENSG00000092010	PSME1 PPI subnetwork	0.76	>=0.20
ENSG00000100911	PSME2 PPI subnetwork	0.72	>=0.20
ENSG00000068878	PSME4 PPI subnetwork	0.42	>=0.20
ENSG00000125818	PSMF1 PPI subnetwork	0.51	>=0.20
ENSG00000121390	PSPC1 PPI subnetwork	0.54	>=0.20
ENSG00000140368	PSTPIP1 PPI subnetwork	0.61	>=0.20
ENSG00000011304	PTBP1 PPI subnetwork	0.04	>=0.20
ENSG00000185920	PTCH1 PPI subnetwork	0.96	>=0.20
ENSG00000171862	PTEN PPI subnetwork	0.06	>=0.20
ENSG00000073756	PTGS2 PPI subnetwork	0.41	>=0.20
ENSG00000160801	PTH1R PPI subnetwork	0.07	>=0.20
ENSG00000187514	PTMA PPI subnetwork	0.1	>=0.20
ENSG00000105894	PTN PPI subnetwork	0.95	>=0.20
ENSG00000104960	PTOV1 PPI subnetwork	0.24	>=0.20
ENSG00000165996	PTPLA PPI subnetwork	0.85	>=0.20
ENSG00000163629	PTPN13 PPI subnetwork	0.96	>=0.20
ENSG00000072135	PTPN18 PPI subnetwork	0.16	>=0.20
ENSG00000134242	PTPN22 PPI subnetwork	0.37	>=0.20
ENSG00000143851	PTPN7 PPI subnetwork	0.84	>=0.20
ENSG00000127329	PTPRB PPI subnetwork	0.47	>=0.20
ENSG00000132334	PTPRE PPI subnetwork	1	>=0.20
ENSG00000142949	PTPRF PPI subnetwork	0.93	>=0.20
ENSG00000153233	PTPRR PPI subnetwork	0.66	>=0.20
ENSG00000177469	PTRF PPI subnetwork	0.96	>=0.20
ENSG00000164611	PTTG1 PPI subnetwork	0.85	>=0.20
MP:0001178	pulmonary hypoplasia	0.94	>=0.20
MP:0010018	pulmonary vascular congestion	0.09	>=0.20
MP:0001385	pup cannibalization	0.39	>=0.20
GO:0072522	purine-containing compound biosynthetic process	0.92	>=0.20
GO:0043101	purine-containing compound salvage	0.72	>=0.20
GO:0009113	purine base biosynthetic process	0.9	>=0.20
GO:0006144	purine base metabolic process	0.49	>=0.20
GO:0070035	purine NTP-dependent helicase activity	0.44	>=0.20
GO:0042451	purine nucleoside biosynthetic process	0.75	>=0.20
GO:0009127	purine nucleoside monophosphate biosynthetic process	0.89	>=0.20
GO:0009126	purine nucleoside monophosphate metabolic process	0.93	>=0.20
GO:0009145	purine nucleoside triphosphate biosynthetic process	0.74	>=0.20
GO:0006164	purine nucleotide biosynthetic process	0.95	>=0.20
GO:0046129	purine ribonucleoside biosynthetic process	0.75	>=0.20
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	0.89	>=0.20
GO:0009167	purine ribonucleoside monophosphate metabolic process	0.93	>=0.20
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	0.75	>=0.20
GO:0009152	purine ribonucleotide biosynthetic process	0.72	>=0.20
GO:0001614	purinergic nucleotide receptor activity	0.85	>=0.20
GO:0035586	purinergic receptor activity	0.84	>=0.20
GO:0035587	purinergic receptor signaling pathway	0.96	>=0.20
MP:0000876	Purkinje cell degeneration	0.46	>=0.20

ENSG00000100994	PYGB PPI subnetwork	0.16	>=0.20
ENSG00000100504	PYGL PPI subnetwork	0.1	>=0.20
GO:0072528	pyrimidine-containing compound biosynthetic process	0.82	>=0.20
GO:0072529	pyrimidine-containing compound catabolic process	0.95	>=0.20
GO:0072527	pyrimidine-containing compound metabolic process	0.9	>=0.20
GO:0072531	pyrimidine-containing compound transmembrane transport	0.5	>=0.20
GO:0006206	pyrimidine base metabolic process	0.87	>=0.20
GO:0046134	pyrimidine nucleoside biosynthetic process	0.72	>=0.20
GO:0046135	pyrimidine nucleoside catabolic process	0.79	>=0.20
GO:0006213	pyrimidine nucleoside metabolic process	0.76	>=0.20
GO:0006220	pyrimidine nucleotide metabolic process	0.87	>=0.20
GO:0006090	pyruvate metabolic process	0.03	>=0.20
ENSG00000172053	QARS PPI subnetwork	0.97	>=0.20
GO:0015697	quaternary ammonium group transport	0.64	>=0.20
GO:0048038	quinone binding	0.04	>=0.20
GO:0042375	quinone cofactor metabolic process	0.94	>=0.20
GO:0070412	R-SMAD binding	0.14	>=0.20
GO:0005097	Rab GTPase activator activity	0.03	>=0.20
GO:0017137	Rab GTPase binding	1	>=0.20
ENSG00000084733	RAB10 PPI subnetwork	1	>=0.20
ENSG00000185236	RAB11B PPI subnetwork	0.23	>=0.20
ENSG00000156675	RAB11FIP1 PPI subnetwork	0.08	>=0.20
ENSG00000107560	RAB11FIP2 PPI subnetwork	0.09	>=0.20
ENSG00000139998	RAB15 PPI subnetwork	1	>=0.20
ENSG00000099246	RAB18 PPI subnetwork	0.61	>=0.20
ENSG00000138069	RAB1A PPI subnetwork	0.09	>=0.20
ENSG00000069974	RAB27A PPI subnetwork	0.91	>=0.20
ENSG00000104388	RAB2A PPI subnetwork	0.99	>=0.20
ENSG00000172794	RAB37 PPI subnetwork	0.99	>=0.20
ENSG00000105649	RAB3A PPI subnetwork	1	>=0.20
ENSG00000169213	RAB3B PPI subnetwork	1	>=0.20
ENSG00000105514	RAB3D PPI subnetwork	1	>=0.20
ENSG00000168118	RAB4A PPI subnetwork	0.75	>=0.20
ENSG00000175582	RAB6A PPI subnetwork	0.3	>=0.20
ENSG00000154917	RAB6B PPI subnetwork	0.14	>=0.20
ENSG00000075785	RAB7A PPI subnetwork	0.2	>=0.20
ENSG00000167461	RAB8A PPI subnetwork	0.99	>=0.20
ENSG00000166128	RAB8B PPI subnetwork	0.22	>=0.20
ENSG00000029725	RABEP1 PPI subnetwork	0.24	>=0.20
ENSG00000154710	RABGEF1 PPI subnetwork	0.87	>=0.20
ENSG00000137955	RABGGTB PPI subnetwork	0.95	>=0.20
GO:0048365	Rac GTPase binding	0.81	>=0.20
ENSG00000136238	RAC1 PPI subnetwork	0.42	>=0.20
ENSG00000128340	RAC2 PPI subnetwork	0.21	>=0.20
ENSG00000169750	RAC3 PPI subnetwork	0.06	>=0.20
ENSG00000161800	RACGAP1 PPI subnetwork	0.23	>=0.20
ENSG00000070950	RAD18 PPI subnetwork	1	>=0.20

ENSG00000164754	RAD21 PPI subnetwork	0.92	>=0.20
ENSG00000179262	RAD23A PPI subnetwork	0.77	>=0.20
ENSG00000119318	RAD23B PPI subnetwork	0.73	>=0.20
ENSG00000113522	RAD50 PPI subnetwork	0.88	>=0.20
ENSG00000051180	RAD51 PPI subnetwork	1	>=0.20
ENSG00000182185	RAD51B PPI subnetwork	1	>=0.20
ENSG00000002016	RAD52 PPI subnetwork	0.96	>=0.20
ENSG00000172613	RAD9A PPI subnetwork	0.99	>=0.20
ENSG00000151164	RAD9B PPI subnetwork	0.99	>=0.20
ENSG00000039560	RAI14 PPI subnetwork	0.32	>=0.20
ENSG00000006451	RALA PPI subnetwork	0.95	>=0.20
ENSG00000017797	RALBP1 PPI subnetwork	0.05	>=0.20
ENSG00000160271	RALGDS PPI subnetwork	0.26	>=0.20
ENSG00000125970	RALY PPI subnetwork	0.33	>=0.20
ENSG00000184672	RALYL PPI subnetwork	0.53	>=0.20
GO:0008536	Ran GTPase binding	0.89	>=0.20
ENSG00000132341	RAN PPI subnetwork	0.47	>=0.20
ENSG00000153201	RANBP2 PPI subnetwork	0.52	>=0.20
ENSG00000100401	RANGAP1 PPI subnetwork	0.27	>=0.20
ENSG00000116473	RAP1A PPI subnetwork	0.27	>=0.20
ENSG00000127314	RAP1B PPI subnetwork	0.94	>=0.20
ENSG00000076864	RAP1GAP PPI subnetwork	0.99	>=0.20
ENSG00000125249	RAP2A PPI subnetwork	0.4	>=0.20
ENSG00000107263	RAPGEF1 PPI subnetwork	0.45	>=0.20
ENSG00000091428	RAPGEF4 PPI subnetwork	0.97	>=0.20
ENSG00000113643	RARS PPI subnetwork	0.82	>=0.20
GO:0005099	Ras GTPase activator activity	0.03	>=0.20
GO:0017016	Ras GTPase binding	0.95	>=0.20
GO:0005088	Ras guanyl-nucleotide exchange factor activity	0.29	>=0.20
GO:0007265	Ras protein signal transduction	0.27	>=0.20
ENSG00000111344	RASAL1 PPI subnetwork	0.71	>=0.20
ENSG00000075391	RASAL2 PPI subnetwork	0.74	>=0.20
ENSG00000100302	RASD2 PPI subnetwork	0.81	>=0.20
ENSG00000058335	RASGRF1 PPI subnetwork	0.19	>=0.20
ENSG00000136653	RASSF5 PPI subnetwork	0.9	>=0.20
ENSG00000139687	RB1 PPI subnetwork	0.03	>=0.20
ENSG00000162521	RBBP4 PPI subnetwork	0.06	>=0.20
ENSG00000117222	RBBP5 PPI subnetwork	0.11	>=0.20
ENSG00000102054	RBBP7 PPI subnetwork	0.03	>=0.20
ENSG00000101773	RBBP8 PPI subnetwork	0.36	>=0.20
ENSG00000078328	RBFOX1 PPI subnetwork	1	>=0.20
ENSG00000080839	RBL1 PPI subnetwork	0.45	>=0.20
ENSG00000182872	RBM10 PPI subnetwork	0.85	>=0.20
ENSG00000134453	RBM17 PPI subnetwork	0.42	>=0.20
ENSG00000122965	RBM19 PPI subnetwork	0.92	>=0.20
ENSG00000184863	RBM33 PPI subnetwork	0.08	>=0.20
ENSG00000131051	RBM39 PPI subnetwork	0.43	>=0.20

ENSG00000127993	RBM48 PPI subnetwork	0.49	>=0.20
ENSG00000076053	RBM7 PPI subnetwork	0.94	>=0.20
ENSG00000144642	RBMS3 PPI subnetwork	0.09	>=0.20
ENSG00000168214	RBPJ PPI subnetwork	0.52	>=0.20
ENSG00000157110	RBPMS PPI subnetwork	0.78	>=0.20
ENSG00000100387	RBX1 PPI subnetwork	0.55	>=0.20
ENSG00000180198	RCC1 PPI subnetwork	0.45	>=0.20
ENSG00000179051	RCC2 PPI subnetwork	0.68	>=0.20
ENSG00000117906	RCN2 PPI subnetwork	0.69	>=0.20
ENSG00000204356	RDBP PPI subnetwork	0.04	>=0.20
ENSG00000206268	RDBP PPI subnetwork	0.04	>=0.20
ENSG00000206357	RDBP PPI subnetwork	0.04	>=0.20
ENSG00000137710	RDX PPI subnetwork	0.17	>=0.20
REACTOME_3_:UTR:MEDIATE	REACTOME_3_:UTR:MEDIATED_TRANSLATIONAL_REGULATIC	0.86	>=0.20
REACTOME_A_THIRD_PROTEC	REACTOME_A_THIRD_PROTEOLYTIC_CLEAVAGE_RELEASES_N	0.13	>=0.20
REACTOME_ABORTIVE_ELONC	REACTOME_ABORTIVE_ELONGATION_OF_HIV:1_TRANSCRIPT	0.21	>=0.20
REACTOME_ACETYLCHOLINE_	REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM	0.92	>=0.20
REACTOME_ACETYLCHOLINE_	REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE	0.95	>=0.20
REACTOME_ACTIVATED_TAK1	REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIV	0.12	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_APCC_AND_APCCCDC20_MEDI	0.78	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLIC	0.97	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_BH3:ONLY_PROTEINS	0.65	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_CA:PERMEABLE_KAINATE_RECI	1	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_CHAPERONES_BY_ATF6:ALPHA	0.14	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_G_PROTEIN_GATED_POTASSIU	1	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_GABAB_RECEPTORS	1	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_GENES_BY_ATF4	0.39	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_C	1	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_NICOTINIC_ACETYLCHOLINE_RI	0.92	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLU	1	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_THE_AP:1_FAMILY_OF_TRANSC	0.79	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_C	0.73	>=0.20
REACTOME_ACTIVATION_OF_	REACTOME_ACTIVATION_OF_THE_PRE:REPLICATIVE_COMPL	0.98	>=0.20
REACTOME_ADAPTIVE_IMMU	REACTOME_ADAPTIVE_IMMUNE_SYSTEM	0.14	>=0.20
REACTOME_ADHERENS_JUNC	REACTOME_ADHERENS_JUNCTIONS_INTERACTIONS	1	>=0.20
REACTOME_ADP_SIGNALLING	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPT	0.85	>=0.20
REACTOME_ADP_SIGNALLING	REACTOME_ADP_SIGNALLING_THROUGH_P2Y_PURINOCEPT	0.95	>=0.20
REACTOME_AMINE:DERIVED_	REACTOME_AMINE:DERIVED_HORMONES	0.98	>=0.20
REACTOME_AMINE_COMPOU	REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	0.43	>=0.20
REACTOME_AMINE_LIGAND:E	REACTOME_AMINE_LIGAND:BINDING_RECEPTORS	1	>=0.20
REACTOME_AMINO_ACID_AN	REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSP	0.33	>=0.20
REACTOME_AMINO_ACID_TR	REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASM	0.05	>=0.20
REACTOME_ANTIGEN_PRESEN	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_	0.94	>=0.20
REACTOME_ANTIGEN_PROCE	REACTOME_ANTIGEN_PROCESSING:CROSS_PRESENTATION	0.74	>=0.20
REACTOME_ANTIGEN_PROCE	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION__PRO	0.43	>=0.20
REACTOME_ANTIVIRAL_MECH	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN:STIMULATED_(	0.74	>=0.20
REACTOME_APC:CDC20_MED	REACTOME_APC:CDC20_MEDIATED_DEGRADATION_OF_NEK	0.85	>=0.20

REACTOME_APCC:MEDIATED_	REACTOME_APCC:MEDIATED_DEGRADATION_OF_CELL_CYCL	0.74	>=0.20
REACTOME_APCCCDC20_MEI	REACTOME_APCCCDC20_MEDIATED_DEGRADATION_OF_CY(	0.89	>=0.20
REACTOME_APCCCDC20_MEI	REACTOME_APCCCDC20_MEDIATED_DEGRADATION_OF_MI	0.8	>=0.20
REACTOME_APCCCDC20_MEI	REACTOME_APCCCDC20_MEDIATED_DEGRADATION_OF_SE(	0.77	>=0.20
REACTOME_APCCCDH1_MEDI	REACTOME_APCCCDH1_MEDIATED_DEGRADATION_OF_CDC	0.76	>=0.20
REACTOME_APOPTOTIC_CLEA	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELL_ADHESION__P	0.48	>=0.20
REACTOME_APOPTOTIC_CLEA	REACTOME_APOPTOTIC_CLEAVAGE_OF_CELLULAR_PROTEIN	0.13	>=0.20
REACTOME_AQUAPORIN:MEI	REACTOME_AQUAPORIN:MEDIATED_TRANSPORT	0.71	>=0.20
REACTOME_AUTODEGRADAT	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1APCC	0.73	>=0.20
REACTOME_AUTODEGRADAT	REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LI	0.75	>=0.20
REACTOME_AXON_GUIDANCI	REACTOME_AXON_GUIDANCE	0.96	>=0.20
REACTOME_BASIGIN_INTERA(	REACTOME_BASIGIN_INTERACTIONS	0.31	>=0.20
REACTOME_BETA:CATENIN_P	REACTOME_BETA:CATENIN_PHOSPHORYLATION_CASCADE	0.06	>=0.20
REACTOME_BETA_DEFENSINS	REACTOME_BETA_DEFENSINS	0.53	>=0.20
REACTOME_BILE_SALT_AND_	REACTOME_BILE_SALT_AND_ORGANIC_ANION_SLC_TRANSP	0.75	>=0.20
REACTOME_BMAL1CLOCKNP/	REACTOME_BMAL1CLOCKNPAS2_ACTIVATES_GENE_EXPRESS	0.08	>=0.20
REACTOME_BOTULINUM_NEI	REACTOME_BOTULINUM_NEUROTOXICITY	0.98	>=0.20
REACTOME_BRANCHED:CHAII	REACTOME_BRANCHED:CHAIN_AMINO_ACID_CATABOLISM	0.45	>=0.20
REACTOME_CA:DEPENDENT_I	REACTOME_CA:DEPENDENT_EVENTS	0.7	>=0.20
REACTOME_CALCITONIN:LIKE	REACTOME_CALCITONIN:LIKE_LIGAND_RECEPTORS	0.55	>=0.20
REACTOME_CALMODULIN_IN	REACTOME_CALMODULIN_INDUCED_EVENTS	0.69	>=0.20
REACTOME_CALNEXINCALRET	REACTOME_CALNEXINCALRETICULIN_CYCLE	0.48	>=0.20
REACTOME_CAM_PATHWAY	REACTOME_CAM_PATHWAY	0.69	>=0.20
REACTOME_CAP:DEPENDENT_	REACTOME_CAP:DEPENDENT_TRANSLATION_INITIATION	0.73	>=0.20
REACTOME_CASPASE:MEDIAT	REACTOME_CASPASE:MEDIATED_CLEAVAGE_OF_CYTOSKELE	0.48	>=0.20
REACTOME_CD28_CO:STIMUI	REACTOME_CD28_CO:STIMULATION	0.36	>=0.20
REACTOME_CD28_DEPENDEN	REACTOME_CD28_DEPENDENT_PI3KAKT_SIGNALING	0.36	>=0.20
REACTOME_CD28_DEPENDEN	REACTOME_CD28_DEPENDENT_VAV1_PATHWAY	0.49	>=0.20
REACTOME_CDC20PHOSPHO:	REACTOME_CDC20PHOSPHO:APCC_MEDIATED_DEGRADATIC	0.73	>=0.20
REACTOME_CDC6_ASSOCIATI	REACTOME_CDC6_ASSOCIATION_WITH_THE_ORCORIGIN_CC	0.46	>=0.20
REACTOME_CDK:MEDIATED_I	REACTOME_CDK:MEDIATED_PHOSPHORYLATION_AND_REM	0.67	>=0.20
REACTOME_CDO_IN_MYOGEI	REACTOME_CDO_IN_MYOGENESIS	0.89	>=0.20
REACTOME_CDT1_ASSOCIATI	REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6ORCORIG	0.73	>=0.20
REACTOME_CELL:CELL_COMM	REACTOME_CELL:CELL_COMMUNICATION	0.88	>=0.20
REACTOME_CELL:CELL_JUNCT	REACTOME_CELL:CELL_JUNCTION_ORGANIZATION	1	>=0.20
REACTOME_CELL:EXTRACELLU	REACTOME_CELL:EXTRACELLULAR_MATRIX_INTERACTIONS	0.79	>=0.20
REACTOME_CELL_CYCLE	REACTOME_CELL_CYCLE	0.59	>=0.20
REACTOME_CELL_CYCLE_CHE	REACTOME_CELL_CYCLE_CHECKPOINTS	0.89	>=0.20
REACTOME_CELL_CYCLE_MIT(	REACTOME_CELL_CYCLE_MITOTIC	0.49	>=0.20
REACTOME_CELL_DEATH_SIG	REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AI	0.45	>=0.20
REACTOME_CELL_JUNCTION_	REACTOME_CELL_JUNCTION_ORGANIZATION	0.98	>=0.20
REACTOME_CENTROSOME_M	REACTOME_CENTROSOME_MATURATION	0.27	>=0.20
REACTOME_CGMP_EFFECTS	REACTOME_CGMP_EFFECTS	0.64	>=0.20
REACTOME_CHAPERONIN:ME	REACTOME_CHAPERONIN:MEDIATED_PROTEIN_FOLDING	0.37	>=0.20
REACTOME_CHEMOKINE_REC	REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.26	>=0.20
REACTOME_CHROMOSOME_I	REACTOME_CHROMOSOME_MAINTENANCE	0.95	>=0.20
REACTOME_CIRCADIAN_CLOC	REACTOME_CIRCADIAN_CLOCK	0.08	>=0.20

REACTOME_CITRIC_ACID_CYC	REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE	0.55	>=0.20
REACTOME_CLASS_A1_RHOD	REACTOME_CLASS_A1_RHODOPSIN:LIKE_RECEPTORS	0.8	>=0.20
REACTOME_CLASS_B2_SECRE	REACTOME_CLASS_B2_SECRETIN_FAMILY_RECEPTORS	0.91	>=0.20
REACTOME_CLASS_C3_METAI	REACTOME_CLASS_C3_METABOTROPIC_GLUTAMATEPHERO	1	>=0.20
REACTOME_CLASS_I_MHC_M	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSIN	0.5	>=0.20
REACTOME_CONVERSION_FR	REACTOME_CONVERSION_FROM_APCCCDC20_TO_APCCCDH	0.87	>=0.20
REACTOME_COOPERATION_C	REACTOME_COOPERATION_OF_PREFOLDIN_AND_TRICCCT_	0.62	>=0.20
REACTOME_COPI_MEDIATED_	REACTOME_COPI_MEDIATED_TRANSPORT	0.1	>=0.20
REACTOME_COSTIMULATION_	REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	0.49	>=0.20
REACTOME_CREB_PHOSPHOF	REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACT	1	>=0.20
REACTOME_CREB_PHOSPHOF	REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACT	0.92	>=0.20
REACTOME_CRMPS_IN_SEMA	REACTOME_CRMPS_IN_SEMA3A_SIGNALING	0.59	>=0.20
REACTOME_CROSS:PRESENTA	REACTOME_CROSS:PRESENTATION_OF_SOLUBLE_EXOGENO	0.66	>=0.20
REACTOME_CTLA4_INHIBITOF	REACTOME_CTLA4_INHIBITORY_SIGNALING	0.03	>=0.20
REACTOME_CYCLIN_AB1_ASS	REACTOME_CYCLIN_AB1_ASSOCIATED_EVENTS_DURING_G2	0.83	>=0.20
REACTOME_CYCLIN_ACDK2:A	REACTOME_CYCLIN_ACDK2:ASSOCIATED_EVENTS_AT_S_PHA	0.57	>=0.20
REACTOME_CYCLIN_D_ASSOC	REACTOME_CYCLIN_D_ASSOCIATED_EVENTS_IN_G1	0.22	>=0.20
REACTOME_CYCLIN_E_ASSOC	REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1S_T	0.57	>=0.20
REACTOME_CYTOKINE_SIGNA	REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	0.08	>=0.20
REACTOME_CYTOSOLIC_TRNA	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	0.62	>=0.20
REACTOME_DAG_AND_IP3_SI	REACTOME_DAG_AND_IP3_SIGNALING	0.77	>=0.20
REACTOME_DCC_MEDIATED_	REACTOME_DCC_MEDIATED_ATTRACTIVE_SIGNALING	0.92	>=0.20
REACTOME_DEADENYLATION	REACTOME_DEADENYLATION:DEPENDENT_MRNA_DECAY	0.67	>=0.20
REACTOME_DEADENYLATION_	REACTOME_DEADENYLATION_OF_MRNA	0.17	>=0.20
REACTOME_DEATH_RECEPTO	REACTOME_DEATH_RECEPTOR__SIGNALLING	0.95	>=0.20
REACTOME_DEFENSINS	REACTOME_DEFENSINS	0.15	>=0.20
REACTOME_DEGRADATION_C	REACTOME_DEGRADATION_OF_BETA:CATENIN_BY_THE_DES	0.4	>=0.20
REACTOME_DEPOLARIZATION	REACTOME_DEPOLARIZATION_OF_THE_PRESYNAPTIC_TERM	1	>=0.20
REACTOME_DEPOSITION_OF_	REACTOME_DEPOSITION_OF_NEW_CENPA:CONTAINING_NU	0.97	>=0.20
REACTOME_DESTABILIZATION	REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_	0.76	>=0.20
REACTOME_DESTABILIZATION	REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	0.81	>=0.20
REACTOME_DESTABILIZATION	REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPRO	0.9	>=0.20
REACTOME_DEVELOPMENTAI	REACTOME_DEVELOPMENTAL_BIOLOGY	0.04	>=0.20
REACTOME_DNA_REPLICATIO	REACTOME_DNA_REPLICATION	0.56	>=0.20
REACTOME_DNA_REPLICATIO	REACTOME_DNA_REPLICATION_PRE:INITIATION	0.78	>=0.20
REACTOME_DNA_STRAND_EL	REACTOME_DNA_STRAND_ELONGATION	0.94	>=0.20
REACTOME_DOPAMINE_NEUI	REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYC	1	>=0.20
REACTOME_DOUBLE:STRAND_	REACTOME_DOUBLE:STRAND_BREAK_REPAIR	0.96	>=0.20
REACTOME_DOWNSTREAM_S	REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	0.03	>=0.20
REACTOME_DOWNSTREAM_S	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGI	0.05	>=0.20
REACTOME_DOWNSTREAM_T	REACTOME_DOWNSTREAM_TCR_SIGNALING	0.91	>=0.20
REACTOME_DSCAM_INTERAC	REACTOME_DSCAM_INTERACTIONS	0.8	>=0.20
REACTOME_DUAL_INCISION_	REACTOME_DUAL_INCISION_REACTION_IN_GG:NER	0.99	>=0.20
REACTOME_DUAL_INCISION_	REACTOME_DUAL_INCISION_REACTION_IN_TC:NER	0.81	>=0.20
REACTOME_E2F:ENABLED_INI	REACTOME_E2F:ENABLED_INHIBITION_OF_PRE:REPLICATION	0.93	>=0.20
REACTOME_E2F_MEDIATED_I	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICA	0.54	>=0.20
REACTOME_EARLY_PHASE_OI	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	0.23	>=0.20

REACTOME_EFFECTS_OF_PIP2	REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	1	>=0.20
REACTOME_EGFR_DOWNREG	REACTOME_EGFR_DOWNREGULATION	0.67	>=0.20
REACTOME_EGFR_INTERACTS	REACTOME_EGFR_INTERACTS_WITH_PHOSPHOLIPASE_C:GA	0.73	>=0.20
REACTOME_EICOSANOID_LIG	REACTOME_EICOSANOID_LIGAND:BINDING_RECEPTORS	0.06	>=0.20
REACTOME_ELONGATION_AR	REACTOME_ELONGATION_ARREST_AND_RECOVERY	0.07	>=0.20
REACTOME_ENDOSOMAL_SO	REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_F	0.79	>=0.20
REACTOME_ENERGY_DEPEND	REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_	0.2	>=0.20
REACTOME_ER:PHAGOSOME_	REACTOME_ER:PHAGOSOME_PATHWAY	0.83	>=0.20
REACTOME_ETHANOL_OXIDA	REACTOME_ETHANOL_OXIDATION	0.15	>=0.20
REACTOME_EUKARYOTIC_TRA	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION	0.87	>=0.20
REACTOME_EUKARYOTIC_TRA	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION	0.73	>=0.20
REACTOME_EUKARYOTIC_TRA	REACTOME_EUKARYOTIC_TRANSLATION_TERMINATION	0.94	>=0.20
REACTOME_EXTENSION_OF_T	REACTOME_EXTENSION_OF_TELOMERES	0.84	>=0.20
REACTOME_EXTRINSIC_PATH	REACTOME_EXTRINSIC_PATHWAY_FOR_APOPTOSIS	0.95	>=0.20
REACTOME_FACTORS_INVOL	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEV	0.12	>=0.20
REACTOME_FANCONI_ANEMI	REACTOME_FANCONI_ANEMIA_PATHWAY	1	>=0.20
REACTOME_FGFR_LIGAND_BI	REACTOME_FGFR_LIGAND_BINDING_AND_ACTIVATION	0.76	>=0.20
REACTOME_FGFR1_LIGAND_B	REACTOME_FGFR1_LIGAND_BINDING_AND_ACTIVATION	0.98	>=0.20
REACTOME_FGFR1C_LIGAND_	REACTOME_FGFR1C_LIGAND_BINDING_AND_ACTIVATION	0.98	>=0.20
REACTOME_FGFR2_LIGAND_B	REACTOME_FGFR2_LIGAND_BINDING_AND_ACTIVATION	0.98	>=0.20
REACTOME_FGFR2C_LIGAND_	REACTOME_FGFR2C_LIGAND_BINDING_AND_ACTIVATION	0.98	>=0.20
REACTOME_FGFR3_LIGAND_B	REACTOME_FGFR3_LIGAND_BINDING_AND_ACTIVATION	0.98	>=0.20
REACTOME_FGFR3C_LIGAND_	REACTOME_FGFR3C_LIGAND_BINDING_AND_ACTIVATION	0.98	>=0.20
REACTOME_FGFR4_LIGAND_B	REACTOME_FGFR4_LIGAND_BINDING_AND_ACTIVATION	0.89	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_A_POOL_OF_FREE_40S_SUBUI	0.92	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU	0.94	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_HIV:1_ELONGATION_COMPLEX	0.25	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_HIV:1_ELONGATION_COMPLEX	0.26	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_INCISION_COMPLEX_IN_GG:NI	0.99	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_CO	0.26	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_THE_EARLY_ELONGATION_COI	0.48	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_THE_HIV:1_EARLY_ELONGATIC	0.48	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND	0.89	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_TRANSCRIPTION:COUPLED_NE	0.81	>=0.20
REACTOME_FORMATION_OF_	REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMED	0.39	>=0.20
REACTOME_FRS2:MEDIATED_	REACTOME_FRS2:MEDIATED_ACTIVATION	0.27	>=0.20
REACTOME_FRS2:MEDIATED_	REACTOME_FRS2:MEDIATED_CASCADE	0.37	>=0.20
REACTOME_G:PROTEIN_ACTI	REACTOME_G:PROTEIN_ACTIVATION	0.98	>=0.20
REACTOME_G:PROTEIN_BETA	REACTOME_G:PROTEIN_BETAGAMMA_SIGNALLING	0.93	>=0.20
REACTOME_G:PROTEIN_MED	REACTOME_G:PROTEIN_MEDIATED_EVENTS	0.88	>=0.20
REACTOME_G_ALPHA_1213_S	REACTOME_G_ALPHA_1213_SIGNALLING_EVENTS	0.3	>=0.20
REACTOME_G_ALPHA_I_SIGN	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	0.95	>=0.20
REACTOME_G_ALPHA_Q_SIGI	REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	0.98	>=0.20
REACTOME_G_ALPHA_S_SIGN	REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	0.81	>=0.20
REACTOME_G_ALPHA_Z_SIGN	REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	0.99	>=0.20
REACTOME_G_BETAGAMMA_	REACTOME_G_BETAGAMMA_SIGNALLING_THROUGH_PI3KG	0.91	>=0.20
REACTOME_G_BETAGAMMA_	REACTOME_G_BETAGAMMA_SIGNALLING_THROUGH_PLC_B	0.99	>=0.20

REACTOME_G_PROTEIN_GAT	REACTOME_G_PROTEIN_GATED_POTASSIUM_CHANNELS	1	>=0.20
REACTOME_G0_AND_EARLY_	REACTOME_G0_AND_EARLY_G1	0.56	>=0.20
REACTOME_G1_PHASE	REACTOME_G1_PHASE	0.22	>=0.20
REACTOME_G1S:SPECIFIC_TR/	REACTOME_G1S:SPECIFIC_TRANSCRIPTION	0.6	>=0.20
REACTOME_G1S_DNA_DAMA	REACTOME_G1S_DNA_DAMAGE_CHECKPOINTS	0.68	>=0.20
REACTOME_G1S_TRANSITION	REACTOME_G1S_TRANSITION	0.71	>=0.20
REACTOME_G2M_CHECKPOIN	REACTOME_G2M_CHECKPOINTS	0.97	>=0.20
REACTOME_G2M_TRANSITIOI	REACTOME_G2M_TRANSITION	0.33	>=0.20
REACTOME_GABA_A_RECEPT	REACTOME_GABA_A_RECEPTOR_ACTIVATION	1	>=0.20
REACTOME_GABA_B_RECEPT	REACTOME_GABA_B_RECEPTOR_ACTIVATION	1	>=0.20
REACTOME_GABA_RECEPTOR	REACTOME_GABA_RECEPTOR_ACTIVATION	1	>=0.20
REACTOME_GABA_SYNTHESIS	REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DE	0.8	>=0.20
REACTOME_GAP:FILLING_DN/	REACTOME_GAP:FILLING_DNA_REPAIR_SYNTHESIS_AND_LIG	0.93	>=0.20
REACTOME_GAP:FILLING_DN/	REACTOME_GAP:FILLING_DNA_REPAIR_SYNTHESIS_AND_LIG	0.93	>=0.20
REACTOME_GAP_JUNCTION_/	REACTOME_GAP_JUNCTION_ASSEMBLY	0.3	>=0.20
REACTOME_GAP_JUNCTION_T	REACTOME_GAP_JUNCTION_TRAFFICKING	0.43	>=0.20
REACTOME_GAP_JUNCTION_T	REACTOME_GAP_JUNCTION_TRAFFICKING_AND_REGULATIC	0.43	>=0.20
REACTOME_GENERATION_OF	REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLEC	0.97	>=0.20
REACTOME_GENERIC_TRANSC	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	0.32	>=0.20
REACTOME_GLOBAL_GENOM	REACTOME_GLOBAL_GENOMIC_NER_GG:NER	0.97	>=0.20
REACTOME_GLUCAGON:TYPE	REACTOME_GLUCAGON:TYPE_LIGAND_RECEPTORS	0.98	>=0.20
REACTOME_GLUCAGON_SIGN	REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGUL	0.67	>=0.20
REACTOME_GLUTAMATE_BIN	REACTOME_GLUTAMATE_BINDING_ACTIVATION_OF_AMPA_	0.98	>=0.20
REACTOME_GLUTAMATE_NEU	REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CY	0.99	>=0.20
REACTOME_GLUTATHIONE_C	REACTOME_GLUTATHIONE_CONJUGATION	0.56	>=0.20
REACTOME_GLUTATHIONE_S	REACTOME_GLUTATHIONE_SYNTHESIS_AND_RECYCLING	0.82	>=0.20
REACTOME_GOLGI_TO_ER_RE	REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	0.1	>=0.20
REACTOME_GPCR_LIGAND_B	REACTOME_GPCR_LIGAND_BINDING	0.89	>=0.20
REACTOME_GPVI:MEDIATED_	REACTOME_GPVI:MEDIATED_ACTIVATION_CASCADE	0.09	>=0.20
REACTOME_GRB2_EVENTS_IN	REACTOME_GRB2_EVENTS_IN_ERBB2_SIGNALING	0.29	>=0.20
REACTOME_GTP_HYDROLYSIS	REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_	0.86	>=0.20
REACTOME_HIGHLY_CALCIUM	REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_	0.89	>=0.20
REACTOME_HIV:1_ELONGATI	REACTOME_HIV:1_ELONGATION_ARREST_AND_RECOVERY	0.07	>=0.20
REACTOME_HIV:1_TRANSCRIF	REACTOME_HIV:1_TRANSCRIPTION_ELONGATION	0.25	>=0.20
REACTOME_HIV:1_TRANSCRIF	REACTOME_HIV:1_TRANSCRIPTION_INITIATION	0.72	>=0.20
REACTOME_HOMOLOGOUS_R	REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR	0.97	>=0.20
REACTOME_HOMOLOGOUS_R	REACTOME_HOMOLOGOUS_RECOMBINATION_REPAIR_OF_I	0.97	>=0.20
REACTOME_HORMONE_LIGAI	REACTOME_HORMONE_LIGAND:BINDING_RECEPTORS	0.93	>=0.20
REACTOME_HOST_INTERACTI	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	0.44	>=0.20
REACTOME_IMMUNOREGULA	REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEE	0.32	>=0.20
REACTOME_INACTIVATION_O	REACTOME_INACTIVATION_OF_APCC_VIA_DIRECT_INHIBITIC	0.85	>=0.20
REACTOME_INCRETIN_SYNTH	REACTOME_INCRETIN_SYNTHESIS_SECRETION_AND_INACTIV	0.39	>=0.20
REACTOME_INFLUENZA_INFE	REACTOME_INFLUENZA_INFECTION	0.66	>=0.20
REACTOME_INFLUENZA_LIFE_	REACTOME_INFLUENZA_LIFE_CYCLE	0.75	>=0.20
REACTOME_INFLUENZA_VIRA	REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_	0.91	>=0.20
REACTOME_INHIBITION__OF_	REACTOME_INHIBITION__OF_VOLTAGE_GATED_CA2_CHANN	1	>=0.20
REACTOME_INHIBITION_OF_I	REACTOME_INHIBITION_OF_INSULIN_SECRETION_BY_ADREN	1	>=0.20

REACTOME_INHIBITION_OF_F	REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_D	0.16	>=0.20
REACTOME_INHIBITION_OF_T	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_O	0.85	>=0.20
REACTOME_INSULIN_RECEPTO	REACTOME_INSULIN_RECEPTOR_RECYCLING	0.78	>=0.20
REACTOME_INSULIN_RECEPTO	REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	0.06	>=0.20
REACTOME_INSULIN_SYNTHE	REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	0.99	>=0.20
REACTOME_INTEGRATION_OF	REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	0.34	>=0.20
REACTOME_INTERACTION_BE	REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	1	>=0.20
REACTOME_INTERACTIONS_O	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR	0.78	>=0.20
REACTOME_INTERFERON_ALP	REACTOME_INTERFERON_ALPHABETA_SIGNALING	0.5	>=0.20
REACTOME_INTERFERON_GA	REACTOME_INTERFERON_GAMMA_SIGNALING	0.84	>=0.20
REACTOME_INTERFERON_SIG	REACTOME_INTERFERON_SIGNALING	0.63	>=0.20
REACTOME_INTERLEUKIN:1_S	REACTOME_INTERLEUKIN:1_SIGNALING	0.04	>=0.20
REACTOME_INTERLEUKIN:2_S	REACTOME_INTERLEUKIN:2_SIGNALING	0.07	>=0.20
REACTOME_INTERLEUKIN:3_5	REACTOME_INTERLEUKIN:3_5_AND_GM:CSF_SIGNALING	0.06	>=0.20
REACTOME_INTERLEUKIN:6_S	REACTOME_INTERLEUKIN:6_SIGNALING	0.08	>=0.20
REACTOME_INTERLEUKIN_RE	REACTOME_INTERLEUKIN_RECEPTOR_SHC_SIGNALING	0.17	>=0.20
REACTOME_INWARDLY_RECT	REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	0.96	>=0.20
REACTOME_ION_CHANNEL_T	REACTOME_ION_CHANNEL_TRANSPORT	1	>=0.20
REACTOME_ION_TRANSPORT	REACTOME_ION_TRANSPORT_BY_P:TYPE_ATPASES	0.92	>=0.20
REACTOME_IONOTROPIC_ACT	REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTOR	1	>=0.20
REACTOME_IRAK2_MEDIATED	REACTOME_IRAK2_MEDIATED_ACTIVATION_OF_TAK1_COMI	0.79	>=0.20
REACTOME_IRON_UPTAKE_AI	REACTOME_IRON_UPTAKE_AND_TRANSPORT	0.28	>=0.20
REACTOME_IRS:MEDIATED_SI	REACTOME_IRS:MEDIATED_SIGNALLING	0.06	>=0.20
REACTOME_IRS:RELATED_EVE	REACTOME_IRS:RELATED_EVENTS	0.06	>=0.20
REACTOME_ISG15_ANTIVIRAL	REACTOME_ISG15_ANTIVIRAL_MECHANISM	0.74	>=0.20
REACTOME_JNK_C:JUN_KINAS	REACTOME_JNK_C:JUN_KINASES_PHOSPHORYLATION_AND_	0.86	>=0.20
REACTOME_KINESINS	REACTOME_KINESINS	0.97	>=0.20
REACTOME_L13A:MEDIATED_	REACTOME_L13A:MEDIATED_TRANSLATIONAL_SILENCING_C	0.86	>=0.20
REACTOME_L1CAM_INTERAC	REACTOME_L1CAM_INTERACTIONS	0.8	>=0.20
REACTOME_LAGGING_STRAN	REACTOME_LAGGING_STRAND_SYNTHESIS	0.93	>=0.20
REACTOME_LEADING_STRANI	REACTOME_LEADING_STRAND_SYNTHESIS	0.88	>=0.20
REACTOME_LIGAND:GATED_I	REACTOME_LIGAND:GATED_ION_CHANNEL_TRANSPORT	1	>=0.20
REACTOME_LOSS_OF_NLP_FF	REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	0.25	>=0.20
REACTOME_LOSS_OF_PROTEI	REACTOME_LOSS_OF_PROTEINS_REQUIRED_FOR_INTERPHA	0.25	>=0.20
REACTOME_LYSOSOME_VESIC	REACTOME_LYSOSOME_VESICLE_BIOGENESIS	0.34	>=0.20
REACTOME_M_PHASE	REACTOME_M_PHASE	0.4	>=0.20
REACTOME_MAP_KINASE_AC	REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	0.04	>=0.20
REACTOME_MAPK_TARGETS_	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_	0.05	>=0.20
REACTOME_MEIOSIS	REACTOME_MEIOSIS	1	>=0.20
REACTOME_MEIOTIC_RECOM	REACTOME_MEIOTIC_RECOMBINATION	1	>=0.20
REACTOME_MEIOTIC_SYNAPS	REACTOME_MEIOTIC_SYNAPSIS	0.98	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_MRNA	0.59	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_NON:CODING_RNA	0.88	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_NUCLEOTIDES	0.23	>=0.20
REACTOME_METABOLISM_OF	REACTOME_METABOLISM_OF_PORPHYRINS	0.4	>=0.20
REACTOME_METAL_ION_SLC_	REACTOME_METAL_ION_SLC_TRANSPORTERS	0.03	>=0.20
REACTOME_MG1_TRANSITIOI	REACTOME_MG1_TRANSITION	0.78	>=0.20

REACTOME_MICRORNA_MIRI	REACTOME_MICRORNA_MIRNA_BIOGENESIS	0.36	>=0.20
REACTOME_MITOTIC_G1:G1S	REACTOME_MITOTIC_G1:G1S_PHASES	0.57	>=0.20
REACTOME_MITOTIC_G2:G2M	REACTOME_MITOTIC_G2:G2M_PHASES	0.26	>=0.20
REACTOME_MITOTIC_M:MG1	REACTOME_MITOTIC_M:MG1_PHASES	0.63	>=0.20
REACTOME_MITOTIC_PROME	REACTOME_MITOTIC_PROMETAPHASE	0.46	>=0.20
REACTOME_MITOTIC_SPINDL	REACTOME_MITOTIC_SPINDLE_CHECKPOINT	0.77	>=0.20
REACTOME_MRNA_CAPPING	REACTOME_MRNA_CAPPING	0.77	>=0.20
REACTOME_MRNA_DECAY_B'	REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE	0.84	>=0.20
REACTOME_MTOR_SIGNALLIN	REACTOME_MTOR_SIGNALLING	0.08	>=0.20
REACTOME_MUSCLE_CONTRA	REACTOME_MUSCLE_CONTRACTION	0.75	>=0.20
REACTOME_MYOGENESIS	REACTOME_MYOGENESIS	0.89	>=0.20
REACTOME_N:GLYCAN_ANTEI	REACTOME_N:GLYCAN_ANTENNAE_ELONGATION	0.87	>=0.20
REACTOME_N:GLYCAN_ANTEI	REACTOME_N:GLYCAN_ANTENNAE_ELONGATION_IN_THE_M	0.89	>=0.20
REACTOME_NACL:_DEPENDEI	REACTOME_NACL:_DEPENDENT_NEUROTRANSMITTER_TRAN	0.58	>=0.20
REACTOME_NCAM_SIGNALIN	REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT:GROWT	0.99	>=0.20
REACTOME_NCAM1_INTERAC	REACTOME_NCAM1_INTERACTIONS	1	>=0.20
REACTOME_NEF:MEDIATES_D	REACTOME_NEF:MEDIATES_DOWN_MODULATION_OF_CELL	0.5	>=0.20
REACTOME_NEF_MEDIATED_	REACTOME_NEF_MEDIATED_DOWNREGULATION_OF_MHC_	0.78	>=0.20
REACTOME_NEGATIVE_REGU	REACTOME_NEGATIVE_REGULATION_OF_FGFR_SIGNALING	0.36	>=0.20
REACTOME_NEGATIVE_REGU	REACTOME_NEGATIVE_REGULATORS_OF_RIG:IMDA5_SIGNA	0.42	>=0.20
REACTOME_NEPHRIN_INTERA	REACTOME_NEPHRIN_INTERACTIONS	0.85	>=0.20
REACTOME_NETRIN:1_SIGNAI	REACTOME_NETRIN:1_SIGNALING	1	>=0.20
REACTOME_NEURONAL_SYST	REACTOME_NEURONAL_SYSTEM	1	>=0.20
REACTOME_NEUROTRANSMI	REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND	1	>=0.20
REACTOME_NEUROTRANSMI	REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	0.93	>=0.20
REACTOME_NF:KB_ACTIVATIC	REACTOME_NF:KB_ACTIVATION_THROUGH_FADDRIP:1_PAT	0.38	>=0.20
REACTOME_NF:KB_IS_ACTIVA	REACTOME_NF:KB_IS_ACTIVATED_AND_SIGNALS_SURVIVAL	0.78	>=0.20
REACTOME_NICD_TRAFFICS_T	REACTOME_NICD_TRAFFICS_TO_NUCLEUS	0.38	>=0.20
REACTOME_NITRIC_OXIDE_ST	REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLA	0.67	>=0.20
REACTOME_NOD12_SIGNALIN	REACTOME_NOD12_SIGNALING_PATHWAY	0.34	>=0.20
REACTOME_NONSENSE:MEDI	REACTOME_NONSENSE:MEDIATED_DECAY	0.88	>=0.20
REACTOME_NONSENSE_MED	REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_	0.88	>=0.20
REACTOME_NONSENSE_MED	REACTOME_NONSENSE_MEDIATED_DECAY_INDEPENDENT_(	0.92	>=0.20
REACTOME_NOREPINEPHRINI	REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEA	1	>=0.20
REACTOME_NOTCH:HLH_TRA	REACTOME_NOTCH:HLH_TRANSCRIPTION_PATHWAY	0.38	>=0.20
REACTOME_NRAGE_SIGNALS_	REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	0.51	>=0.20
REACTOME_NRIF_SIGNALS_CI	REACTOME_NRIF_SIGNALS_CELL_DEATH_FROM_THE_NUCLE	0.9	>=0.20
REACTOME_NUCLEAR_SIGNAI	REACTOME_NUCLEAR_SIGNALING_BY_ERBB4	0.19	>=0.20
REACTOME_NUCLEOSOME_A	REACTOME_NUCLEOSOME_ASSEMBLY	0.97	>=0.20
REACTOME_NUCLEOTIDE:BIN	REACTOME_NUCLEOTIDE:BINDING_DOMAIN_LEUCINE_RICH	0.31	>=0.20
REACTOME_NUCLEOTIDE:LIKE	REACTOME_NUCLEOTIDE:LIKE_PURINERGIC_RECEPTORS	0.89	>=0.20
REACTOME_NUCLEOTIDE_EX(	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	0.92	>=0.20
REACTOME_O:LINKED_GLYCO	REACTOME_O:LINKED_GLYCOSYLATION_OF_MUCINS	0.81	>=0.20
REACTOME_OLFACTORY_SIGN	REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.99	>=0.20
REACTOME_OPIOID_SIGNALL	REACTOME_OPIOID_SIGNALLING	0.84	>=0.20
REACTOME_ORC1_REMOVAL_	REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	0.6	>=0.20
REACTOME_ORGANIC_CATIOI	REACTOME_ORGANIC_CATIONANIONZWITTERION_TRANSPC	0.76	>=0.20

REACTOME_OTHER_SEMAPH(	REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	0.82	>=0.20
REACTOME_P2Y_RECEPTORS	REACTOME_P2Y_RECEPTORS	0.93	>=0.20
REACTOME_P38MAPK_EVENT	REACTOME_P38MAPK_EVENTS	0.26	>=0.20
REACTOME_P53:DEPENDENT_	REACTOME_P53:DEPENDENT_G1_DNA_DAMAGE_RESPONSE	0.7	>=0.20
REACTOME_P53:DEPENDENT_	REACTOME_P53:DEPENDENT_G1S_DNA_DAMAGE_CHECKPC	0.7	>=0.20
REACTOME_P75_NTR_RECEPT	REACTOME_P75_NTR_RECEPTOR:MEDIATED_SIGNALLING	0.43	>=0.20
REACTOME_P75NTR_RECRUIT	REACTOME_P75NTR_RECRUITS_SIGNALLING_COMPLEXES	0.92	>=0.20
REACTOME_P75NTR_SIGNALS	REACTOME_P75NTR_SIGNALS_VIA_NF:KB	0.77	>=0.20
REACTOME_PACKAGING_OF_	REACTOME_PACKAGING_OF_TELOMERE_ENDS	0.98	>=0.20
REACTOME_PAUSING_AND_R	REACTOME_PAUSING_AND_RECOVERY_OF_ELONGATION	0.07	>=0.20
REACTOME_PAUSING_AND_R	REACTOME_PAUSING_AND_RECOVERY_OF_HIV:1_ELONGAT	0.07	>=0.20
REACTOME_PAUSING_AND_R	REACTOME_PAUSING_AND_RECOVERY_OF_TAT:MEDIATED_	0.06	>=0.20
REACTOME_PD:1_SIGNALING	REACTOME_PD:1_SIGNALING	0.88	>=0.20
REACTOME_PECAM1_INTERA	REACTOME_PECAM1_INTERACTIONS	0.42	>=0.20
REACTOME_PEPTIDE_CHAIN_	REACTOME_PEPTIDE_CHAIN_ELONGATION	0.88	>=0.20
REACTOME_PEPTIDE_HORMC	REACTOME_PEPTIDE_HORMONE_BIOSYNTHESIS	0.87	>=0.20
REACTOME_PEPTIDE_LIGAND	REACTOME_PEPTIDE_LIGAND:BINDING_RECEPTORS	0.64	>=0.20
REACTOME_PERK_REGULATEI	REACTOME_PERK_REGULATED_GENE_EXPRESSION	0.39	>=0.20
REACTOME_PHOSPHOLIPASE_	REACTOME_PHOSPHOLIPASE_C:MEDIATED_CASCADE	0.73	>=0.20
REACTOME_PHOSPHORYLATI(	REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_C	0.97	>=0.20
REACTOME_PHOSPHORYLATI(	REACTOME_PHOSPHORYLATION_OF_THE_APCC	0.83	>=0.20
REACTOME_PI:3K_CASCADE	REACTOME_PI:3K_CASCADE	0.04	>=0.20
REACTOME_PI3K_CASCADE	REACTOME_PI3K_CASCADE	0.1	>=0.20
REACTOME_PIP3_ACTIVATES_	REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	0.03	>=0.20
REACTOME_PKA:MEDIATED_F	REACTOME_PKA:MEDIATED_PHOSPHORYLATION_OF_CREB	0.76	>=0.20
REACTOME_PKA_ACTIVATION	REACTOME_PKA_ACTIVATION	0.65	>=0.20
REACTOME_PKA_ACTIVATION	REACTOME_PKA_ACTIVATION_IN_GLUCAGON_SIGNALLING	0.6	>=0.20
REACTOME_PKB:MEDIATED_E	REACTOME_PKB:MEDIATED_EVENTS	0.03	>=0.20
REACTOME_PLATELET_ADHES	REACTOME_PLATELET_ADHESION_TO_EXPOSED_COLLAGEN	0.2	>=0.20
REACTOME_PLATELET_CALCIU	REACTOME_PLATELET_CALCIUM_HOMEOSTASIS	0.46	>=0.20
REACTOME_PLATELET_HOME	REACTOME_PLATELET_HOMEOSTASIS	0.17	>=0.20
REACTOME_PLC:GAMMA1_SI	REACTOME_PLC:GAMMA1_SIGNALLING	0.72	>=0.20
REACTOME_PLC_BETA_MEDIA	REACTOME_PLC_BETA_MEDIATED_EVENTS	0.86	>=0.20
REACTOME_PLCG1_EVENTS_I	REACTOME_PLCG1_EVENTS_IN_ERBB2_SIGNALING	0.68	>=0.20
REACTOME_POLYMERASE_SW	REACTOME_POLYMERASE_SWITCHING	0.88	>=0.20
REACTOME_POLYMERASE_SW	REACTOME_POLYMERASE_SWITCHING_ON_THE_C:STRAND_	0.88	>=0.20
REACTOME_POST:CHAPERON	REACTOME_POST:CHAPERONIN_TUBULIN_FOLDING_PATHW	0.84	>=0.20
REACTOME_POST:TRANSLATI(	REACTOME_POST:TRANSLATIONAL_MODIFICATION_SYNTHE	0.83	>=0.20
REACTOME_POST_NMDA_RE(	REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	1	>=0.20
REACTOME_POSTSYNAPTIC_N	REACTOME_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RE(	0.92	>=0.20
REACTOME_POTASSIUM_CHA	REACTOME_POTASSIUM_CHANNELS	1	>=0.20
REACTOME_PREFOLDIN_MED	REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRA	0.62	>=0.20
REACTOME_PRESYNAPTIC_FU	REACTOME_PRESYNAPTIC_FUNCTION_OF_KAINATE_RECEPT(	1	>=0.20
REACTOME_PRESYNAPTIC_NI	REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECE	0.97	>=0.20
REACTOME_PROCESSING_OF_	REACTOME_PROCESSING_OF_INTRONLESS_PRE:MRNAS	0.49	>=0.20
REACTOME_PROCESSIVE_SYN	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_C:STRAND_OI	0.93	>=0.20
REACTOME_PROCESSIVE_SYN	REACTOME_PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STI	0.95	>=0.20

REACTOME_PROLACTIN_RECE	REACTOME_PROLACTIN_RECEPTOR_SIGNALING	0.05	>=0.20
REACTOME_PROSTACYCLIN_S	REACTOME_PROSTACYCLIN_SIGNALLING_THROUGH_PROSTA	0.97	>=0.20
REACTOME_PROTEIN_FOLDIN	REACTOME_PROTEIN_FOLDING	0.51	>=0.20
REACTOME_PROTEOLYTIC_CL	REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX	0.95	>=0.20
REACTOME_PURINE_METABC	REACTOME_PURINE_METABOLISM	0.2	>=0.20
REACTOME_PURINE_RIBONU	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_	0.94	>=0.20
REACTOME_PURINE_SALVAGE	REACTOME_PURINE_SALVAGE	0.25	>=0.20
REACTOME_PYRIMIDINE_MET	REACTOME_PYRIMIDINE_METABOLISM	0.25	>=0.20
REACTOME_PYRUVATE_META	REACTOME_PYRUVATE_METABOLISM	0.09	>=0.20
REACTOME_PYRUVATE_META	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TC	0.1	>=0.20
REACTOME_RAP1_SIGNALLIN	REACTOME_RAP1_SIGNALLING	0.45	>=0.20
REACTOME_RAS_ACTIVATION	REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH	1	>=0.20
REACTOME_RECRUITMENT_O	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PR(	0.27	>=0.20
REACTOME_RECRUITMENT_O	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTR	0.47	>=0.20
REACTOME_RECYCLING_PATH	REACTOME_RECYCLING_PATHWAY_OF_L1	0.09	>=0.20
REACTOME_REGULATED_PRO	REACTOME_REGULATED_PROTEOLYSIS_OF_P75NTR	0.49	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_ACTIVATED_PAK:2P34_BY_PR(	0.71	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_AMPK_ACTIVITY_VIA_LKB1	0.17	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_APCC_ACTIVATORS_BETWEEN	0.67	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_APOPTOSIS	0.86	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_DNA_REPLICATION	0.5	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_IFNA_SIGNALING	0.28	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_IFNG_SIGNALING	0.1	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_INSULIN_SECRETION	0.97	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_ACE	0.86	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_INSULIN_SECRETION_BY_GLU(	0.99	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_KIT_SIGNALING	0.17	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	0.74	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEI	0.58	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_	0.72	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENASE_	0.17	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_SIGNALING_BY_CBL	0.2	>=0.20
REACTOME_REGULATION_OF	REACTOME_REGULATION_OF_WATER_BALANCE_BY_RENAL_	0.89	>=0.20
REACTOME_REGULATORY_RN	REACTOME_REGULATORY_RNA_PATHWAYS	0.36	>=0.20
REACTOME_REMOVAL_OF_LI	REACTOME_REMOVAL_OF_LICENSING_FACTORS_FROM_ORI	0.61	>=0.20
REACTOME_REMOVAL_OF_TH	REACTOME_REMOVAL_OF_THE_FLAP_INTERMEDIATE	0.97	>=0.20
REACTOME_REPAIR_SYNTHES	REACTOME_REPAIR_SYNTHESIS_FOR_GAP:FILLING_BY_DNA_	0.94	>=0.20
REACTOME_REPAIR_SYNTHES	REACTOME_REPAIR_SYNTHESIS_OF_PATCH_27:30_BASES_LO	0.94	>=0.20
REACTOME_RESPIRATORY_EL	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.99	>=0.20
REACTOME_RESPIRATORY_EL	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYN	0.97	>=0.20
REACTOME_RETROGRADE_NE	REACTOME_RETROGRADE_NEUROTROPHIN_SIGNALLING	0.16	>=0.20
REACTOME_RHO_GTPASE_CY	REACTOME_RHO_GTPASE_CYCLE	0.25	>=0.20
REACTOME_RIBOSOMAL_SCA	REACTOME_RIBOSOMAL_SCANNING_AND_START_CODON_F	0.85	>=0.20
REACTOME_RIG:IMDA5_MED	REACTOME_RIG:IMDA5_MEDIATED_INDUCTION_OF_IFN:ALF	0.21	>=0.20
REACTOME_RNA_POL_II_CTD	REACTOME_RNA_POL_II_CTD_PHOSPHORYLATION_AND_INT	0.76	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_CHAIN_ELONGATION	0.99	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_PROMOTER_CLEARANCE	0.99	>=0.20

REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_PROMOTER_ESCAPE	0.99	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_PROMOTER_OPENING	0.93	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_RNA_POLYMERASE_III_AN	0.9	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION	0.98	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATIC	0.98	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINA	0.98	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_HIV:1_PROMOTER_ESCAP	0.72	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_PRE:TRANSCRIPTION_EVE	0.3	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_PROMOTER_ESCAPE	0.72	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_ELONGA	0.26	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_INITIATI	0.72	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_INITIATI	0.72	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_PRE:INIT	0.72	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_ABORTIVE_AND_RETRAC	0.74	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	0.99	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION	0.74	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT	0.95	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT	0.98	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT	0.99	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIAT	0.93	>=0.20
REACTOME_RNA_POLYMERAS	REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMIN	0.81	>=0.20
REACTOME_S_PHASE	REACTOME_S_PHASE	0.75	>=0.20
REACTOME_SCF:BETA:TRCP_M	REACTOME_SCF:BETA:TRCP_MEDIATED_DEGRADATION_OF_	0.66	>=0.20
REACTOME_SCFSKP2:MEDIAT	REACTOME_SCFSKP2:MEDIATED_DEGRADATION_OF_P27P21	0.58	>=0.20
REACTOME_SEMA3A_PAK_DE	REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	0.19	>=0.20
REACTOME_SEMA4D_IN_SEM	REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	0.1	>=0.20
REACTOME_SEMA4D_INDUCE	REACTOME_SEMA4D_INDUCED_CELL_MIGRATION_AND_GR	0.43	>=0.20
REACTOME_SEMAPHORIN_IN	REACTOME_SEMAPHORIN_INTERACTIONS	0.12	>=0.20
REACTOME_SEROTONIN_NEU	REACTOME_SEROTONIN_NEUROTRANSMITTER_RELEASE_CY	1	>=0.20
REACTOME_SEROTONIN_REC	REACTOME_SEROTONIN_RECEPTORS	1	>=0.20
REACTOME_SHC:MEDIATED_C	REACTOME_SHC:MEDIATED_CASCADE	0.61	>=0.20
REACTOME_SHC1_EVENTS_IN	REACTOME_SHC1_EVENTS_IN_ERBB4_SIGNALING	0.19	>=0.20
REACTOME_SIGNAL_AMPLIFI	REACTOME_SIGNAL_AMPLIFICATION	0.71	>=0.20
REACTOME_SIGNAL_TRANSDU	REACTOME_SIGNAL_TRANSDUCTION_BY_L1	0.09	>=0.20
REACTOME_SIGNALING_BY_B	REACTOME_SIGNALING_BY_BMP	0.92	>=0.20
REACTOME_SIGNALING_BY_E	REACTOME_SIGNALING_BY_EGFR	0.03	>=0.20
REACTOME_SIGNALING_BY_E	REACTOME_SIGNALING_BY_ERBB2	0.03	>=0.20
REACTOME_SIGNALING_BY_F	REACTOME_SIGNALING_BY_FGFR	0.04	>=0.20
REACTOME_SIGNALING_BY_IN	REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	0.13	>=0.20
REACTOME_SIGNALING_BY_N	REACTOME_SIGNALING_BY_NODAL	0.11	>=0.20
REACTOME_SIGNALING_BY_N	REACTOME_SIGNALING_BY_NOTCH	0.17	>=0.20
REACTOME_SIGNALING_BY_P	REACTOME_SIGNALING_BY_PDGF	0.08	>=0.20
REACTOME_SIGNALING_BY_R	REACTOME_SIGNALING_BY_RHO_GTPASES	0.25	>=0.20
REACTOME_SIGNALING_BY_R	REACTOME_SIGNALING_BY_ROBO_RECEPTOR	0.99	>=0.20
REACTOME_SIGNALING_BY_T	REACTOME_SIGNALING_BY_TGF_BETA	0.2	>=0.20
REACTOME_SIGNALING_BY_W	REACTOME_SIGNALING_BY_WNT	0.4	>=0.20
REACTOME_SIGNALLING_TO_	REACTOME_SIGNALLING_TO_ERKS	0.32	>=0.20

REACTOME_SIGNALLING_TO_	REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN	0.61	>=0.20
REACTOME_SIGNALLING_TO_	REACTOME_SIGNALLING_TO_RAS	0.23	>=0.20
REACTOME_SLC:MEDIATED_T	REACTOME_SLC:MEDIATED_TRANSMEMBRANE_TRANSPORT	0.19	>=0.20
REACTOME_SMOOTH_MUSCL	REACTOME_SMOOTH_MUSCLE_CONTRACTION	0.39	>=0.20
REACTOME_SNRNP_ASSEMBL	REACTOME_SNRNP_ASSEMBLY	0.88	>=0.20
REACTOME_SPHINGOLIPID_D	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	0.87	>=0.20
REACTOME_SRP:DEPENDENT_	REACTOME_SRP:DEPENDENT_COTRANSLATIONAL_PROTEIN_	0.73	>=0.20
REACTOME_STABILIZATION_C	REACTOME_STABILIZATION_OF_P53	0.75	>=0.20
REACTOME_STRIATED_MUSCL	REACTOME_STRIATED_MUSCLE_CONTRACTION	0.91	>=0.20
REACTOME_SWITCHING_OF_(	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST:REPLICAT	0.6	>=0.20
REACTOME_SYNTHESIS_AND_	REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLE	0.91	>=0.20
REACTOME_SYNTHESIS_OF_D	REACTOME_SYNTHESIS_OF_DNA	0.73	>=0.20
REACTOME_SYNTHESIS_OF_G	REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSIT	0.91	>=0.20
REACTOME_SYNTHESIS_OF_S	REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N:GLYCAN_BIO	0.47	>=0.20
REACTOME_SYNTHESIS_SECRI	REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_	0.19	>=0.20
REACTOME_SYNTHESIS_SECRI	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF	0.37	>=0.20
REACTOME_SYNTHESIS_SECRI	REACTOME_SYNTHESIS_SECRETION_AND_INACTIVATION_OF	0.92	>=0.20
REACTOME_TAK1_ACTIVATES_	REACTOME_TAK1_ACTIVATES_NFKB_BY_PHOSPHORYLATION	0.13	>=0.20
REACTOME_TANDEM_PORE_I	REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNE	0.71	>=0.20
REACTOME_TAT:MEDIATED_E	REACTOME_TAT:MEDIATED_ELONGATION_OF_THE_HIV:1_TI	0.25	>=0.20
REACTOME_TAT:MEDIATED_H	REACTOME_TAT:MEDIATED_HIV:1_ELONGATION_ARREST_AI	0.06	>=0.20
REACTOME_TCR_SIGNALING	REACTOME_TCR_SIGNALING	0.85	>=0.20
REACTOME_TELOMERE_C:STR	REACTOME_TELOMERE_C:STRAND_LAGGING_STRAND_SYNT	0.92	>=0.20
REACTOME_TELOMERE_MAIN	REACTOME_TELOMERE_MAINTENANCE	0.9	>=0.20
REACTOME_TERMINATION_O	REACTOME_TERMINATION_OF_O:GLYCAN_BIOSYNTHESIS	0.06	>=0.20
REACTOME_TETRAHYDROBIO	REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYC	0.08	>=0.20
REACTOME_THE_CITRIC_ACID	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATOI	0.74	>=0.20
REACTOME_THE_NLRP3_INFL	REACTOME_THE_NLRP3_INFLAMMASOME	0.42	>=0.20
REACTOME_THE_ROLE_OF_N	REACTOME_THE_ROLE_OF_NEF_IN_HIV:1_REPLICATION_AN	0.41	>=0.20
REACTOME_THROMBIN_SIGN	REACTOME_THROMBIN_SIGNALLING_THROUGH_PROTEINAS	0.56	>=0.20
REACTOME_THROMBOXANE_	REACTOME_THROMBOXANE_SIGNALLING_THROUGH_TP_RE	0.98	>=0.20
REACTOME_TIGHT_JUNCTION	REACTOME_TIGHT_JUNCTION_INTERACTIONS	0.95	>=0.20
REACTOME_TOLL_LIKE_RECEI	REACTOME_TOLL_LIKE_RECEPTOR_3_TLR3_CASCADE	0.04	>=0.20
REACTOME_TRAF3:DEPENDEN	REACTOME_TRAF3:DEPENDENT_IRF_ACTIVATION_PATHWAY	0.55	>=0.20
REACTOME_TRAF6_MEDIATEI	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_PROINFLAM	0.03	>=0.20
REACTOME_TRAF6_MEDIATEI	REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	0.56	>=0.20
REACTOME_TRAF6_MEDIATEI	REACTOME_TRAF6_MEDIATED_NF:KB_ACTIVATION	0.05	>=0.20
REACTOME_TRAFFICKING_OF	REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	0.98	>=0.20
REACTOME_TRAFFICKING_OF	REACTOME_TRAFFICKING_OF_GLUR2:CONTAINING_AMPA_R	0.57	>=0.20
REACTOME_TRANSCRIPTION	REACTOME_TRANSCRIPTION	0.26	>=0.20
REACTOME_TRANSCRIPTION:(	REACTOME_TRANSCRIPTION:COUPLED_NER_TC:NER	0.87	>=0.20
REACTOME_TRANSCRIPTION_	REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	0.29	>=0.20
REACTOME_TRANSFERRIN_EN	REACTOME_TRANSFERRIN_ENDOCYTOSIS_AND_RECYCLING	0.45	>=0.20
REACTOME_TRANSLATION	REACTOME_TRANSLATION	0.53	>=0.20
REACTOME_TRANSLATION_IN	REACTOME_TRANSLATION_INITIATION_COMPLEX_FORMATI	0.83	>=0.20
REACTOME_TRANSLOCATION	REACTOME_TRANSLOCATION_OF_ZAP:70_TO_IMMUNOLOG	0.99	>=0.20
REACTOME_TRANSMEMBRAN	REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MC	0.36	>=0.20

REACTOME_TRANSMISSION_A	REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	1	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGAR	0.17	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_INORGANIC_CATIONSANIONS_	0.76	>=0.20
REACTOME_TRANSPORT_OF_	REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATU	0.78	>=0.20
REACTOME_TRIF_MEDIATED_	REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	0.04	>=0.20
REACTOME_TRNA_AMINOAC	REACTOME_TRNA_AMINOACYLATION	0.61	>=0.20
REACTOME_UBIQUITIN:DEPEI	REACTOME_UBIQUITIN:DEPENDENT_DEGRADATION_OF_CYC	0.68	>=0.20
REACTOME_UBIQUITIN:DEPEI	REACTOME_UBIQUITIN:DEPENDENT_DEGRADATION_OF_CYC	0.68	>=0.20
REACTOME_UNBLOCKING_OF	REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMA	1	>=0.20
REACTOME_UNWINDING_OF_	REACTOME_UNWINDING_OF_DNA	0.93	>=0.20
REACTOME_VIF:MEDIATED_D	REACTOME_VIF:MEDIATED_DEGRADATION_OF_APOBEC3G	0.71	>=0.20
REACTOME_VIRAL_MESSENGI	REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	0.63	>=0.20
REACTOME_VIRAL_MRNA_TR	REACTOME_VIRAL_MRNA_TRANSLATION	0.92	>=0.20
REACTOME_VOLTAGE_GATED	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	1	>=0.20
REACTOME_VPR:MEDIATED_I	REACTOME_VPR:MEDIATED_NUCLEAR_IMPORT_OF_PICS	0.71	>=0.20
REACTOME_VPU_MEDIATED_	REACTOME_VPU_MEDIATED_DEGRADATION_OF_CD4	0.68	>=0.20
REACTOME_ZINC_INFLUX_INT	REACTOME_ZINC_INFLUX_INTO_CELLS_BY_THE_SLC39_GENI	0.09	>=0.20
REACTOME_ZINC_TRANSPORT	REACTOME_ZINC_TRANSPORTERS	0.23	>=0.20
GO:0048019	receptor antagonist activity	0.71	>=0.20
GO:0043113	receptor clustering	1	>=0.20
GO:0043235	receptor complex	0.14	>=0.20
GO:0030547	receptor inhibitor activity	0.71	>=0.20
GO:0030159	receptor signaling complex scaffold activity	0.35	>=0.20
GO:0005057	receptor signaling protein activity	0.44	>=0.20
GO:0004702	receptor signaling protein serine/threonine kinase activity	0.22	>=0.20
GO:0035825	reciprocal DNA recombination	1	>=0.20
GO:0007131	reciprocal meiotic recombination	1	>=0.20
GO:0000725	recombinational repair	0.93	>=0.20
ENSG00000004700	RECQL PPI subnetwork	0.98	>=0.20
GO:0055037	recycling endosome	0.06	>=0.20
GO:0055038	recycling endosome membrane	0.52	>=0.20
MP:0005172	reduced eye pigmentation	0.51	>=0.20
MP:0001921	reduced fertility	0.19	>=0.20
MP:0004814	reduced linear vestibular evoked potential	1	>=0.20
MP:0001475	reduced long term depression	1	>=0.20
MP:0001473	reduced long term potentiation	1	>=0.20
MP:0001922	reduced male fertility	0.9	>=0.20
MP:0001380	reduced male mating frequency	0.97	>=0.20
ENSG00000068615	REEP1 PPI subnetwork	0.11	>=0.20
ENSG00000165476	REEP3 PPI subnetwork	0.51	>=0.20
ENSG00000168476	REEP4 PPI subnetwork	0.25	>=0.20
ENSG00000129625	REEP5 PPI subnetwork	0.69	>=0.20
GO:0003002	regionalization	1	>=0.20
GO:0045055	regulated secretory pathway	0.82	>=0.20
GO:0010510	regulation of acetyl-CoA biosynthetic process from pyruvate	0.65	>=0.20
GO:0032956	regulation of actin cytoskeleton organization	0.57	>=0.20
GO:0032970	regulation of actin filament-based process	0.59	>=0.20

GO:0030834	regulation of actin filament depolymerization	0.42	>=0.20
GO:0030832	regulation of actin filament length	0.5	>=0.20
GO:0030833	regulation of actin filament polymerization	0.44	>=0.20
GO:0008064	regulation of actin polymerization or depolymerization	0.51	>=0.20
GO:0001508	regulation of action potential	1	>=0.20
GO:0019228	regulation of action potential in neuron	1	>=0.20
GO:0046006	regulation of activated T cell proliferation	0.7	>=0.20
GO:0032925	regulation of activin receptor signaling pathway	0.86	>=0.20
GO:0002673	regulation of acute inflammatory response	0.56	>=0.20
GO:0002819	regulation of adaptive immune response	0.96	>=0.20
GO:0002822	regulation of adaptive immune response based on somatic re	0.96	>=0.20
GO:0045761	regulation of adenylate cyclase activity	1	>=0.20
GO:0010578	regulation of adenylate cyclase activity involved in G-protein	0.96	>=0.20
GO:2000311	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole pı	1	>=0.20
GO:0046634	regulation of alpha-beta T cell activation	0.92	>=0.20
GO:0046637	regulation of alpha-beta T cell differentiation	0.58	>=0.20
GO:0046640	regulation of alpha-beta T cell proliferation	0.99	>=0.20
GO:0000381	regulation of alternative nuclear mRNA splicing, via spliceoso	0.97	>=0.20
GO:0051952	regulation of amine transport	0.99	>=0.20
GO:0022603	regulation of anatomical structure morphogenesis	0.31	>=0.20
GO:0090066	regulation of anatomical structure size	0.15	>=0.20
GO:0045765	regulation of angiogenesis	0.03	>=0.20
GO:0002577	regulation of antigen processing and presentation	0.8	>=0.20
GO:0032098	regulation of appetite	0.77	>=0.20
GO:0032312	regulation of ARF GTPase activity	0.34	>=0.20
GO:0032012	regulation of ARF protein signal transduction	0.27	>=0.20
GO:0048710	regulation of astrocyte differentiation	0.89	>=0.20
GO:0030516	regulation of axon extension	0.97	>=0.20
GO:0048841	regulation of axon extension involved in axon guidance	0.85	>=0.20
GO:0050770	regulation of axonogenesis	1	>=0.20
GO:0050864	regulation of B cell activation	0.51	>=0.20
GO:0045577	regulation of B cell differentiation	0.15	>=0.20
GO:0002712	regulation of B cell mediated immunity	0.93	>=0.20
GO:0030888	regulation of B cell proliferation	0.68	>=0.20
GO:0050795	regulation of behavior	0.95	>=0.20
GO:0051098	regulation of binding	0.03	>=0.20
GO:0070167	regulation of biomineral tissue development	0.96	>=0.20
GO:0008217	regulation of blood pressure	0.36	>=0.20
GO:0043535	regulation of blood vessel endothelial cell migration	0.43	>=0.20
GO:0050880	regulation of blood vessel size	0.13	>=0.20
GO:0030510	regulation of BMP signaling pathway	0.89	>=0.20
GO:0030500	regulation of bone mineralization	0.95	>=0.20
GO:0051924	regulation of calcium ion transport	1	>=0.20
GO:0051925	regulation of calcium ion transport via voltage-gated calcium	1	>=0.20
GO:0030817	regulation of cAMP biosynthetic process	1	>=0.20
GO:0030814	regulation of cAMP metabolic process	1	>=0.20
GO:0060828	regulation of canonical Wnt receptor signaling pathway	1	>=0.20

GO:0055117	regulation of cardiac muscle contraction	0.98	>=0.20
GO:0055024	regulation of cardiac muscle tissue development	0.93	>=0.20
GO:0051890	regulation of cardioblast differentiation	0.95	>=0.20
GO:0061035	regulation of cartilage development	0.51	>=0.20
GO:0050433	regulation of catecholamine secretion	0.98	>=0.20
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	0.78	>=0.20
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	0.78	>=0.20
GO:0010810	regulation of cell-substrate adhesion	0.8	>=0.20
GO:0050865	regulation of cell activation	0.13	>=0.20
GO:0030155	regulation of cell adhesion	0.15	>=0.20
GO:0071156	regulation of cell cycle arrest	0.58	>=0.20
GO:0010564	regulation of cell cycle process	0.56	>=0.20
GO:0060284	regulation of cell development	1	>=0.20
GO:0010453	regulation of cell fate commitment	0.93	>=0.20
GO:0042659	regulation of cell fate specification	0.58	>=0.20
GO:0001558	regulation of cell growth	0.17	>=0.20
GO:0031341	regulation of cell killing	1	>=0.20
GO:0022604	regulation of cell morphogenesis	0.9	>=0.20
GO:0010769	regulation of cell morphogenesis involved in differentiation	1	>=0.20
GO:0031344	regulation of cell projection organization	1	>=0.20
GO:0008360	regulation of cell shape	0.3	>=0.20
GO:0008361	regulation of cell size	0.96	>=0.20
GO:0033238	regulation of cellular amine metabolic process	0.96	>=0.20
GO:0006521	regulation of cellular amino acid metabolic process	0.96	>=0.20
GO:0044087	regulation of cellular component biogenesis	0.82	>=0.20
GO:0032535	regulation of cellular component size	0.8	>=0.20
GO:0060341	regulation of cellular localization	0.12	>=0.20
GO:0090287	regulation of cellular response to growth factor stimulus	0.62	>=0.20
GO:0080135	regulation of cellular response to stress	0.33	>=0.20
GO:0046605	regulation of centrosome cycle	0.75	>=0.20
GO:0010824	regulation of centrosome duplication	0.77	>=0.20
GO:0045073	regulation of chemokine biosynthetic process	1	>=0.20
GO:0032642	regulation of chemokine production	0.88	>=0.20
GO:0050920	regulation of chemotaxis	0.63	>=0.20
GO:0032330	regulation of chondrocyte differentiation	0.68	>=0.20
GO:0033044	regulation of chromosome organization	0.97	>=0.20
GO:0051983	regulation of chromosome segregation	0.97	>=0.20
GO:0051196	regulation of coenzyme metabolic process	0.74	>=0.20
GO:0051193	regulation of cofactor metabolic process	0.74	>=0.20
GO:0031279	regulation of cyclase activity	1	>=0.20
GO:0030802	regulation of cyclic nucleotide biosynthetic process	0.99	>=0.20
GO:0030799	regulation of cyclic nucleotide metabolic process	0.99	>=0.20
GO:0000079	regulation of cyclin-dependent protein kinase activity	0.79	>=0.20
GO:2000116	regulation of cysteine-type endopeptidase activity	0.17	>=0.20
GO:0001959	regulation of cytokine-mediated signaling pathway	0.1	>=0.20
GO:0042035	regulation of cytokine biosynthetic process	0.2	>=0.20
GO:0002718	regulation of cytokine production involved in immune respor	0.41	>=0.20

GO:0050707	regulation of cytokine secretion	0.63	>=0.20
GO:0032465	regulation of cytokinesis	0.98	>=0.20
GO:0051493	regulation of cytoskeleton organization	0.77	>=0.20
GO:0050688	regulation of defense response to virus	0.78	>=0.20
GO:0050691	regulation of defense response to virus by host	0.95	>=0.20
GO:0050690	regulation of defense response to virus by virus	0.81	>=0.20
GO:0050773	regulation of dendrite development	1	>=0.20
GO:0048814	regulation of dendrite morphogenesis	1	>=0.20
GO:0048638	regulation of developmental growth	0.77	>=0.20
GO:0090329	regulation of DNA-dependent DNA replication	0.98	>=0.20
GO:0051101	regulation of DNA binding	0.23	>=0.20
GO:0051052	regulation of DNA metabolic process	0.55	>=0.20
GO:0000018	regulation of DNA recombination	0.99	>=0.20
GO:0006282	regulation of DNA repair	0.96	>=0.20
GO:0006275	regulation of DNA replication	0.86	>=0.20
GO:0045995	regulation of embryonic development	0.96	>=0.20
GO:0010594	regulation of endothelial cell migration	0.28	>=0.20
GO:0001936	regulation of endothelial cell proliferation	0.27	>=0.20
GO:0007176	regulation of epidermal growth factor-activated receptor act	0.81	>=0.20
GO:0042058	regulation of epidermal growth factor receptor signaling patl	0.6	>=0.20
GO:0045682	regulation of epidermis development	0.9	>=0.20
GO:0010632	regulation of epithelial cell migration	1	>=0.20
GO:0050678	regulation of epithelial cell proliferation	0.63	>=0.20
GO:0010717	regulation of epithelial to mesenchymal transition	0.97	>=0.20
GO:0070372	regulation of ERK1 and ERK2 cascade	0.76	>=0.20
GO:0090175	regulation of establishment of planar polarity	0.97	>=0.20
GO:0090178	regulation of establishment of planar polarity involved in neu	0.99	>=0.20
GO:0060079	regulation of excitatory postsynaptic membrane potential	1	>=0.20
GO:0044062	regulation of excretion	0.9	>=0.20
GO:0017157	regulation of exocytosis	0.99	>=0.20
GO:0061387	regulation of extent of cell growth	0.96	>=0.20
GO:0045598	regulation of fat cell differentiation	0.9	>=0.20
GO:0040036	regulation of fibroblast growth factor receptor signaling path	1	>=0.20
GO:0008277	regulation of G-protein coupled receptor protein signaling pa	1	>=0.20
GO:2000045	regulation of G1/S transition of mitotic cell cycle	0.93	>=0.20
GO:0010389	regulation of G2/M transition of mitotic cell cycle	0.99	>=0.20
GO:0010470	regulation of gastrulation	0.28	>=0.20
GO:0040029	regulation of gene expression, epigenetic	0.41	>=0.20
GO:0060968	regulation of gene silencing	0.99	>=0.20
GO:0045685	regulation of glial cell differentiation	0.96	>=0.20
GO:0014013	regulation of gliogenesis	0.96	>=0.20
GO:0014048	regulation of glutamate secretion	1	>=0.20
GO:0044126	regulation of growth of symbiont in host	0.93	>=0.20
GO:0033124	regulation of GTP catabolic process	0.63	>=0.20
GO:0043087	regulation of GTPase activity	0.58	>=0.20
GO:0008016	regulation of heart contraction	0.85	>=0.20
GO:0060420	regulation of heart growth	0.92	>=0.20

GO:2000826	regulation of heart morphogenesis	0.99	>=0.20
GO:0002027	regulation of heart rate	0.99	>=0.20
GO:0031063	regulation of histone deacetylation	0.56	>=0.20
GO:0051569	regulation of histone H3-K4 methylation	0.97	>=0.20
GO:0031060	regulation of histone methylation	0.76	>=0.20
GO:0031056	regulation of histone modification	0.95	>=0.20
GO:0032844	regulation of homeostatic process	0.09	>=0.20
GO:0046883	regulation of hormone secretion	0.46	>=0.20
GO:0002920	regulation of humoral immune response	0.61	>=0.20
GO:0043122	regulation of I-kappaB kinase/NF-kappaB cascade	0.55	>=0.20
GO:0002697	regulation of immune effector process	0.2	>=0.20
GO:0050776	regulation of immune response	0.07	>=0.20
GO:0002889	regulation of immunoglobulin mediated immune response	0.95	>=0.20
GO:0002637	regulation of immunoglobulin production	0.65	>=0.20
GO:0051023	regulation of immunoglobulin secretion	0.46	>=0.20
GO:0043567	regulation of insulin-like growth factor receptor signaling pat	1	>=0.20
GO:0050796	regulation of insulin secretion	0.43	>=0.20
GO:0032647	regulation of interferon-alpha production	0.9	>=0.20
GO:0032648	regulation of interferon-beta production	0.96	>=0.20
GO:0032649	regulation of interferon-gamma production	0.82	>=0.20
GO:0032653	regulation of interleukin-10 production	0.96	>=0.20
GO:0032655	regulation of interleukin-12 production	0.79	>=0.20
GO:0032660	regulation of interleukin-17 production	1	>=0.20
GO:0045076	regulation of interleukin-2 biosynthetic process	0.63	>=0.20
GO:0032663	regulation of interleukin-2 production	0.58	>=0.20
GO:0032673	regulation of interleukin-4 production	0.74	>=0.20
GO:0032675	regulation of interleukin-6 production	0.08	>=0.20
GO:2000602	regulation of interphase of mitotic cell cycle	0.94	>=0.20
GO:0010627	regulation of intracellular protein kinase cascade	0.07	>=0.20
GO:0034765	regulation of ion transmembrane transport	1	>=0.20
GO:0032412	regulation of ion transmembrane transporter activity	1	>=0.20
GO:0043269	regulation of ion transport	1	>=0.20
GO:0045191	regulation of isotype switching	0.99	>=0.20
GO:0048302	regulation of isotype switching to IgG isotypes	1	>=0.20
GO:0046425	regulation of JAK-STAT cascade	0.68	>=0.20
GO:0046328	regulation of JNK cascade	0.15	>=0.20
GO:0090183	regulation of kidney development	0.98	>=0.20
GO:0002694	regulation of leukocyte activation	0.32	>=0.20
GO:2000106	regulation of leukocyte apoptotic process	0.57	>=0.20
GO:0002688	regulation of leukocyte chemotaxis	0.29	>=0.20
GO:0043300	regulation of leukocyte degranulation	0.64	>=0.20
GO:0001910	regulation of leukocyte mediated cytotoxicity	0.99	>=0.20
GO:0002703	regulation of leukocyte mediated immunity	0.88	>=0.20
GO:0002685	regulation of leukocyte migration	0.28	>=0.20
GO:0070663	regulation of leukocyte proliferation	0.78	>=0.20
GO:0051340	regulation of ligase activity	0.87	>=0.20
GO:0040012	regulation of locomotion	0.04	>=0.20

GO:0048169	regulation of long-term neuronal synaptic plasticity	1	>=0.20
GO:0051339	regulation of lyase activity	1	>=0.20
GO:0051249	regulation of lymphocyte activation	0.46	>=0.20
GO:0045619	regulation of lymphocyte differentiation	0.64	>=0.20
GO:0002706	regulation of lymphocyte mediated immunity	0.96	>=0.20
GO:0050670	regulation of lymphocyte proliferation	0.7	>=0.20
GO:0010743	regulation of macrophage derived foam cell differentiation	0.03	>=0.20
GO:0045649	regulation of macrophage differentiation	0.58	>=0.20
GO:0043405	regulation of MAP kinase activity	0.04	>=0.20
GO:0043408	regulation of MAPK cascade	0.08	>=0.20
GO:0033003	regulation of mast cell activation	0.91	>=0.20
GO:0033006	regulation of mast cell activation involved in immune respon	0.77	>=0.20
GO:0043304	regulation of mast cell degranulation	0.67	>=0.20
GO:0045652	regulation of megakaryocyte differentiation	0.92	>=0.20
GO:0042391	regulation of membrane potential	1	>=0.20
GO:0010464	regulation of mesenchymal cell proliferation	1	>=0.20
GO:0010959	regulation of metal ion transport	1	>=0.20
GO:0032886	regulation of microtubule-based process	0.99	>=0.20
GO:0070507	regulation of microtubule cytoskeleton organization	0.99	>=0.20
GO:0031114	regulation of microtubule depolymerization	1	>=0.20
GO:0031110	regulation of microtubule polymerization or depolymerizatio	0.99	>=0.20
GO:0046902	regulation of mitochondrial membrane permeability	0.99	>=0.20
GO:0007088	regulation of mitosis	0.71	>=0.20
GO:0007346	regulation of mitotic cell cycle	0.63	>=0.20
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.93	>=0.20
GO:0032944	regulation of mononuclear cell proliferation	0.73	>=0.20
GO:0060688	regulation of morphogenesis of a branching structure	0.98	>=0.20
GO:0050684	regulation of mRNA processing	0.75	>=0.20
GO:0043900	regulation of multi-organism process	0.68	>=0.20
GO:0051147	regulation of muscle cell differentiation	0.96	>=0.20
GO:0006937	regulation of muscle contraction	0.99	>=0.20
GO:0048634	regulation of muscle organ development	0.79	>=0.20
GO:0090257	regulation of muscle system process	0.95	>=0.20
GO:0045637	regulation of myeloid cell differentiation	0.03	>=0.20
GO:0002761	regulation of myeloid leukocyte differentiation	0.77	>=0.20
GO:0002886	regulation of myeloid leukocyte mediated immunity	0.57	>=0.20
GO:0010830	regulation of myotube differentiation	0.72	>=0.20
GO:0032814	regulation of natural killer cell activation	0.98	>=0.20
GO:0042269	regulation of natural killer cell mediated cytotoxicity	0.95	>=0.20
GO:0002715	regulation of natural killer cell mediated immunity	0.95	>=0.20
GO:0051960	regulation of nervous system development	1	>=0.20
GO:2000177	regulation of neural precursor cell proliferation	0.99	>=0.20
GO:0050767	regulation of neurogenesis	1	>=0.20
GO:0031644	regulation of neurological system process	1	>=0.20
GO:0043523	regulation of neuron apoptotic process	1	>=0.20
GO:0045664	regulation of neuron differentiation	1	>=0.20
GO:0010975	regulation of neuron projection development	1	>=0.20

GO:0048168	regulation of neuronal synaptic plasticity	1	>=0.20
GO:0001505	regulation of neurotransmitter levels	1	>=0.20
GO:0046928	regulation of neurotransmitter secretion	1	>=0.20
GO:0051588	regulation of neurotransmitter transport	1	>=0.20
GO:0045428	regulation of nitric oxide biosynthetic process	0.28	>=0.20
GO:0008593	regulation of Notch signaling pathway	1	>=0.20
GO:0051783	regulation of nuclear division	0.71	>=0.20
GO:0048024	regulation of nuclear mRNA splicing, via spliceosome	0.79	>=0.20
GO:0030808	regulation of nucleotide biosynthetic process	0.99	>=0.20
GO:0030811	regulation of nucleotide catabolic process	0.65	>=0.20
GO:0006140	regulation of nucleotide metabolic process	0.83	>=0.20
GO:0042481	regulation of odontogenesis	1	>=0.20
GO:0048713	regulation of oligodendrocyte differentiation	0.99	>=0.20
GO:0003156	regulation of organ formation	1	>=0.20
GO:0046620	regulation of organ growth	0.93	>=0.20
GO:2000027	regulation of organ morphogenesis	0.99	>=0.20
GO:0033043	regulation of organelle organization	0.48	>=0.20
GO:0030278	regulation of ossification	0.65	>=0.20
GO:0045667	regulation of osteoblast differentiation	0.81	>=0.20
GO:0060393	regulation of pathway-restricted SMAD protein phosphorylat	0.76	>=0.20
GO:0090276	regulation of peptide hormone secretion	0.4	>=0.20
GO:0002791	regulation of peptide secretion	0.41	>=0.20
GO:0090087	regulation of peptide transport	0.41	>=0.20
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	0.28	>=0.20
GO:0006885	regulation of pH	0.99	>=0.20
GO:0050764	regulation of phagocytosis	0.26	>=0.20
GO:0010517	regulation of phospholipase activity	0.45	>=0.20
GO:0010543	regulation of platelet activation	0.2	>=0.20
GO:0060078	regulation of postsynaptic membrane potential	1	>=0.20
GO:0002700	regulation of production of molecular mediator of immune r	0.36	>=0.20
GO:0061136	regulation of proteasomal protein catabolic process	0.97	>=0.20
GO:0042176	regulation of protein catabolic process	0.3	>=0.20
GO:0043254	regulation of protein complex assembly	0.44	>=0.20
GO:0043244	regulation of protein complex disassembly	0.84	>=0.20
GO:0090311	regulation of protein deacetylation	0.51	>=0.20
GO:0042306	regulation of protein import into nucleus	0.06	>=0.20
GO:0032271	regulation of protein polymerization	0.65	>=0.20
GO:0070613	regulation of protein processing	0.17	>=0.20
GO:0050708	regulation of protein secretion	0.28	>=0.20
GO:0061097	regulation of protein tyrosine kinase activity	0.68	>=0.20
GO:0031396	regulation of protein ubiquitination	0.85	>=0.20
GO:0031272	regulation of pseudopodium assembly	0.87	>=0.20
GO:0033121	regulation of purine nucleotide catabolic process	0.65	>=0.20
GO:0032313	regulation of Rab GTPase activity	0.12	>=0.20
GO:0032483	regulation of Rab protein signal transduction	0.12	>=0.20
GO:0032318	regulation of Ras GTPase activity	0.1	>=0.20
GO:0046578	regulation of Ras protein signal transduction	0.15	>=0.20

GO:0010469	regulation of receptor activity	0.65	>=0.20
GO:2000241	regulation of reproductive process	0.62	>=0.20
GO:0002831	regulation of response to biotic stimulus	0.82	>=0.20
GO:0060759	regulation of response to cytokine stimulus	0.08	>=0.20
GO:2001020	regulation of response to DNA damage stimulus	0.99	>=0.20
GO:0032095	regulation of response to food	0.79	>=0.20
GO:0032319	regulation of Rho GTPase activity	0.6	>=0.20
GO:0035023	regulation of Rho protein signal transduction	0.7	>=0.20
GO:0043484	regulation of RNA splicing	0.61	>=0.20
GO:0051046	regulation of secretion	0.45	>=0.20
GO:0051090	regulation of sequence-specific DNA binding transcription fac	0.03	>=0.20
GO:2001014	regulation of skeletal muscle cell differentiation	0.77	>=0.20
GO:0048742	regulation of skeletal muscle fiber development	0.94	>=0.20
GO:0048641	regulation of skeletal muscle tissue development	0.84	>=0.20
GO:0051056	regulation of small GTPase mediated signal transduction	0.05	>=0.20
GO:0014910	regulation of smooth muscle cell migration	0.47	>=0.20
GO:0048660	regulation of smooth muscle cell proliferation	0.07	>=0.20
GO:0006940	regulation of smooth muscle contraction	0.98	>=0.20
GO:0008589	regulation of smoothened signaling pathway	0.97	>=0.20
GO:2000736	regulation of stem cell differentiation	0.97	>=0.20
GO:0070302	regulation of stress-activated protein kinase signaling cascad	0.25	>=0.20
GO:0051153	regulation of striated muscle cell differentiation	0.94	>=0.20
GO:0006942	regulation of striated muscle contraction	1	>=0.20
GO:0016202	regulation of striated muscle tissue development	0.79	>=0.20
GO:0043903	regulation of symbiosis, encompassing mutualism through pa	0.97	>=0.20
GO:0050807	regulation of synapse organization	1	>=0.20
GO:0050803	regulation of synapse structure and activity	1	>=0.20
GO:0048167	regulation of synaptic plasticity	1	>=0.20
GO:0050804	regulation of synaptic transmission	1	>=0.20
GO:0032228	regulation of synaptic transmission, GABAergic	1	>=0.20
GO:0051966	regulation of synaptic transmission, glutamatergic	1	>=0.20
GO:0044057	regulation of system process	0.63	>=0.20
GO:0003073	regulation of systemic arterial blood pressure	0.99	>=0.20
GO:0002825	regulation of T-helper 1 type immune response	0.95	>=0.20
GO:0045622	regulation of T-helper cell differentiation	0.89	>=0.20
GO:0050863	regulation of T cell activation	0.62	>=0.20
GO:0045580	regulation of T cell differentiation	0.77	>=0.20
GO:0001914	regulation of T cell mediated cytotoxicity	1	>=0.20
GO:0002709	regulation of T cell mediated immunity	1	>=0.20
GO:0042129	regulation of T cell proliferation	0.85	>=0.20
GO:0032204	regulation of telomere maintenance	0.78	>=0.20
GO:0032006	regulation of TOR signaling cascade	0.37	>=0.20
GO:0032784	regulation of transcription elongation, DNA-dependent	0.63	>=0.20
GO:0034339	regulation of transcription from RNA polymerase II promoter	0.07	>=0.20
GO:0000083	regulation of transcription involved in G1/S phase of mitotic	0.55	>=0.20
GO:2000677	regulation of transcription regulatory region DNA binding	1	>=0.20
GO:0017015	regulation of transforming growth factor beta receptor signa	0.63	>=0.20

GO:0006417	regulation of translation	0.12	>=0.20
GO:0006446	regulation of translational initiation	0.64	>=0.20
GO:0090092	regulation of transmembrane receptor protein serine/threon	0.81	>=0.20
GO:0034762	regulation of transmembrane transport	0.5	>=0.20
GO:0022898	regulation of transmembrane transporter activity	1	>=0.20
GO:0051969	regulation of transmission of nerve impulse	1	>=0.20
GO:0032409	regulation of transporter activity	1	>=0.20
GO:0035150	regulation of tube size	0.12	>=0.20
GO:0002828	regulation of type 2 immune response	0.49	>=0.20
GO:0060338	regulation of type I interferon-mediated signaling pathway	0.88	>=0.20
GO:0032479	regulation of type I interferon production	0.85	>=0.20
GO:0051438	regulation of ubiquitin-protein ligase activity	0.87	>=0.20
GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitc	0.9	>=0.20
GO:0010574	regulation of vascular endothelial growth factor production	0.24	>=0.20
GO:0030947	regulation of vascular endothelial growth factor receptor sigr	0.46	>=0.20
GO:0019229	regulation of vasoconstriction	0.27	>=0.20
GO:0042312	regulation of vasodilation	0.33	>=0.20
GO:0060627	regulation of vesicle-mediated transport	0.24	>=0.20
GO:0045069	regulation of viral genome replication	0.64	>=0.20
GO:0050792	regulation of viral reproduction	0.36	>=0.20
GO:0046782	regulation of viral transcription	0.47	>=0.20
GO:0030111	regulation of Wnt receptor signaling pathway	0.98	>=0.20
GO:0000975	regulatory region DNA binding	0.03	>=0.20
GO:0001067	regulatory region nucleic acid binding	0.03	>=0.20
ENSG00000162924	REL PPI subnetwork	0.1	>=0.20
ENSG00000104856	RELB PPI subnetwork	0.05	>=0.20
ENSG00000088320	REM1 PPI subnetwork	0.98	>=0.20
MP:0003446	renal hypoplasia	0.99	>=0.20
MP:0003215	renal interstitial fibrosis	0.11	>=0.20
GO:0072001	renal system development	0.98	>=0.20
GO:0003014	renal system process	0.73	>=0.20
MP:0004154	renal tubular necrosis	0.41	>=0.20
GO:0061326	renal tubule development	1	>=0.20
GO:0061333	renal tubule morphogenesis	0.98	>=0.20
GO:0072087	renal vesicle development	1	>=0.20
GO:0072077	renal vesicle morphogenesis	1	>=0.20
GO:0005657	replication fork	0.8	>=0.20
GO:0030894	replisome	0.99	>=0.20
GO:0048608	reproductive structure development	0.74	>=0.20
ENSG00000135597	REPS1 PPI subnetwork	0.45	>=0.20
ENSG00000169891	REPS2 PPI subnetwork	0.3	>=0.20
ENSG00000142599	RERE PPI subnetwork	0.97	>=0.20
GO:0070469	respiratory chain	0.98	>=0.20
GO:0045271	respiratory chain complex I	0.98	>=0.20
MP:0001954	respiratory distress	0.36	>=0.20
GO:0022904	respiratory electron transport chain	1	>=0.20
MP:0001953	respiratory failure	0.79	>=0.20

GO:0007585	respiratory gaseous exchange	0.76	>=0.20
GO:0060541	respiratory system development	0.75	>=0.20
GO:0003016	respiratory system process	0.99	>=0.20
GO:0030323	respiratory tube development	0.67	>=0.20
GO:0014823	response to activity	0.7	>=0.20
GO:0043279	response to alkaloid	0.91	>=0.20
GO:0014075	response to amine stimulus	0.91	>=0.20
GO:0043200	response to amino acid stimulus	0.7	>=0.20
GO:0001975	response to amphetamine	1	>=0.20
GO:0051592	response to calcium ion	0.77	>=0.20
GO:0042220	response to cocaine	1	>=0.20
GO:0009409	response to cold	0.96	>=0.20
GO:0043331	response to dsRNA	0.99	>=0.20
GO:0034976	response to endoplasmic reticulum stress	0.87	>=0.20
GO:0032355	response to estradiol stimulus	0.44	>=0.20
GO:0043627	response to estrogen stimulus	0.42	>=0.20
GO:0045471	response to ethanol	0.23	>=0.20
GO:0043330	response to exogenous dsRNA	0.79	>=0.20
GO:0071774	response to fibroblast growth factor stimulus	0.41	>=0.20
GO:0034405	response to fluid shear stress	0.51	>=0.20
GO:0060992	response to fungicide	0.99	>=0.20
GO:0009620	response to fungus	0.88	>=0.20
GO:0010332	response to gamma radiation	0.88	>=0.20
GO:0033762	response to glucagon stimulus	0.32	>=0.20
GO:0070848	response to growth factor stimulus	0.47	>=0.20
GO:0009408	response to heat	0.32	>=0.20
GO:0009635	response to herbicide	0.43	>=0.20
GO:0042542	response to hydrogen peroxide	0.22	>=0.20
GO:0055093	response to hyperoxia	0.52	>=0.20
GO:0017085	response to insecticide	0.91	>=0.20
GO:0034341	response to interferon-gamma	0.88	>=0.20
GO:0070555	response to interleukin-1	0.44	>=0.20
GO:0070670	response to interleukin-4	0.74	>=0.20
GO:0010039	response to iron ion	0.95	>=0.20
GO:0009416	response to light stimulus	1	>=0.20
GO:0009612	response to mechanical stimulus	0.91	>=0.20
GO:0051597	response to methylmercury	0.9	>=0.20
GO:0051385	response to mineralocorticoid stimulus	0.6	>=0.20
GO:0035094	response to nicotine	1	>=0.20
GO:0010243	response to organic nitrogen	0.7	>=0.20
GO:0006979	response to oxidative stress	0.05	>=0.20
GO:0048265	response to pain	1	>=0.20
GO:0032494	response to peptidoglycan	0.48	>=0.20
GO:0032570	response to progesterone stimulus	0.58	>=0.20
GO:0034694	response to prostaglandin stimulus	0.89	>=0.20
GO:0009314	response to radiation	0.94	>=0.20
GO:0000302	response to reactive oxygen species	0.17	>=0.20

GO:0032526	response to retinoic acid	0.79	>=0.20
GO:0009266	response to temperature stimulus	0.58	>=0.20
GO:0035966	response to topologically incorrect protein	0.99	>=0.20
GO:0014073	response to tropane	1	>=0.20
GO:0034612	response to tumor necrosis factor	0.22	>=0.20
GO:0034340	response to type I interferon	0.98	>=0.20
GO:0006986	response to unfolded protein	0.99	>=0.20
GO:0009615	response to virus	0.76	>=0.20
GO:0033189	response to vitamin A	0.73	>=0.20
GO:0033280	response to vitamin D	0.25	>=0.20
GO:0010165	response to X-ray	1	>=0.20
GO:0010043	response to zinc ion	0.76	>=0.20
GO:0060041	retina development in camera-type eye	1	>=0.20
GO:0060042	retina morphogenesis in camera-type eye	0.99	>=0.20
MP:0001326	retinal degeneration	0.61	>=0.20
GO:0031290	retinal ganglion cell axon guidance	1	>=0.20
MP:0008518	retinal outer nuclear layer degeneration	0.52	>=0.20
MP:0008450	retinal photoreceptor degeneration	0.84	>=0.20
MP:0008451	retinal rod cell degeneration	0.89	>=0.20
GO:0042573	retinoic acid metabolic process	0.94	>=0.20
GO:0048384	retinoic acid receptor signaling pathway	0.84	>=0.20
GO:0001523	retinoid metabolic process	0.55	>=0.20
GO:0042572	retinol metabolic process	0.23	>=0.20
GO:0042147	retrograde transport, endosome to Golgi	0.05	>=0.20
GO:0000301	retrograde transport, vesicle recycling within Golgi	0.96	>=0.20
GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	0.7	>=0.20
ENSG00000135945	REV1 PPI subnetwork	0.87	>=0.20
ENSG00000009413	REV3L PPI subnetwork	0.85	>=0.20
ENSG00000035928	RFC1 PPI subnetwork	0.78	>=0.20
ENSG00000049541	RFC2 PPI subnetwork	0.86	>=0.20
ENSG00000133119	RFC3 PPI subnetwork	0.74	>=0.20
ENSG00000163918	RFC4 PPI subnetwork	0.94	>=0.20
ENSG00000111445	RFC5 PPI subnetwork	0.65	>=0.20
ENSG00000132005	RFX1 PPI subnetwork	0.05	>=0.20
ENSG00000087903	RFX2 PPI subnetwork	0.48	>=0.20
ENSG00000206282	RGL2 PPI subnetwork	0.74	>=0.20
ENSG00000169220	RGS14 PPI subnetwork	0.07	>=0.20
ENSG00000138835	RGS3 PPI subnetwork	0.8	>=0.20
ENSG00000182901	RGS7 PPI subnetwork	0.5	>=0.20
ENSG00000106615	RHEB PPI subnetwork	0.99	>=0.20
GO:0005100	Rho GTPase activator activity	0.52	>=0.20
GO:0017048	Rho GTPase binding	0.46	>=0.20
GO:0005089	Rho guanyl-nucleotide exchange factor activity	0.66	>=0.20
GO:0007266	Rho protein signal transduction	0.61	>=0.20
ENSG00000067560	RHOA PPI subnetwork	0.83	>=0.20
ENSG00000143878	RHOB PPI subnetwork	0.28	>=0.20
ENSG00000173156	RHOD PPI subnetwork	0.48	>=0.20

ENSG00000177105	RHOG PPI subnetwork	0.05	>=0.20
ENSG00000126785	RHOJ PPI subnetwork	0.2	>=0.20
ENSG00000131941	RHPN2 PPI subnetwork	0.14	>=0.20
GO:0048511	rhythmic process	0.7	>=0.20
MP:0000153	rib bifurcation	0.97	>=0.20
MP:0000154	rib fusion	0.97	>=0.20
GO:0030529	ribonucleoprotein complex	0.61	>=0.20
GO:0022618	ribonucleoprotein complex assembly	0.94	>=0.20
GO:0043021	ribonucleoprotein complex binding	0.35	>=0.20
GO:0022613	ribonucleoprotein complex biogenesis	0.95	>=0.20
GO:0071826	ribonucleoprotein complex subunit organization	0.92	>=0.20
GO:0035770	ribonucleoprotein granule	0.52	>=0.20
GO:0042455	ribonucleoside biosynthetic process	0.75	>=0.20
GO:0009156	ribonucleoside monophosphate biosynthetic process	0.84	>=0.20
GO:0009161	ribonucleoside monophosphate metabolic process	0.89	>=0.20
GO:0009201	ribonucleoside triphosphate biosynthetic process	0.72	>=0.20
GO:0009260	ribonucleotide biosynthetic process	0.66	>=0.20
GO:0042274	ribosomal small subunit biogenesis	1	>=0.20
GO:0005840	ribosome	0.9	>=0.20
GO:0043022	ribosome binding	0.74	>=0.20
GO:0042254	ribosome biogenesis	0.99	>=0.20
ENSG00000177963	RIC8A PPI subnetwork	0.38	>=0.20
ENSG00000164327	RICTOR PPI subnetwork	0.17	>=0.20
ENSG00000080345	RIF1 PPI subnetwork	0.1	>=0.20
MP:0004158	right aortic arch	0.88	>=0.20
MP:0000531	right pulmonary isomerism	1	>=0.20
ENSG00000079841	RIMS1 PPI subnetwork	0.98	>=0.20
ENSG00000176406	RIMS2 PPI subnetwork	0.7	>=0.20
ENSG00000174791	RIN1 PPI subnetwork	0.11	>=0.20
ENSG00000100599	RIN3 PPI subnetwork	0.13	>=0.20
ENSG00000204227	RING1 PPI subnetwork	0.05	>=0.20
ENSG00000206287	RING1 PPI subnetwork	0.05	>=0.20
ENSG00000137275	RIPK1 PPI subnetwork	0.58	>=0.20
ENSG00000104312	RIPK2 PPI subnetwork	0.68	>=0.20
ENSG00000129465	RIPK3 PPI subnetwork	0.16	>=0.20
ENSG00000143622	RIT1 PPI subnetwork	0.63	>=0.20
ENSG00000117000	RLF PPI subnetwork	0.72	>=0.20
GO:0008186	RNA-dependent ATPase activity	0.17	>=0.20
GO:0006278	RNA-dependent DNA replication	0.68	>=0.20
GO:0031123	RNA 3'-end processing	0.27	>=0.20
GO:0009452	RNA capping	0.95	>=0.20
GO:0006401	RNA catabolic process	0.92	>=0.20
GO:0006405	RNA export from nucleus	0.53	>=0.20
GO:0003724	RNA helicase activity	0.45	>=0.20
GO:0006403	RNA localization	0.53	>=0.20
GO:0001510	RNA methylation	0.89	>=0.20
GO:0008173	RNA methyltransferase activity	0.98	>=0.20

GO:0043631	RNA polyadenylation	0.87	>=0.20
GO:0034062	RNA polymerase activity	0.98	>=0.20
GO:0030880	RNA polymerase complex	0.96	>=0.20
GO:0008353	RNA polymerase II carboxy-terminal domain kinase activity	0.59	>=0.20
GO:0000982	RNA polymerase II core promoter proximal region sequence-	0.46	>=0.20
GO:0001078	RNA polymerase II core promoter proximal region sequence-	0.45	>=0.20
GO:0001077	RNA polymerase II core promoter proximal region sequence-	0.53	>=0.20
GO:0000979	RNA polymerase II core promoter sequence-specific DNA bin	0.75	>=0.20
GO:0003705	RNA polymerase II distal enhancer sequence-specific DNA bir	0.05	>=0.20
GO:0001012	RNA polymerase II regulatory region DNA binding	0.55	>=0.20
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA b	0.79	>=0.20
GO:0001105	RNA polymerase II transcription coactivator activity	0.79	>=0.20
GO:0001104	RNA polymerase II transcription cofactor activity	0.83	>=0.20
GO:0001085	RNA polymerase II transcription factor binding	0.07	>=0.20
GO:0001076	RNA polymerase II transcription factor binding transcription f	0.83	>=0.20
GO:0001190	RNA polymerase II transcription factor binding transcription f	0.79	>=0.20
GO:0008380	RNA splicing	0.47	>=0.20
GO:0000375	RNA splicing, via transesterification reactions	0.51	>=0.20
GO:0000377	RNA splicing, via transesterification reactions with bulged ad	0.53	>=0.20
GO:0050658	RNA transport	0.51	>=0.20
ENSG00000115963	RND3 PPI subnetwork	0.2	>=0.20
ENSG00000123091	RNF11 PPI subnetwork	0.54	>=0.20
ENSG00000013561	RNF14 PPI subnetwork	0.81	>=0.20
ENSG00000163162	RNF149 PPI subnetwork	0.88	>=0.20
ENSG00000121481	RNF2 PPI subnetwork	0.23	>=0.20
ENSG00000092098	RNF31 PPI subnetwork	0.45	>=0.20
ENSG00000181852	RNF41 PPI subnetwork	0.78	>=0.20
ENSG00000111880	RNGTT PPI subnetwork	0.39	>=0.20
ENSG00000101654	RNMT PPI subnetwork	0.33	>=0.20
ENSG00000185008	ROBO2 PPI subnetwork	0.97	>=0.20
ENSG00000067900	ROCK1 PPI subnetwork	0.65	>=0.20
ENSG00000134318	ROCK2 PPI subnetwork	0.54	>=0.20
ENSG00000067836	ROGDI PPI subnetwork	1	>=0.20
ENSG00000047936	ROS1 PPI subnetwork	0.14	>=0.20
GO:0021903	rostrocaudal neural tube patterning	0.99	>=0.20
ENSG00000130589	RP4-697K14.7 PPI subnetwork	0.32	>=0.20
ENSG00000132383	RPA1 PPI subnetwork	1	>=0.20
ENSG00000117748	RPA2 PPI subnetwork	0.99	>=0.20
ENSG00000106399	RPA3 PPI subnetwork	0.99	>=0.20
ENSG00000204086	RPA4 PPI subnetwork	0.99	>=0.20
ENSG00000005175	RPAP3 PPI subnetwork	0.03	>=0.20
ENSG00000117133	RPF1 PPI subnetwork	0.53	>=0.20
ENSG00000197498	RPF2 PPI subnetwork	0.64	>=0.20
ENSG00000156313	RPGR PPI subnetwork	0.32	>=0.20
ENSG00000089169	RPH3A PPI subnetwork	1	>=0.20
ENSG00000198755	RPL10A PPI subnetwork	0.68	>=0.20
ENSG00000142676	RPL11 PPI subnetwork	0.59	>=0.20

ENSG00000197958	RPL12 PPI subnetwork	0.78	>=0.20
ENSG00000142541	RPL13A PPI subnetwork	0.98	>=0.20
ENSG00000188846	RPL14 PPI subnetwork	0.76	>=0.20
ENSG00000174748	RPL15 PPI subnetwork	0.51	>=0.20
ENSG00000063177	RPL18 PPI subnetwork	0.74	>=0.20
ENSG00000108298	RPL19 PPI subnetwork	0.96	>=0.20
ENSG00000122026	RPL21 PPI subnetwork	0.55	>=0.20
ENSG00000116251	RPL22 PPI subnetwork	0.67	>=0.20
ENSG00000125691	RPL23 PPI subnetwork	0.46	>=0.20
ENSG00000198242	RPL23A PPI subnetwork	0.37	>=0.20
ENSG00000114391	RPL24 PPI subnetwork	0.9	>=0.20
ENSG00000161970	RPL26 PPI subnetwork	0.74	>=0.20
ENSG00000037241	RPL26L1 PPI subnetwork	0.89	>=0.20
ENSG00000166441	RPL27A PPI subnetwork	0.77	>=0.20
ENSG00000108107	RPL28 PPI subnetwork	0.34	>=0.20
ENSG00000162244	RPL29 PPI subnetwork	0.99	>=0.20
ENSG00000071082	RPL31 PPI subnetwork	0.45	>=0.20
ENSG00000144713	RPL32 PPI subnetwork	0.97	>=0.20
ENSG00000109475	RPL34 PPI subnetwork	0.83	>=0.20
ENSG00000136942	RPL35 PPI subnetwork	0.98	>=0.20
ENSG00000182899	RPL35A PPI subnetwork	0.79	>=0.20
ENSG00000130255	RPL36 PPI subnetwork	0.92	>=0.20
ENSG00000145592	RPL37 PPI subnetwork	0.95	>=0.20
ENSG00000197756	RPL37A PPI subnetwork	0.91	>=0.20
ENSG00000172809	RPL38 PPI subnetwork	0.77	>=0.20
ENSG00000198918	RPL39 PPI subnetwork	0.97	>=0.20
ENSG00000140986	RPL3L PPI subnetwork	0.93	>=0.20
ENSG00000089009	RPL6 PPI subnetwork	0.67	>=0.20
ENSG00000147604	RPL7 PPI subnetwork	0.2	>=0.20
ENSG00000148303	RPL7A PPI subnetwork	0.59	>=0.20
ENSG00000161016	RPL8 PPI subnetwork	0.9	>=0.20
ENSG00000163682	RPL9 PPI subnetwork	0.61	>=0.20
ENSG00000089157	RPLP0 PPI subnetwork	0.09	>=0.20
ENSG00000137818	RPLP1 PPI subnetwork	0.87	>=0.20
ENSG00000163902	RPN1 PPI subnetwork	0.51	>=0.20
ENSG00000118705	RPN2 PPI subnetwork	0.12	>=0.20
ENSG00000101413	RPRD1B PPI subnetwork	0.24	>=0.20
ENSG00000124614	RPS10 PPI subnetwork	0.78	>=0.20
ENSG00000112306	RPS12 PPI subnetwork	0.79	>=0.20
ENSG00000164587	RPS14 PPI subnetwork	0.69	>=0.20
ENSG00000115268	RPS15 PPI subnetwork	0.86	>=0.20
ENSG00000105193	RPS16 PPI subnetwork	0.81	>=0.20
ENSG00000184779	RPS17 PPI subnetwork	0.81	>=0.20
ENSG00000182774	RPS17L PPI subnetwork	0.81	>=0.20
ENSG00000096150	RPS18 PPI subnetwork	0.38	>=0.20
ENSG00000105372	RPS19 PPI subnetwork	0.48	>=0.20
ENSG00000140988	RPS2 PPI subnetwork	0.47	>=0.20

ENSG00000008988	RPS20 PPI subnetwork	0.68	>=0.20
ENSG00000171858	RPS21 PPI subnetwork	0.82	>=0.20
ENSG00000186468	RPS23 PPI subnetwork	0.31	>=0.20
ENSG00000118181	RPS25 PPI subnetwork	0.37	>=0.20
ENSG00000197728	RPS26 PPI subnetwork	0.7	>=0.20
ENSG00000177954	RPS27 PPI subnetwork	0.72	>=0.20
ENSG00000143947	RPS27A PPI subnetwork	0.05	>=0.20
ENSG00000213741	RPS29 PPI subnetwork	0.85	>=0.20
ENSG00000149273	RPS3 PPI subnetwork	0.25	>=0.20
ENSG00000198034	RPS4X PPI subnetwork	0.56	>=0.20
ENSG00000129824	RPS4Y1 PPI subnetwork	0.8	>=0.20
ENSG00000137154	RPS6 PPI subnetwork	0.26	>=0.20
ENSG00000117676	RPS6KA1 PPI subnetwork	0.15	>=0.20
ENSG00000177189	RPS6KA3 PPI subnetwork	0.74	>=0.20
ENSG00000162302	RPS6KA4 PPI subnetwork	0.39	>=0.20
ENSG00000100784	RPS6KA5 PPI subnetwork	0.04	>=0.20
ENSG00000175634	RPS6KB2 PPI subnetwork	0.04	>=0.20
ENSG00000171863	RPS7 PPI subnetwork	0.86	>=0.20
ENSG00000142937	RPS8 PPI subnetwork	0.62	>=0.20
ENSG00000170889	RPS9 PPI subnetwork	0.63	>=0.20
ENSG00000168028	RPSA PPI subnetwork	0.51	>=0.20
ENSG00000144580	RQCD1 PPI subnetwork	0.3	>=0.20
ENSG00000166592	RRAD PPI subnetwork	0.59	>=0.20
ENSG00000126458	RRAS PPI subnetwork	0.11	>=0.20
ENSG00000133818	RRAS2 PPI subnetwork	0.07	>=0.20
ENSG00000171848	RRM2 PPI subnetwork	1	>=0.20
GO:0019843	rRNA binding	0.85	>=0.20
GO:0016072	rRNA metabolic process	0.99	>=0.20
GO:0006364	rRNA processing	0.97	>=0.20
GO:0009303	rRNA transcription	1	>=0.20
ENSG00000067533	RRP15 PPI subnetwork	0.64	>=0.20
ENSG00000179041	RRS1 PPI subnetwork	0.8	>=0.20
ENSG00000081019	RSBN1 PPI subnetwork	0.04	>=0.20
ENSG00000171490	RSL1D1 PPI subnetwork	0.74	>=0.20
ENSG00000137876	RSL24D1 PPI subnetwork	0.75	>=0.20
ENSG00000137815	RTF1 PPI subnetwork	0.46	>=0.20
ENSG00000139970	RTN1 PPI subnetwork	0.98	>=0.20
ENSG00000133318	RTN3 PPI subnetwork	1	>=0.20
ENSG00000115310	RTN4 PPI subnetwork	0.63	>=0.20
GO:0032587	ruffle membrane	0.51	>=0.20
ENSG00000079102	RUNX1T1 PPI subnetwork	0.56	>=0.20
ENSG00000124813	RUNX2 PPI subnetwork	0.37	>=0.20
ENSG00000175792	RUVBL1 PPI subnetwork	0.08	>=0.20
ENSG00000183207	RUVBL2 PPI subnetwork	0.13	>=0.20
ENSG00000163602	RYBP PPI subnetwork	0.16	>=0.20
ENSG00000196218	RYR1 PPI subnetwork	0.86	>=0.20
ENSG00000198626	RYR2 PPI subnetwork	0.4	>=0.20

ENSG00000198838	RYR3 PPI subnetwork	0.88	>=0.20
GO:0051320	S phase	0.91	>=0.20
GO:0000084	S phase of mitotic cell cycle	0.94	>=0.20
ENSG00000160678	S100A1 PPI subnetwork	0.13	>=0.20
ENSG00000163191	S100A11 PPI subnetwork	0.4	>=0.20
ENSG00000196154	S100A4 PPI subnetwork	0.64	>=0.20
ENSG00000197956	S100A6 PPI subnetwork	0.71	>=0.20
ENSG00000160307	S100B PPI subnetwork	0.32	>=0.20
ENSG00000168061	SAC3D1 PPI subnetwork	0.58	>=0.20
ENSG00000211456	SACM1L PPI subnetwork	0.36	>=0.20
MP:0004617	sacral vertebral transformation	0.91	>=0.20
ENSG00000160633	SAFB PPI subnetwork	0.25	>=0.20
ENSG00000130561	SAG PPI subnetwork	0.8	>=0.20
GO:0007431	salivary gland development	1	>=0.20
GO:0007435	salivary gland morphogenesis	1	>=0.20
ENSG00000020577	SAMD4A PPI subnetwork	0.26	>=0.20
ENSG00000100347	SAMM50 PPI subnetwork	0.98	>=0.20
ENSG00000136715	SAP130 PPI subnetwork	0.03	>=0.20
ENSG00000150459	SAP18 PPI subnetwork	0.19	>=0.20
ENSG00000205307	SAP25 PPI subnetwork	0.12	>=0.20
ENSG00000164105	SAP30 PPI subnetwork	0.08	>=0.20
ENSG00000152700	SAR1B PPI subnetwork	0.41	>=0.20
GO:0042383	sarcolemma	0.69	>=0.20
GO:0030017	sarcomere	0.72	>=0.20
GO:0045214	sarcomere organization	0.9	>=0.20
GO:0016528	sarcoplasm	0.28	>=0.20
GO:0016529	sarcoplasmic reticulum	0.39	>=0.20
GO:0033017	sarcoplasmic reticulum membrane	0.4	>=0.20
ENSG00000075856	SART3 PPI subnetwork	0.68	>=0.20
ENSG00000111961	SASH1 PPI subnetwork	0.44	>=0.20
ENSG00000122122	SASH3 PPI subnetwork	0.09	>=0.20
ENSG00000130066	SAT1 PPI subnetwork	0.99	>=0.20
ENSG00000182568	SATB1 PPI subnetwork	0.83	>=0.20
ENSG00000151748	SAV1 PPI subnetwork	0.24	>=0.20
ENSG00000100241	SBF1 PPI subnetwork	1	>=0.20
ENSG00000133812	SBF2 PPI subnetwork	1	>=0.20
ENSG00000156304	SCAF4 PPI subnetwork	0.05	>=0.20
GO:0019005	SCF ubiquitin ligase complex	0.41	>=0.20
ENSG00000092108	SCFD1 PPI subnetwork	0.04	>=0.20
ENSG00000006747	SCIN PPI subnetwork	0.12	>=0.20
ENSG00000010803	SCMH1 PPI subnetwork	0.05	>=0.20
ENSG00000144285	SCN1A PPI subnetwork	0.68	>=0.20
ENSG00000136531	SCN2A PPI subnetwork	0.44	>=0.20
ENSG00000198301	SDAD1 PPI subnetwork	0.52	>=0.20
ENSG00000115884	SDC1 PPI subnetwork	0.64	>=0.20
ENSG00000169439	SDC2 PPI subnetwork	0.19	>=0.20
ENSG00000124145	SDC4 PPI subnetwork	0.13	>=0.20

ENSG00000137575	SDCBP PPI subnetwork	1	>=0.20
ENSG00000117118	SDHB PPI subnetwork	0.66	>=0.20
ENSG00000168497	SDPR PPI subnetwork	0.06	>=0.20
ENSG00000157020	SEC13 PPI subnetwork	0.39	>=0.20
ENSG00000121542	SEC22A PPI subnetwork	0.05	>=0.20
ENSG00000176986	SEC24C PPI subnetwork	0.15	>=0.20
ENSG00000138674	SEC31A PPI subnetwork	0.34	>=0.20
ENSG00000058262	SEC61A1 PPI subnetwork	0.16	>=0.20
ENSG00000132432	SEC61G PPI subnetwork	0.07	>=0.20
ENSG00000008952	SEC62 PPI subnetwork	0.27	>=0.20
ENSG00000025796	SEC63 PPI subnetwork	0.78	>=0.20
GO:0019932	second-messenger-mediated signaling	0.89	>=0.20
GO:0015291	secondary active transmembrane transporter activity	0.5	>=0.20
MP:0001939	secondary sex reversal	0.45	>=0.20
GO:0030667	secretory granule membrane	0.75	>=0.20
GO:0007379	segment specification	0.98	>=0.20
GO:0035282	segmentation	0.99	>=0.20
ENSG00000085415	SEH1L PPI subnetwork	0.57	>=0.20
MP:0002064	seizures	0.89	>=0.20
GO:0008430	selenium binding	0.93	>=0.20
ENSG00000188404	SELL PPI subnetwork	0.15	>=0.20
ENSG00000110876	SELPLG PPI subnetwork	0.78	>=0.20
MP:0001154	seminiferous tubule degeneration	0.56	>=0.20
ENSG00000163904	SENP2 PPI subnetwork	0.99	>=0.20
ENSG00000161956	SENP3 PPI subnetwork	0.71	>=0.20
ENSG00000138468	SENP7 PPI subnetwork	0.41	>=0.20
MP:0004740	sensorineural hearing loss	0.93	>=0.20
GO:0007423	sensory organ development	1	>=0.20
GO:0007600	sensory perception	1	>=0.20
GO:0007606	sensory perception of chemical stimulus	1	>=0.20
GO:0050953	sensory perception of light stimulus	1	>=0.20
GO:0050954	sensory perception of mechanical stimulus	1	>=0.20
GO:0019233	sensory perception of pain	1	>=0.20
GO:0007608	sensory perception of smell	1	>=0.20
GO:0007605	sensory perception of sound	1	>=0.20
GO:0050909	sensory perception of taste	1	>=0.20
ENSG00000138758	SEPT11 PPI subnetwork	1	>=0.20
ENSG00000100167	SEPT3 PPI subnetwork	1	>=0.20
ENSG00000108387	SEPT4 PPI subnetwork	1	>=0.20
ENSG00000184702	SEPT5 PPI subnetwork	1	>=0.20
ENSG00000125354	SEPT6 PPI subnetwork	1	>=0.20
ENSG00000164402	SEPT8 PPI subnetwork	1	>=0.20
GO:0031105	septin complex	0.99	>=0.20
GO:0032156	septin cytoskeleton	0.99	>=0.20
GO:0000981	sequence-specific DNA binding RNA polymerase II transcripti	0.04	>=0.20
GO:0030730	sequestering of triglyceride	0.06	>=0.20
GO:0004993	serotonin receptor activity	1	>=0.20

GO:0007210	serotonin receptor signaling pathway	1	>=0.20
ENSG00000196136	SERPINA3 PPI subnetwork	0.08	>=0.20
ENSG00000149257	SERPINH1 PPI subnetwork	0.21	>=0.20
ENSG00000099381	SETD1A PPI subnetwork	0.61	>=0.20
ENSG00000181555	SETD2 PPI subnetwork	0.69	>=0.20
ENSG00000145391	SETD7 PPI subnetwork	0.25	>=0.20
GO:0000803	sex chromosome	0.99	>=0.20
GO:0007530	sex determination	0.99	>=0.20
GO:0007548	sex differentiation	0.8	>=0.20
GO:0019953	sexual reproduction	0.93	>=0.20
ENSG00000168066	SF1 PPI subnetwork	0.15	>=0.20
ENSG00000099995	SF3A1 PPI subnetwork	0.09	>=0.20
ENSG00000183431	SF3A3 PPI subnetwork	0.04	>=0.20
ENSG00000115524	SF3B1 PPI subnetwork	0.09	>=0.20
ENSG00000143368	SF3B4 PPI subnetwork	0.05	>=0.20
ENSG00000175793	SFN PPI subnetwork	0.05	>=0.20
ENSG00000116560	SFPQ PPI subnetwork	0.09	>=0.20
ENSG00000104332	SFRP1 PPI subnetwork	1	>=0.20
ENSG00000145423	SFRP2 PPI subnetwork	0.99	>=0.20
ENSG00000106483	SFRP4 PPI subnetwork	1	>=0.20
ENSG00000120057	SFRP5 PPI subnetwork	1	>=0.20
ENSG00000173349	SFT2D3 PPI subnetwork	0.11	>=0.20
ENSG00000107819	SFXN3 PPI subnetwork	0.31	>=0.20
ENSG00000108823	SGCA PPI subnetwork	0.99	>=0.20
ENSG00000163069	SGCB PPI subnetwork	1	>=0.20
ENSG00000170624	SGCD PPI subnetwork	1	>=0.20
ENSG00000102683	SGCG PPI subnetwork	1	>=0.20
ENSG00000118515	SGK1 PPI subnetwork	0.06	>=0.20
ENSG00000182319	SGK223 PPI subnetwork	0.19	>=0.20
ENSG00000129810	SGOL1 PPI subnetwork	0.65	>=0.20
ENSG00000163535	SGOL2 PPI subnetwork	0.83	>=0.20
ENSG00000126821	SGPP1 PPI subnetwork	1	>=0.20
ENSG00000163082	SGPP2 PPI subnetwork	0.99	>=0.20
ENSG00000104969	SGTA PPI subnetwork	0.42	>=0.20
ENSG00000197860	SGTB PPI subnetwork	1	>=0.20
ENSG00000183918	SH2D1A PPI subnetwork	0.62	>=0.20
ENSG00000125731	SH2D3A PPI subnetwork	0.12	>=0.20
GO:0017124	SH3 domain binding	0.94	>=0.20
GO:0005070	SH3/SH2 adaptor activity	0.29	>=0.20
ENSG00000087266	SH3BP2 PPI subnetwork	0.16	>=0.20
ENSG00000130147	SH3BP4 PPI subnetwork	0.1	>=0.20
ENSG00000141985	SH3GL1 PPI subnetwork	1	>=0.20
ENSG00000107295	SH3GL2 PPI subnetwork	0.94	>=0.20
ENSG00000140600	SH3GL3 PPI subnetwork	0.56	>=0.20
ENSG00000147010	SH3KBP1 PPI subnetwork	0.23	>=0.20
ENSG00000161681	SHANK1 PPI subnetwork	0.86	>=0.20
ENSG00000162105	SHANK2 PPI subnetwork	0.36	>=0.20

ENSG00000171241	SHCBP1 PPI subnetwork	0.15	>=0.20
ENSG00000127922	SHFM1 PPI subnetwork	0.17	>=0.20
MP:0001196	shiny skin	0.18	>=0.20
ENSG00000108061	SHOC2 PPI subnetwork	0.14	>=0.20
MP:0003109	short femur	0.26	>=0.20
MP:0002765	short fibula	0.88	>=0.20
MP:0004351	short humerus	0.77	>=0.20
MP:0004830	short incisors	0.57	>=0.20
MP:0000547	short limbs	0.12	>=0.20
MP:0000088	short mandible	0.88	>=0.20
MP:0000097	short maxilla	0.8	>=0.20
MP:0004471	short nasal bone	0.41	>=0.20
MP:0008582	short photoreceptor inner segment	1	>=0.20
MP:0008587	short photoreceptor outer segment	0.99	>=0.20
MP:0000091	short premaxilla	0.83	>=0.20
MP:0004355	short radius	1	>=0.20
MP:0004672	short ribs	0.69	>=0.20
MP:0000445	short snout	0.79	>=0.20
MP:0004321	short sternum	0.97	>=0.20
MP:0001407	short stride length	0.23	>=0.20
MP:0002764	short tibia	0.46	>=0.20
MP:0004359	short ulna	0.96	>=0.20
MP:0004704	short vertebral column	0.86	>=0.20
MP:0002563	shortened circadian period	0.93	>=0.20
MP:0000435	shortened head	0.83	>=0.20
ENSG00000164403	SHROOM1 PPI subnetwork	0.45	>=0.20
ENSG00000146950	SHROOM2 PPI subnetwork	0.03	>=0.20
ENSG00000138771	SHROOM3 PPI subnetwork	0.07	>=0.20
ENSG00000196470	SIAH1 PPI subnetwork	1	>=0.20
GO:0008373	sialyltransferase activity	0.32	>=0.20
ENSG00000147955	SIGMAR1 PPI subnetwork	0.31	>=0.20
GO:0023061	signal release	0.68	>=0.20
GO:0005048	signal sequence binding	0.27	>=0.20
GO:0072331	signal transduction by p53 class mediator	0.78	>=0.20
GO:0072332	signal transduction by p53 class mediator resulting in inducti	0.96	>=0.20
GO:0042770	signal transduction in response to DNA damage	0.62	>=0.20
GO:0072395	signal transduction involved in cell cycle checkpoint	0.91	>=0.20
GO:0072422	signal transduction involved in DNA damage checkpoint	0.91	>=0.20
GO:0072401	signal transduction involved in DNA integrity checkpoint	0.91	>=0.20
GO:0072404	signal transduction involved in G1/S transition checkpoint	0.91	>=0.20
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	0.91	>=0.20
GO:0072474	signal transduction involved in mitotic cell cycle G1/S checkp	0.91	>=0.20
GO:0072431	signal transduction involved in mitotic cell cycle G1/S transiti	0.91	>=0.20
GO:0023019	signal transduction involved in regulation of gene expression	0.99	>=0.20
GO:0035591	signaling adaptor activity	0.09	>=0.20
GO:0008180	signalosome	0.49	>=0.20
ENSG00000170145	SIK2 PPI subnetwork	0.27	>=0.20

ENSG00000160584	SIK3 PPI subnetwork	0.14	>=0.20
ENSG00000052723	SIKE1 PPI subnetwork	0.93	>=0.20
ENSG00000127511	SIN3B PPI subnetwork	0.06	>=0.20
GO:0003697	single-stranded DNA binding	0.29	>=0.20
GO:0003727	single-stranded RNA binding	0.13	>=0.20
GO:0007338	single fertilization	1	>=0.20
MP:0003604	single kidney	0.99	>=0.20
ENSG00000197555	SIPA1L1 PPI subnetwork	0.15	>=0.20
ENSG00000198053	SIRPA PPI subnetwork	0.04	>=0.20
ENSG00000096717	SIRT1 PPI subnetwork	0.12	>=0.20
ENSG00000068903	SIRT2 PPI subnetwork	0.98	>=0.20
GO:0007062	sister chromatid cohesion	0.93	>=0.20
GO:0000819	sister chromatid segregation	0.95	>=0.20
GO:0030427	site of polarized growth	0.99	>=0.20
MP:0002766	situs inversus	0.95	>=0.20
ENSG00000126778	SIX1 PPI subnetwork	0.91	>=0.20
ENSG00000154839	SKA1 PPI subnetwork	0.79	>=0.20
MP:0009417	skeletal muscle atrophy	0.11	>=0.20
GO:0035914	skeletal muscle cell differentiation	0.84	>=0.20
GO:0003009	skeletal muscle contraction	0.98	>=0.20
GO:0048741	skeletal muscle fiber development	0.99	>=0.20
MP:0009414	skeletal muscle fiber necrosis	0.97	>=0.20
GO:0060538	skeletal muscle organ development	0.97	>=0.20
GO:0007519	skeletal muscle tissue development	0.97	>=0.20
GO:0001501	skeletal system development	0.73	>=0.20
GO:0048705	skeletal system morphogenesis	0.96	>=0.20
ENSG00000157933	SKI PPI subnetwork	0.43	>=0.20
ENSG00000136603	SKIL PPI subnetwork	0.42	>=0.20
GO:0043588	skin development	0.94	>=0.20
ENSG00000039123	SKIV2L2 PPI subnetwork	0.64	>=0.20
ENSG00000113558	SKP1 PPI subnetwork	0.14	>=0.20
ENSG00000155926	SLA PPI subnetwork	0.05	>=0.20
ENSG00000110436	SLC1A2 PPI subnetwork	0.72	>=0.20
ENSG00000108528	SLC25A11 PPI subnetwork	0.15	>=0.20
ENSG00000177542	SLC25A22 PPI subnetwork	0.79	>=0.20
ENSG00000151729	SLC25A4 PPI subnetwork	0.19	>=0.20
ENSG00000005022	SLC25A5 PPI subnetwork	0.05	>=0.20
ENSG00000181856	SLC2A4 PPI subnetwork	0.04	>=0.20
ENSG00000198569	SLC34A3 PPI subnetwork	0.55	>=0.20
ENSG00000164889	SLC4A2 PPI subnetwork	0.76	>=0.20
ENSG00000188687	SLC4A5 PPI subnetwork	0.83	>=0.20
ENSG00000100170	SLC5A1 PPI subnetwork	0.69	>=0.20
ENSG00000013293	SLC7A14 PPI subnetwork	0.11	>=0.20
ENSG00000099960	SLC7A4 PPI subnetwork	0.11	>=0.20
ENSG00000183023	SLC8A1 PPI subnetwork	0.96	>=0.20
ENSG00000090020	SLC9A1 PPI subnetwork	0.06	>=0.20
ENSG00000109062	SLC9A3R1 PPI subnetwork	0.58	>=0.20

ENSG00000065054	SLC9A3R2 PPI subnetwork	0.56	>=0.20
ENSG00000065613	SLK PPI subnetwork	0.89	>=0.20
GO:0046332	SMAD binding	0.11	>=0.20
GO:0007183	SMAD protein complex assembly	0.71	>=0.20
GO:0060395	SMAD protein signal transduction	0.89	>=0.20
ENSG00000137834	SMAD6 PPI subnetwork	0.56	>=0.20
ENSG00000101665	SMAD7 PPI subnetwork	0.39	>=0.20
MP:0004462	small basisphenoid bone	0.4	>=0.20
MP:0000852	small cerebellum	0.96	>=0.20
GO:0019783	small conjugating protein-specific protease activity	0.92	>=0.20
GO:0032182	small conjugating protein binding	0.8	>=0.20
GO:0019787	small conjugating protein ligase activity	0.85	>=0.20
MP:0005352	small cranium	0.91	>=0.20
MP:0000018	small ears	0.86	>=0.20
GO:0031267	small GTPase binding	0.92	>=0.20
GO:0007264	small GTPase mediated signal transduction	0.36	>=0.20
GO:0005083	small GTPase regulator activity	0.05	>=0.20
MP:0002989	small kidney	0.76	>=0.20
MP:0001306	small lens	0.98	>=0.20
MP:0003641	small lung	0.71	>=0.20
MP:0002217	small lymph nodes	0.2	>=0.20
MP:0004592	small mandible	1	>=0.20
GO:0005732	small nucleolar ribonucleoprotein complex	0.98	>=0.20
MP:0002741	small olfactory bulb	0.98	>=0.20
MP:0004310	small otic vesicle	0.93	>=0.20
MP:0001127	small ovary	0.98	>=0.20
MP:0009172	small pancreatic islets	0.39	>=0.20
MP:0004418	small parietal bone	0.66	>=0.20
MP:0008135	small Peyer's patches	0.81	>=0.20
GO:0015935	small ribosomal subunit	0.98	>=0.20
MP:0001157	small seminal vesicle	0.71	>=0.20
MP:0001153	small seminiferous tubules	0.95	>=0.20
MP:0000692	small spleen	0.14	>=0.20
MP:0000936	small telencephalic vesicles	0.89	>=0.20
MP:0001147	small testis	0.81	>=0.20
MP:0010103	small thoracic cage	0.27	>=0.20
MP:0000706	small thymus	0.37	>=0.20
MP:0001093	small trigeminal ganglion	1	>=0.20
ENSG00000080503	SMARCA2 PPI subnetwork	0.21	>=0.20
ENSG00000127616	SMARCA4 PPI subnetwork	0.06	>=0.20
ENSG00000153147	SMARCA5 PPI subnetwork	0.42	>=0.20
ENSG00000173473	SMARCC1 PPI subnetwork	0.04	>=0.20
ENSG00000139613	SMARCC2 PPI subnetwork	0.27	>=0.20
ENSG00000066117	SMARCD1 PPI subnetwork	0.27	>=0.20
ENSG00000108604	SMARCD2 PPI subnetwork	0.73	>=0.20
ENSG00000082014	SMARCD3 PPI subnetwork	0.75	>=0.20
ENSG00000073584	SMARCE1 PPI subnetwork	0.11	>=0.20

ENSG00000136824	SMC2 PPI subnetwork	0.18	>=0.20
ENSG00000108055	SMC3 PPI subnetwork	0.14	>=0.20
ENSG00000113810	SMC4 PPI subnetwork	0.31	>=0.20
ENSG00000100796	SMEK1 PPI subnetwork	0.81	>=0.20
ENSG00000138041	SMEK2 PPI subnetwork	0.9	>=0.20
ENSG00000172062	SMN1 PPI subnetwork	0.39	>=0.20
ENSG00000205571	SMN2 PPI subnetwork	0.39	>=0.20
ENSG00000128602	SMO PPI subnetwork	0.45	>=0.20
GO:0005790	smooth endoplasmic reticulum	0.54	>=0.20
GO:0051145	smooth muscle cell differentiation	1	>=0.20
GO:0014909	smooth muscle cell migration	0.51	>=0.20
GO:0048659	smooth muscle cell proliferation	0.05	>=0.20
GO:0006939	smooth muscle contraction	1	>=0.20
GO:0048745	smooth muscle tissue development	0.98	>=0.20
GO:0007224	smoothened signaling pathway	0.98	>=0.20
ENSG00000198742	SMURF1 PPI subnetwork	0.7	>=0.20
ENSG00000108854	SMURF2 PPI subnetwork	0.79	>=0.20
GO:0005484	SNAP receptor activity	0.55	>=0.20
ENSG00000092531	SNAP23 PPI subnetwork	0.91	>=0.20
ENSG00000132639	SNAP25 PPI subnetwork	0.94	>=0.20
ENSG00000065609	SNAP91 PPI subnetwork	0.81	>=0.20
ENSG00000023608	SNAPC1 PPI subnetwork	0.71	>=0.20
ENSG00000104976	SNAPC2 PPI subnetwork	0.89	>=0.20
ENSG00000164975	SNAPC3 PPI subnetwork	0.84	>=0.20
ENSG00000165684	SNAPC4 PPI subnetwork	0.94	>=0.20
ENSG00000174446	SNAPC5 PPI subnetwork	0.92	>=0.20
GO:0000149	SNARE binding	0.89	>=0.20
GO:0031201	SNARE complex	0.37	>=0.20
ENSG00000145335	SNCA PPI subnetwork	0.72	>=0.20
ENSG00000163877	SNIP1 PPI subnetwork	0.11	>=0.20
GO:0017069	snRNA binding	0.72	>=0.20
GO:0016073	snRNA metabolic process	0.85	>=0.20
GO:0016180	snRNA processing	0.7	>=0.20
ENSG00000144028	SNRNP200 PPI subnetwork	0.06	>=0.20
ENSG00000060688	SNRNP40 PPI subnetwork	0.09	>=0.20
ENSG00000077312	SNRPA PPI subnetwork	0.08	>=0.20
ENSG00000101400	SNTA1 PPI subnetwork	0.82	>=0.20
ENSG00000100603	SNW1 PPI subnetwork	0.07	>=0.20
ENSG00000130340	SNX9 PPI subnetwork	0.37	>=0.20
GO:0035176	social behavior	1	>=0.20
ENSG00000120833	SOCS2 PPI subnetwork	0.03	>=0.20
ENSG00000180008	SOCS4 PPI subnetwork	0.06	>=0.20
ENSG00000170677	SOCS6 PPI subnetwork	0.08	>=0.20
GO:0005272	sodium channel activity	1	>=0.20
GO:0034706	sodium channel complex	1	>=0.20
GO:0071436	sodium ion export	1	>=0.20
GO:0035725	sodium ion transmembrane transport	1	>=0.20

GO:0015081	sodium ion transmembrane transporter activity	0.96	>=0.20
GO:0006814	sodium ion transport	1	>=0.20
GO:0005283	sodium:amino acid symporter activity	0.8	>=0.20
GO:0017153	sodium:dicarboxylate symporter activity	0.99	>=0.20
GO:0015298	solute:cation antiporter activity	0.98	>=0.20
GO:0015294	solute:cation symporter activity	0.76	>=0.20
GO:0015295	solute:hydrogen symporter activity	0.83	>=0.20
GO:0015370	solute:sodium symporter activity	0.63	>=0.20
GO:0015300	solute:solute antiporter activity	0.99	>=0.20
GO:0016444	somatic cell DNA recombination	0.99	>=0.20
GO:0002200	somatic diversification of immune receptors	0.94	>=0.20
GO:0002562	somatic diversification of immune receptors via germline rec	0.99	>=0.20
GO:0016445	somatic diversification of immunoglobulins	0.91	>=0.20
GO:0002208	somatic diversification of immunoglobulins involved in immu	1	>=0.20
GO:0016447	somatic recombination of immunoglobulin gene segments	1	>=0.20
GO:0002204	somatic recombination of immunoglobulin genes involved in	1	>=0.20
GO:0035019	somatic stem cell maintenance	0.98	>=0.20
GO:0061053	somite development	1	>=0.20
GO:0001756	somitogenesis	1	>=0.20
ENSG00000154556	SORBS2 PPI subnetwork	0.07	>=0.20
ENSG00000115904	SOS1 PPI subnetwork	0.04	>=0.20
ENSG00000100485	SOS2 PPI subnetwork	0.44	>=0.20
ENSG00000100146	SOX10 PPI subnetwork	0.97	>=0.20
ENSG00000185591	SP1 PPI subnetwork	0.09	>=0.20
ENSG00000172845	SP3 PPI subnetwork	0.26	>=0.20
ENSG00000008294	SPAG9 PPI subnetwork	0.29	>=0.20
ENSG00000113140	SPARC PPI subnetwork	0.71	>=0.20
ENSG00000152583	SPARCL1 PPI subnetwork	0.9	>=0.20
ENSG00000145375	SPATA5 PPI subnetwork	0.84	>=0.20
ENSG00000161888	SPC24 PPI subnetwork	0.82	>=0.20
ENSG00000152253	SPC25 PPI subnetwork	0.81	>=0.20
ENSG00000128487	SPECC1 PPI subnetwork	0.38	>=0.20
ENSG00000100014	SPECC1L PPI subnetwork	0.47	>=0.20
GO:0010092	specification of organ identity	1	>=0.20
GO:0009799	specification of symmetry	1	>=0.20
ENSG00000072195	SPEG PPI subnetwork	0.04	>=0.20
ENSG00000065526	SPEN PPI subnetwork	0.72	>=0.20
GO:0035036	sperm-egg recognition	0.94	>=0.20
GO:0030317	sperm motility	0.55	>=0.20
GO:0007286	spermatid development	0.95	>=0.20
GO:0048515	spermatid differentiation	0.95	>=0.20
GO:0007283	spermatogenesis	0.96	>=0.20
MP:0002812	spherocytosis	0.47	>=0.20
GO:0046520	sphingoid biosynthetic process	0.95	>=0.20
GO:0046519	sphingoid metabolic process	0.62	>=0.20
GO:0046625	sphingolipid binding	0.24	>=0.20
GO:0030148	sphingolipid biosynthetic process	0.94	>=0.20

GO:0030149	sphingolipid catabolic process	0.47	>=0.20
GO:0006665	sphingolipid metabolic process	0.68	>=0.20
GO:0006684	sphingomyelin metabolic process	0.71	>=0.20
ENSG00000186787	SPIN2B PPI subnetwork	0.34	>=0.20
ENSG00000204271	SPIN3 PPI subnetwork	0.34	>=0.20
MP:0003054	spina bifida	0.63	>=0.20
MP:0005297	spina bifida occulta	0.99	>=0.20
GO:0021527	spinal cord association neuron differentiation	1	>=0.20
GO:0021510	spinal cord development	1	>=0.20
GO:0021513	spinal cord dorsal/ventral patterning	0.99	>=0.20
GO:0021511	spinal cord patterning	0.99	>=0.20
MP:0006054	spinal hemorrhage	0.57	>=0.20
GO:0005819	spindle	0.64	>=0.20
GO:0051225	spindle assembly	0.96	>=0.20
GO:0071173	spindle assembly checkpoint	0.93	>=0.20
GO:0090307	spindle assembly involved in mitosis	0.92	>=0.20
GO:0031577	spindle checkpoint	0.85	>=0.20
GO:0051653	spindle localization	0.87	>=0.20
GO:0005876	spindle microtubule	0.75	>=0.20
GO:0051233	spindle midzone	0.53	>=0.20
GO:0007051	spindle organization	0.99	>=0.20
GO:0000922	spindle pole	0.38	>=0.20
ENSG00000133710	SPINK5 PPI subnetwork	0.86	>=0.20
MP:0000694	spleen hypoplasia	0.34	>=0.20
GO:0000245	spliceosomal complex assembly	0.84	>=0.20
GO:0000387	spliceosomal snRNP assembly	0.99	>=0.20
MP:0004678	split xiphoid process	0.65	>=0.20
ENSG00000169682	SPNS1 PPI subnetwork	0.29	>=0.20
MP:0004029	spontaneous chromosome breakage	0.48	>=0.20
MP:0000951	sporadic seizures	0.96	>=0.20
GO:0002040	sprouting angiogenesis	0.93	>=0.20
ENSG00000163554	SPTA1 PPI subnetwork	0.83	>=0.20
ENSG00000197694	SPTAN1 PPI subnetwork	0.46	>=0.20
ENSG00000070182	SPTB PPI subnetwork	0.82	>=0.20
ENSG00000115306	SPTBN1 PPI subnetwork	0.37	>=0.20
ENSG00000090054	SPTLC1 PPI subnetwork	0.69	>=0.20
ENSG00000137767	SQRDL PPI subnetwork	0.31	>=0.20
ENSG00000080603	SRCAP PPI subnetwork	0.5	>=0.20
ENSG00000153914	SREK1 PPI subnetwork	0.21	>=0.20
ENSG00000153006	SREK1IP1 PPI subnetwork	0.13	>=0.20
ENSG00000112658	SRF PPI subnetwork	0.04	>=0.20
ENSG00000163486	SRGAP2 PPI subnetwork	0.08	>=0.20
ENSG00000196220	SRGAP3 PPI subnetwork	0.53	>=0.20
ENSG00000140319	SRP14 PPI subnetwork	0.17	>=0.20
ENSG00000100883	SRP54 PPI subnetwork	0.7	>=0.20
ENSG00000144867	SRPRB PPI subnetwork	0.21	>=0.20
ENSG00000167978	SRRM2 PPI subnetwork	0.3	>=0.20

ENSG00000136450	SRSF1 PPI subnetwork	0.05	>=0.20
ENSG00000188529	SRSF10 PPI subnetwork	0.15	>=0.20
ENSG00000141380	SS18 PPI subnetwork	0.68	>=0.20
ENSG00000138385	SSB PPI subnetwork	0.66	>=0.20
ENSG00000106028	SSBP1 PPI subnetwork	0.15	>=0.20
ENSG00000124783	SSR1 PPI subnetwork	0.86	>=0.20
ENSG00000149136	SSRP1 PPI subnetwork	0.29	>=0.20
ENSG00000160075	SSU72 PPI subnetwork	0.49	>=0.20
ENSG00000118007	STAG1 PPI subnetwork	0.94	>=0.20
ENSG00000136738	STAM PPI subnetwork	0.06	>=0.20
ENSG00000115145	STAM2 PPI subnetwork	0.76	>=0.20
GO:0001964	startle response	1	>=0.20
ENSG00000170581	STAT2 PPI subnetwork	0.03	>=0.20
ENSG00000124214	STAU1 PPI subnetwork	0.45	>=0.20
GO:0048864	stem cell development	0.97	>=0.20
GO:0048863	stem cell differentiation	0.86	>=0.20
GO:0019827	stem cell maintenance	0.98	>=0.20
GO:0035258	steroid hormone receptor binding	0.04	>=0.20
ENSG00000168439	STIP1 PPI subnetwork	0.35	>=0.20
ENSG00000118046	STK11 PPI subnetwork	0.03	>=0.20
ENSG00000102572	STK24 PPI subnetwork	0.18	>=0.20
ENSG00000115694	STK25 PPI subnetwork	0.37	>=0.20
ENSG00000112079	STK38 PPI subnetwork	0.4	>=0.20
ENSG00000198648	STK39 PPI subnetwork	0.78	>=0.20
ENSG00000101109	STK4 PPI subnetwork	0.88	>=0.20
ENSG00000148175	STOM PPI subnetwork	0.12	>=0.20
ENSG00000125695	STRADA PPI subnetwork	0.17	>=0.20
ENSG00000082146	STRADB PPI subnetwork	0.06	>=0.20
ENSG00000023734	STRAP PPI subnetwork	0.73	>=0.20
GO:0051403	stress-activated MAPK cascade	0.67	>=0.20
GO:0031098	stress-activated protein kinase signaling cascade	0.25	>=0.20
GO:0001725	stress fiber	0.32	>=0.20
GO:0055002	striated muscle cell development	0.97	>=0.20
GO:0051146	striated muscle cell differentiation	0.91	>=0.20
GO:0014855	striated muscle cell proliferation	0.99	>=0.20
GO:0006941	striated muscle contraction	1	>=0.20
GO:0005865	striated muscle thin filament	0.83	>=0.20
GO:0014706	striated muscle tissue development	0.98	>=0.20
GO:0021756	striatum development	0.98	>=0.20
ENSG00000115808	STRN PPI subnetwork	0.41	>=0.20
ENSG00000196792	STRN3 PPI subnetwork	0.99	>=0.20
ENSG00000090372	STRN4 PPI subnetwork	0.99	>=0.20
GO:0005200	structural constituent of cytoskeleton	0.86	>=0.20
GO:0005212	structural constituent of eye lens	0.99	>=0.20
GO:0008307	structural constituent of muscle	0.75	>=0.20
GO:0003735	structural constituent of ribosome	0.97	>=0.20
GO:0043566	structure-specific DNA binding	0.08	>=0.20

ENSG00000163527	STT3B PPI subnetwork	0.98	>=0.20
ENSG00000103266	STUB1 PPI subnetwork	0.8	>=0.20
ENSG00000104915	STX10 PPI subnetwork	0.06	>=0.20
ENSG00000117758	STX12 PPI subnetwork	0.06	>=0.20
ENSG00000124222	STX16 PPI subnetwork	0.06	>=0.20
ENSG00000106089	STX1A PPI subnetwork	1	>=0.20
ENSG00000111450	STX2 PPI subnetwork	0.8	>=0.20
ENSG00000166900	STX3 PPI subnetwork	0.98	>=0.20
ENSG00000103496	STX4 PPI subnetwork	0.87	>=0.20
ENSG00000162236	STX5 PPI subnetwork	0.16	>=0.20
ENSG00000135823	STX6 PPI subnetwork	0.63	>=0.20
ENSG00000079950	STX7 PPI subnetwork	0.55	>=0.20
ENSG00000170310	STX8 PPI subnetwork	0.4	>=0.20
ENSG00000136854	STXBP1 PPI subnetwork	1	>=0.20
ENSG00000076944	STXBP2 PPI subnetwork	0.4	>=0.20
GO:0022838	substrate-specific channel activity	1	>=0.20
GO:0034446	substrate adhesion-dependent cell spreading	0.54	>=0.20
ENSG00000111707	SUDS3 PPI subnetwork	0.31	>=0.20
ENSG00000107882	SUFU PPI subnetwork	0.11	>=0.20
ENSG00000105705	SUGP1 PPI subnetwork	0.04	>=0.20
GO:0015116	sulfate transmembrane transporter activity	0.8	>=0.20
GO:0008484	sulfuric ester hydrolase activity	0.69	>=0.20
ENSG00000188612	SUMO2 PPI subnetwork	0.17	>=0.20
ENSG00000177688	SUMO4 PPI subnetwork	0.06	>=0.20
ENSG00000092201	SUPT16H PPI subnetwork	0.17	>=0.20
ENSG00000196284	SUPT3H PPI subnetwork	0.44	>=0.20
ENSG00000213246	SUPT4H1 PPI subnetwork	0.37	>=0.20
ENSG00000196235	SUPT5H PPI subnetwork	0.34	>=0.20
ENSG00000109111	SUPT6H PPI subnetwork	0.25	>=0.20
ENSG00000148248	SURF4 PPI subnetwork	0.16	>=0.20
ENSG00000148296	SURF6 PPI subnetwork	0.3	>=0.20
ENSG00000152455	SUV39H2 PPI subnetwork	0.05	>=0.20
ENSG00000159164	SV2A PPI subnetwork	1	>=0.20
ENSG00000185518	SV2B PPI subnetwork	0.94	>=0.20
GO:0070603	SWI/SNF-type complex	0.35	>=0.20
GO:0016514	SWI/SNF complex	0.58	>=0.20
GO:0048485	sympathetic nervous system development	1	>=0.20
GO:0015293	symporter activity	0.84	>=0.20
ENSG00000008056	SYN1 PPI subnetwork	0.65	>=0.20
GO:0045202	synapse	1	>=0.20
GO:0007416	synapse assembly	1	>=0.20
GO:0050808	synapse organization	1	>=0.20
GO:0044456	synapse part	1	>=0.20
GO:0007129	synapsis	1	>=0.20
GO:0097060	synaptic membrane	1	>=0.20
GO:0007271	synaptic transmission, cholinergic	0.99	>=0.20
GO:0001963	synaptic transmission, dopaminergic	0.99	>=0.20

GO:0051932	synaptic transmission, GABAergic	1	>=0.20
GO:0035249	synaptic transmission, glutamatergic	1	>=0.20
GO:0008021	synaptic vesicle	1	>=0.20
GO:0048488	synaptic vesicle endocytosis	0.79	>=0.20
GO:0016079	synaptic vesicle exocytosis	1	>=0.20
GO:0030672	synaptic vesicle membrane	1	>=0.20
GO:0048489	synaptic vesicle transport	0.99	>=0.20
GO:0000795	synaptonemal complex	0.96	>=0.20
GO:0007130	synaptonemal complex assembly	0.98	>=0.20
GO:0070193	synaptonemal complex organization	1	>=0.20
GO:0019717	synaptosome	0.9	>=0.20
MP:0000564	syndactyly	0.89	>=0.20
ENSG00000197283	SYNGAP1 PPI subnetwork	0.6	>=0.20
ENSG00000100321	SYNGR1 PPI subnetwork	1	>=0.20
ENSG00000159082	SYNJ1 PPI subnetwork	0.94	>=0.20
ENSG00000078269	SYNJ2 PPI subnetwork	0.73	>=0.20
ENSG00000171992	SYNPO PPI subnetwork	0.35	>=0.20
GO:0017075	syntaxin-1 binding	0.97	>=0.20
GO:0019905	syntaxin binding	0.93	>=0.20
ENSG00000067715	SYT1 PPI subnetwork	1	>=0.20
ENSG00000143858	SYT2 PPI subnetwork	1	>=0.20
ENSG00000213023	SYT3 PPI subnetwork	1	>=0.20
ENSG00000132872	SYT4 PPI subnetwork	1	>=0.20
ENSG00000129990	SYT5 PPI subnetwork	1	>=0.20
GO:0045063	T-helper 1 cell differentiation	0.84	>=0.20
GO:0042088	T-helper 1 type immune response	0.85	>=0.20
GO:0042093	T-helper cell differentiation	0.73	>=0.20
GO:0030315	T-tubule	0.47	>=0.20
GO:0042110	T cell activation	0.33	>=0.20
GO:0002286	T cell activation involved in immune response	0.85	>=0.20
GO:0031295	T cell costimulation	0.8	>=0.20
MP:0002024	T cell derived lymphoma	0.46	>=0.20
GO:0030217	T cell differentiation	0.63	>=0.20
GO:0033077	T cell differentiation in thymus	0.8	>=0.20
GO:0002292	T cell differentiation involved in immune response	0.88	>=0.20
GO:0043029	T cell homeostasis	0.54	>=0.20
GO:0001913	T cell mediated cytotoxicity	1	>=0.20
GO:0002456	T cell mediated immunity	1	>=0.20
GO:0042098	T cell proliferation	0.66	>=0.20
GO:0042101	T cell receptor complex	0.9	>=0.20
GO:0050852	T cell receptor signaling pathway	0.96	>=0.20
GO:0045058	T cell selection	0.99	>=0.20
ENSG00000100324	TAB1 PPI subnetwork	0.12	>=0.20
ENSG00000055208	TAB2 PPI subnetwork	0.6	>=0.20
ENSG00000108264	TADA2A PPI subnetwork	0.13	>=0.20
ENSG00000173011	TADA2B PPI subnetwork	0.26	>=0.20
ENSG00000147133	TAF1 PPI subnetwork	0.29	>=0.20

ENSG00000166337	TAF10 PPI subnetwork	0.19	>=0.20
ENSG00000064995	TAF11 PPI subnetwork	0.28	>=0.20
ENSG00000120656	TAF12 PPI subnetwork	0.27	>=0.20
ENSG00000197780	TAF13 PPI subnetwork	0.55	>=0.20
ENSG00000172660	TAF15 PPI subnetwork	0.07	>=0.20
ENSG00000143498	TAF1A PPI subnetwork	1	>=0.20
ENSG00000115750	TAF1B PPI subnetwork	0.89	>=0.20
ENSG00000103168	TAF1C PPI subnetwork	1	>=0.20
ENSG00000064313	TAF2 PPI subnetwork	0.19	>=0.20
ENSG00000165632	TAF3 PPI subnetwork	0.58	>=0.20
ENSG00000130699	TAF4 PPI subnetwork	0.13	>=0.20
ENSG00000141384	TAF4B PPI subnetwork	0.52	>=0.20
ENSG00000148835	TAF5 PPI subnetwork	0.33	>=0.20
ENSG00000106290	TAF6 PPI subnetwork	0.39	>=0.20
ENSG00000102387	TAF7L PPI subnetwork	0.14	>=0.20
ENSG00000137413	TAF8 PPI subnetwork	0.76	>=0.20
ENSG00000085231	TAF9 PPI subnetwork	0.15	>=0.20
ENSG00000187325	TAF9B PPI subnetwork	0.1	>=0.20
ENSG00000162367	TAL1 PPI subnetwork	0.89	>=0.20
ENSG00000186051	TAL2 PPI subnetwork	0.78	>=0.20
ENSG00000177156	TALDO1 PPI subnetwork	0.54	>=0.20
ENSG00000136560	TANK PPI subnetwork	0.88	>=0.20
ENSG00000160551	TAOK1 PPI subnetwork	0.67	>=0.20
ENSG00000149930	TAOK2 PPI subnetwork	0.41	>=0.20
ENSG00000135090	TAOK3 PPI subnetwork	0.23	>=0.20
ENSG00000168394	TAP1 PPI subnetwork	0.63	>=0.20
ENSG00000206297	TAP1 PPI subnetwork	0.63	>=0.20
ENSG00000112493	TAPBP PPI subnetwork	0.8	>=0.20
ENSG00000206208	TAPBP PPI subnetwork	0.8	>=0.20
ENSG00000206281	TAPBP PPI subnetwork	0.8	>=0.20
ENSG00000139546	TARBP2 PPI subnetwork	0.67	>=0.20
ENSG00000120948	TARDBP PPI subnetwork	0.04	>=0.20
GO:0008527	taste receptor activity	0.37	>=0.20
ENSG00000106052	TAX1BP1 PPI subnetwork	0.42	>=0.20
ENSG00000065882	TBC1D1 PPI subnetwork	0.03	>=0.20
ENSG00000054611	TBC1D22A PPI subnetwork	0.48	>=0.20
ENSG00000136111	TBC1D4 PPI subnetwork	0.13	>=0.20
ENSG00000171530	TBCA PPI subnetwork	1	>=0.20
ENSG00000116957	TBCE PPI subnetwork	0.99	>=0.20
ENSG00000183735	TBK1 PPI subnetwork	0.56	>=0.20
ENSG00000198933	TBKBP1 PPI subnetwork	0.25	>=0.20
ENSG00000101849	TBL1X PPI subnetwork	0.54	>=0.20
ENSG00000177565	TBL1XR1 PPI subnetwork	0.43	>=0.20
ENSG00000112592	TBP PPI subnetwork	0.29	>=0.20
ENSG00000136270	TBRG4 PPI subnetwork	0.5	>=0.20
ENSG00000006638	TBXA2R PPI subnetwork	0.41	>=0.20
ENSG00000187735	TCEA1 PPI subnetwork	0.09	>=0.20

ENSG00000011007	TCEB3 PPI subnetwork	0.51	>=0.20
ENSG00000113649	TCERG1 PPI subnetwork	0.92	>=0.20
ENSG00000140262	TCF12 PPI subnetwork	0.76	>=0.20
ENSG00000071564	TCF3 PPI subnetwork	0.73	>=0.20
ENSG00000196628	TCF4 PPI subnetwork	0.92	>=0.20
ENSG00000120438	TCP1 PPI subnetwork	0.67	>=0.20
ENSG00000139372	TDG PPI subnetwork	0.18	>=0.20
ENSG00000111802	TDP2 PPI subnetwork	0.81	>=0.20
ENSG00000187079	TEAD1 PPI subnetwork	0.51	>=0.20
ENSG00000007866	TEAD3 PPI subnetwork	0.11	>=0.20
ENSG00000197905	TEAD4 PPI subnetwork	0.62	>=0.20
GO:0022029	telencephalon cell migration	0.81	>=0.20
GO:0021537	telencephalon development	0.98	>=0.20
GO:0000782	telomere cap complex	0.77	>=0.20
GO:0000723	telomere maintenance	0.92	>=0.20
GO:0000722	telomere maintenance via recombination	0.98	>=0.20
GO:0032201	telomere maintenance via semi-conservative replication	1	>=0.20
GO:0007004	telomere maintenance via telomerase	0.78	>=0.20
GO:0010833	telomere maintenance via telomere lengthening	0.91	>=0.20
GO:0032200	telomere organization	0.89	>=0.20
GO:0042162	telomeric DNA binding	0.94	>=0.20
GO:0001659	temperature homeostasis	0.94	>=0.20
MP:0005578	teratozoospermia	0.92	>=0.20
ENSG00000147601	TERF1 PPI subnetwork	0.88	>=0.20
ENSG00000132604	TERF2 PPI subnetwork	0.94	>=0.20
ENSG00000166848	TERF2IP PPI subnetwork	0.88	>=0.20
GO:0043195	terminal button	1	>=0.20
GO:0038032	termination of G-protein coupled receptor signaling pathway	1	>=0.20
GO:0006363	termination of RNA polymerase I transcription	0.99	>=0.20
GO:0006369	termination of RNA polymerase II transcription	0.43	>=0.20
GO:0006386	termination of RNA polymerase III transcription	1	>=0.20
GO:0023021	termination of signal transduction	1	>=0.20
ENSG00000164362	TERT PPI subnetwork	0.63	>=0.20
ENSG00000135269	TES PPI subnetwork	0.75	>=0.20
MP:0001940	testis hypoplasia	1	>=0.20
MP:0006262	testis tumor	0.14	>=0.20
GO:0033014	tetrapyrrole biosynthetic process	0.75	>=0.20
ENSG00000136891	TEX10 PPI subnetwork	0.75	>=0.20
ENSG00000198176	TFDP1 PPI subnetwork	0.12	>=0.20
ENSG00000114126	TFDP2 PPI subnetwork	0.08	>=0.20
ENSG00000068323	TFE3 PPI subnetwork	0.15	>=0.20
ENSG00000105329	TGFB1 PPI subnetwork	0.04	>=0.20
ENSG00000092969	TGFB2 PPI subnetwork	0.09	>=0.20
ENSG00000119699	TGFB3 PPI subnetwork	0.13	>=0.20
ENSG00000120708	TGFBI PPI subnetwork	0.32	>=0.20
ENSG00000106799	TGFBR1 PPI subnetwork	0.04	>=0.20
ENSG00000177426	TGIF1 PPI subnetwork	0.35	>=0.20

ENSG00000198959	TGM2 PPI subnetwork	0.54	>=0.20
ENSG00000137574	TGS1 PPI subnetwork	0.12	>=0.20
ENSG00000101158	TH1L PPI subnetwork	0.58	>=0.20
ENSG00000137801	THBS1 PPI subnetwork	0.07	>=0.20
ENSG00000186340	THBS2 PPI subnetwork	0.58	>=0.20
MP:0001219	thick epidermis	0.06	>=0.20
MP:0010724	thick interventricular septum	0.07	>=0.20
MP:0011143	thick lung-associated mesenchyme	0.9	>=0.20
MP:0000890	thin cerebellar molecular layer	1	>=0.20
MP:0006254	thin cerebral cortex	0.3	>=0.20
MP:0000761	thin diaphragm muscle	0.97	>=0.20
MP:0008511	thin retinal inner nuclear layer	0.85	>=0.20
MP:0008515	thin retinal outer nuclear layer	0.93	>=0.20
MP:0008519	thin retinal outer plexiform layer	0.42	>=0.20
GO:0035384	thioester biosynthetic process	0.26	>=0.20
ENSG00000125676	THOC2 PPI subnetwork	0.09	>=0.20
ENSG00000131652	THOC6 PPI subnetwork	0.54	>=0.20
MP:0004618	thoracic vertebral transformation	0.22	>=0.20
ENSG00000054118	THRAP3 PPI subnetwork	0.24	>=0.20
ENSG00000151090	THRB PPI subnetwork	0.4	>=0.20
GO:0004298	threonine-type endopeptidase activity	0.84	>=0.20
GO:0070003	threonine-type peptidase activity	0.84	>=0.20
ENSG00000066654	THUMPD1 PPI subnetwork	0.37	>=0.20
ENSG00000154096	THY1 PPI subnetwork	0.68	>=0.20
GO:0045061	thymic T cell selection	1	>=0.20
MP:0003644	thymus atrophy	0.54	>=0.20
MP:0000711	thymus cortex hypoplasia	0.87	>=0.20
GO:0048538	thymus development	1	>=0.20
MP:0000708	thymus hyperplasia	0.04	>=0.20
MP:0001823	thymus hypoplasia	0.33	>=0.20
GO:0030878	thyroid gland development	1	>=0.20
GO:0046966	thyroid hormone receptor binding	0.63	>=0.20
ENSG00000151923	TIAL1 PPI subnetwork	0.78	>=0.20
GO:0005923	tight junction	0.89	>=0.20
GO:0070830	tight junction assembly	1	>=0.20
ENSG00000111602	TIMELESS PPI subnetwork	0.61	>=0.20
ENSG00000099800	TIMM13 PPI subnetwork	0.89	>=0.20
ENSG00000035862	TIMP2 PPI subnetwork	0.23	>=0.20
ENSG00000092330	TINF2 PPI subnetwork	0.89	>=0.20
GO:0090130	tissue migration	1	>=0.20
GO:0048729	tissue morphogenesis	0.99	>=0.20
GO:0048771	tissue remodeling	0.17	>=0.20
GO:0031432	titin binding	0.94	>=0.20
ENSG00000104067	TJP1 PPI subnetwork	0.92	>=0.20
ENSG00000119139	TJP2 PPI subnetwork	0.34	>=0.20
ENSG00000196781	TLE1 PPI subnetwork	0.45	>=0.20
ENSG00000106829	TLE4 PPI subnetwork	0.95	>=0.20

ENSG00000137076	TLN1 PPI subnetwork	0.64	>=0.20
ENSG00000107807	TLX1 PPI subnetwork	0.16	>=0.20
ENSG00000100926	TM9SF1 PPI subnetwork	0.07	>=0.20
ENSG00000155957	TMBIM4 PPI subnetwork	0.76	>=0.20
ENSG00000170876	TMEM43 PPI subnetwork	0.28	>=0.20
ENSG00000185973	TMLHE PPI subnetwork	0.51	>=0.20
ENSG00000136842	TMOD1 PPI subnetwork	0.21	>=0.20
ENSG00000138594	TMOD3 PPI subnetwork	0.15	>=0.20
ENSG00000120802	TMPO PPI subnetwork	0.4	>=0.20
ENSG00000205542	TMSB4X PPI subnetwork	0.21	>=0.20
ENSG00000139921	TMX1 PPI subnetwork	0.31	>=0.20
ENSG00000041982	TNC PPI subnetwork	0.32	>=0.20
ENSG00000204490	TNF PPI subnetwork	0.93	>=0.20
ENSG00000206439	TNF PPI subnetwork	0.93	>=0.20
ENSG00000118503	TNFAIP3 PPI subnetwork	0.22	>=0.20
ENSG00000104689	TNFRSF10A PPI subnetwork	0.59	>=0.20
ENSG00000120889	TNFRSF10B PPI subnetwork	0.98	>=0.20
ENSG00000173530	TNFRSF10D PPI subnetwork	0.13	>=0.20
ENSG00000141655	TNFRSF11A PPI subnetwork	0.73	>=0.20
ENSG00000067182	TNFRSF1A PPI subnetwork	0.14	>=0.20
ENSG00000028137	TNFRSF1B PPI subnetwork	0.47	>=0.20
ENSG00000120949	TNFRSF8 PPI subnetwork	0.54	>=0.20
ENSG00000121858	TNFSF10 PPI subnetwork	0.55	>=0.20
ENSG00000120659	TNFSF11 PPI subnetwork	0.52	>=0.20
ENSG00000154310	TNIK PPI subnetwork	0.8	>=0.20
ENSG00000145901	TNIP1 PPI subnetwork	0.84	>=0.20
ENSG00000168884	TNIP2 PPI subnetwork	0.48	>=0.20
ENSG00000174292	TNK1 PPI subnetwork	0.05	>=0.20
ENSG00000114854	TNNC1 PPI subnetwork	0.51	>=0.20
ENSG00000129991	TNNI3 PPI subnetwork	0.51	>=0.20
ENSG00000105048	TNNT1 PPI subnetwork	0.99	>=0.20
ENSG00000118194	TNNT2 PPI subnetwork	0.26	>=0.20
ENSG00000083312	TNPO1 PPI subnetwork	0.32	>=0.20
ENSG00000064419	TNPO3 PPI subnetwork	0.16	>=0.20
ENSG00000131746	TNS4 PPI subnetwork	0.12	>=0.20
ENSG00000168477	TNXB PPI subnetwork	0.27	>=0.20
ENSG00000206258	TNXB PPI subnetwork	0.6	>=0.20
ENSG00000141232	TOB1 PPI subnetwork	0.25	>=0.20
GO:0034130	toll-like receptor 1 signaling pathway	0.36	>=0.20
GO:0034134	toll-like receptor 2 signaling pathway	0.37	>=0.20
GO:0034138	toll-like receptor 3 signaling pathway	0.66	>=0.20
GO:0002224	toll-like receptor signaling pathway	0.34	>=0.20
ENSG00000025772	TOMM34 PPI subnetwork	1	>=0.20
ENSG00000130204	TOMM40 PPI subnetwork	0.51	>=0.20
ENSG00000154174	TOMM70A PPI subnetwork	1	>=0.20
GO:0043586	tongue development	0.99	>=0.20
MP:0003997	tonic-clonic seizures	0.78	>=0.20

MP:0002826	tonic seizures	1	>=0.20
GO:0034505	tooth mineralization	0.99	>=0.20
ENSG00000198900	TOP1 PPI subnetwork	0.69	>=0.20
ENSG00000131747	TOP2A PPI subnetwork	0.51	>=0.20
ENSG00000077097	TOP2B PPI subnetwork	0.32	>=0.20
ENSG00000177302	TOP3A PPI subnetwork	1	>=0.20
ENSG00000197579	TOPORS PPI subnetwork	0.97	>=0.20
GO:0031929	TOR signaling cascade	0.61	>=0.20
MP:0010263	total cataracts	1	>=0.20
ENSG00000198846	TOX PPI subnetwork	0.92	>=0.20
ENSG00000103460	TOX3 PPI subnetwork	0.92	>=0.20
ENSG00000092203	TOX4 PPI subnetwork	0.41	>=0.20
ENSG00000141510	TP53 PPI subnetwork	0.07	>=0.20
ENSG00000067369	TP53BP1 PPI subnetwork	0.98	>=0.20
ENSG00000143514	TP53BP2 PPI subnetwork	0.13	>=0.20
ENSG00000172315	TP53RK PPI subnetwork	0.61	>=0.20
ENSG00000078900	TP73 PPI subnetwork	0.75	>=0.20
ENSG00000076554	TPD52 PPI subnetwork	1	>=0.20
ENSG00000111907	TPD52L1 PPI subnetwork	0.73	>=0.20
ENSG00000101150	TPD52L2 PPI subnetwork	1	>=0.20
ENSG00000111669	TPI1 PPI subnetwork	0.59	>=0.20
ENSG00000140416	TPM1 PPI subnetwork	0.84	>=0.20
ENSG00000198467	TPM2 PPI subnetwork	0.25	>=0.20
ENSG00000143549	TPM3 PPI subnetwork	0.59	>=0.20
ENSG00000047410	TPR PPI subnetwork	0.85	>=0.20
ENSG00000102871	TRADD PPI subnetwork	0.4	>=0.20
ENSG00000056558	TRAF1 PPI subnetwork	0.57	>=0.20
ENSG00000127191	TRAF2 PPI subnetwork	0.63	>=0.20
ENSG00000056972	TRAF3IP2 PPI subnetwork	0.55	>=0.20
ENSG00000009790	TRAF3IP3 PPI subnetwork	0.33	>=0.20
ENSG00000076604	TRAF4 PPI subnetwork	0.18	>=0.20
ENSG00000082512	TRAF5 PPI subnetwork	0.86	>=0.20
ENSG00000183763	TRAIP PPI subnetwork	0.91	>=0.20
GO:0005802	trans-Golgi network	0.84	>=0.20
GO:0006283	transcription-coupled nucleotide-excision repair	0.96	>=0.20
GO:0003712	transcription cofactor activity	0.03	>=0.20
GO:0003714	transcription corepressor activity	0.07	>=0.20
GO:0008023	transcription elongation factor complex	0.72	>=0.20
GO:0006362	transcription elongation from RNA polymerase I promoter	0.99	>=0.20
GO:0006368	transcription elongation from RNA polymerase II promoter	0.7	>=0.20
GO:0006385	transcription elongation from RNA polymerase III promoter	1	>=0.20
GO:0006354	transcription elongation, DNA-dependent	0.63	>=0.20
GO:0008134	transcription factor binding	0.04	>=0.20
GO:0000989	transcription factor binding transcription factor activity	0.03	>=0.20
GO:0005667	transcription factor complex	0.18	>=0.20
GO:0005669	transcription factor TFIID complex	0.88	>=0.20
GO:0006360	transcription from RNA polymerase I promoter	1	>=0.20

GO:0006383	transcription from RNA polymerase III promoter	0.99	>=0.20
GO:0006361	transcription initiation from RNA polymerase I promoter	1	>=0.20
GO:0006367	transcription initiation from RNA polymerase II promoter	0.84	>=0.20
GO:0006352	transcription initiation, DNA-dependent	0.78	>=0.20
GO:0044212	transcription regulatory region DNA binding	0.03	>=0.20
GO:0000976	transcription regulatory region sequence-specific DNA bindin	0.92	>=0.20
GO:0017053	transcriptional repressor complex	0.1	>=0.20
GO:0016757	transferase activity, transferring glycosyl groups	0.72	>=0.20
GO:0016758	transferase activity, transferring hexosyl groups	0.88	>=0.20
GO:0033572	transferrin transport	0.56	>=0.20
GO:0005024	transforming growth factor beta-activated receptor activity	0.35	>=0.20
GO:0050431	transforming growth factor beta binding	0.18	>=0.20
GO:0005160	transforming growth factor beta receptor binding	0.8	>=0.20
GO:0007179	transforming growth factor beta receptor signaling pathway	0.82	>=0.20
GO:0005072	transforming growth factor beta receptor, cytoplasmic media	0.23	>=0.20
GO:0000041	transition metal ion transport	0.54	>=0.20
GO:0006412	translation	0.65	>=0.20
GO:0003746	translation elongation factor activity	0.74	>=0.20
GO:0008135	translation factor activity, nucleic acid binding	0.54	>=0.20
GO:0003743	translation initiation factor activity	0.76	>=0.20
GO:0045182	translation regulator activity	0.68	>=0.20
GO:0006414	translational elongation	0.94	>=0.20
GO:0006413	translational initiation	0.91	>=0.20
GO:0006415	translational termination	0.99	>=0.20
GO:0019199	transmembrane receptor protein kinase activity	0.2	>=0.20
GO:0019198	transmembrane receptor protein phosphatase activity	0.89	>=0.20
GO:0004675	transmembrane receptor protein serine/threonine kinase act	0.35	>=0.20
GO:0007178	transmembrane receptor protein serine/threonine kinase sig	0.9	>=0.20
GO:0004714	transmembrane receptor protein tyrosine kinase activity	0.3	>=0.20
GO:0005001	transmembrane receptor protein tyrosine phosphatase activi	0.89	>=0.20
GO:0030133	transport vesicle	0.41	>=0.20
GO:0030658	transport vesicle membrane	0.65	>=0.20
MP:0004110	transposition of great arteries	1	>=0.20
ENSG00000126602	TRAP1 PPI subnetwork	0.62	>=0.20
ENSG00000181029	TRAPPC5 PPI subnetwork	0.33	>=0.20
ENSG00000163519	TRAT1 PPI subnetwork	0.42	>=0.20
MP:0000745	tremors	0.88	>=0.20
ENSG00000101255	TRIB3 PPI subnetwork	0.04	>=0.20
GO:0006099	tricarboxylic acid cycle	0.9	>=0.20
ENSG00000132109	TRIM21 PPI subnetwork	0.74	>=0.20
ENSG00000119401	TRIM32 PPI subnetwork	0.67	>=0.20
ENSG00000204599	TRIM39 PPI subnetwork	0.55	>=0.20
ENSG00000206495	TRIM39 PPI subnetwork	0.55	>=0.20
ENSG00000163462	TRIM46 PPI subnetwork	1	>=0.20
ENSG00000158022	TRIM63 PPI subnetwork	0.96	>=0.20
ENSG00000100815	TRIP11 PPI subnetwork	0.07	>=0.20
ENSG00000153827	TRIP12 PPI subnetwork	0.45	>=0.20

ENSG00000103671	TRIP4 PPI subnetwork	0.05	>=0.20
ENSG00000121486	TRMT1L PPI subnetwork	0.14	>=0.20
GO:0043039	tRNA aminoacylation	0.81	>=0.20
GO:0006418	tRNA aminoacylation for protein translation	0.83	>=0.20
GO:0008175	tRNA methyltransferase activity	0.99	>=0.20
GO:0001829	trophectodermal cell differentiation	0.96	>=0.20
GO:0005523	tropomyosin binding	0.99	>=0.20
ENSG00000138741	TRPC3 PPI subnetwork	0.75	>=0.20
ENSG00000072315	TRPC5 PPI subnetwork	0.99	>=0.20
ENSG00000137672	TRPC6 PPI subnetwork	0.99	>=0.20
ENSG00000196367	TRRAP PPI subnetwork	0.06	>=0.20
ENSG00000165699	TSC1 PPI subnetwork	0.13	>=0.20
ENSG00000103197	TSC2 PPI subnetwork	0.11	>=0.20
ENSG00000102804	TSC22D1 PPI subnetwork	0.17	>=0.20
ENSG00000157514	TSC22D3 PPI subnetwork	0.38	>=0.20
ENSG00000074319	TSG101 PPI subnetwork	0.36	>=0.20
ENSG00000145777	TSLP PPI subnetwork	0.05	>=0.20
ENSG00000113312	TTC1 PPI subnetwork	0.46	>=0.20
ENSG00000198677	TTC37 PPI subnetwork	0.9	>=0.20
ENSG00000125482	TTF1 PPI subnetwork	0.86	>=0.20
ENSG00000116830	TTF2 PPI subnetwork	0.44	>=0.20
ENSG00000100304	TTLL12 PPI subnetwork	0.12	>=0.20
ENSG00000214021	TTLL3 PPI subnetwork	0.52	>=0.20
ENSG00000155657	TTN PPI subnetwork	0.69	>=0.20
ENSG00000167553	TUBA1C PPI subnetwork	0.37	>=0.20
ENSG00000198033	TUBA3C PPI subnetwork	0.43	>=0.20
ENSG00000075886	TUBA3D PPI subnetwork	0.43	>=0.20
ENSG00000127824	TUBA4A PPI subnetwork	0.05	>=0.20
ENSG00000183311	TUBB PPI subnetwork	0.12	>=0.20
ENSG00000196230	TUBB PPI subnetwork	0.12	>=0.20
ENSG00000198211	TUBB3 PPI subnetwork	0.1	>=0.20
ENSG00000104833	TUBB4A PPI subnetwork	0.27	>=0.20
ENSG00000188229	TUBB4B PPI subnetwork	0.24	>=0.20
GO:0060606	tube closure	1	>=0.20
GO:0035295	tube development	0.62	>=0.20
GO:0035148	tube formation	0.99	>=0.20
GO:0035239	tube morphogenesis	0.86	>=0.20
ENSG00000131462	TUBG1 PPI subnetwork	0.8	>=0.20
ENSG00000037042	TUBG2 PPI subnetwork	0.99	>=0.20
ENSG00000130640	TUBGCP2 PPI subnetwork	0.2	>=0.20
GO:0004835	tubulin-tyrosine ligase activity	1	>=0.20
GO:0015631	tubulin binding	0.92	>=0.20
GO:0005031	tumor necrosis factor-activated receptor activity	0.61	>=0.20
GO:0033209	tumor necrosis factor-mediated signaling pathway	0.79	>=0.20
GO:0005164	tumor necrosis factor receptor binding	0.98	>=0.20
GO:0032813	tumor necrosis factor receptor superfamily binding	0.93	>=0.20
ENSG00000149016	TUT1 PPI subnetwork	0.1	>=0.20

ENSG00000136810	TXN PPI subnetwork	0.56	>=0.20
ENSG00000105397	TYK2 PPI subnetwork	0.07	>=0.20
GO:0042092	type 2 immune response	0.37	>=0.20
GO:0060337	type I interferon-mediated signaling pathway	0.99	>=0.20
GO:0032606	type I interferon production	0.75	>=0.20
GO:0007260	tyrosine phosphorylation of STAT protein	0.81	>=0.20
GO:0005689	U12-type spliceosomal complex	0.68	>=0.20
ENSG00000160201	U2AF1 PPI subnetwork	0.1	>=0.20
ENSG00000063244	U2AF2 PPI subnetwork	0.19	>=0.20
ENSG00000163714	U2SURP PPI subnetwork	0.12	>=0.20
ENSG00000137831	UACA PPI subnetwork	0.63	>=0.20
ENSG00000126261	UBA2 PPI subnetwork	1	>=0.20
ENSG00000144744	UBA3 PPI subnetwork	0.92	>=0.20
ENSG00000170315	UBB PPI subnetwork	0.11	>=0.20
ENSG00000150991	UBC PPI subnetwork	0.08	>=0.20
ENSG00000077721	UBE2A PPI subnetwork	0.94	>=0.20
ENSG00000119048	UBE2B PPI subnetwork	0.93	>=0.20
ENSG00000175063	UBE2C PPI subnetwork	0.75	>=0.20
ENSG00000072401	UBE2D1 PPI subnetwork	0.89	>=0.20
ENSG00000131508	UBE2D2 PPI subnetwork	0.67	>=0.20
ENSG00000109332	UBE2D3 PPI subnetwork	0.36	>=0.20
ENSG00000078967	UBE2D4 PPI subnetwork	0.83	>=0.20
ENSG00000170142	UBE2E1 PPI subnetwork	0.86	>=0.20
ENSG00000170035	UBE2E3 PPI subnetwork	0.65	>=0.20
ENSG00000103275	UBE2I PPI subnetwork	0.53	>=0.20
ENSG00000160087	UBE2J2 PPI subnetwork	0.29	>=0.20
ENSG00000078140	UBE2K PPI subnetwork	0.99	>=0.20
ENSG00000130725	UBE2M PPI subnetwork	0.95	>=0.20
ENSG00000177889	UBE2N PPI subnetwork	0.92	>=0.20
ENSG00000107341	UBE2R2 PPI subnetwork	0.39	>=0.20
ENSG00000169139	UBE2V2 PPI subnetwork	1	>=0.20
ENSG00000114062	UBE3A PPI subnetwork	0.48	>=0.20
ENSG00000009335	UBE3C PPI subnetwork	0.15	>=0.20
GO:0006511	ubiquitin-dependent protein catabolic process	0.84	>=0.20
GO:0004842	ubiquitin-protein ligase activity	0.86	>=0.20
GO:0004843	ubiquitin-specific protease activity	0.94	>=0.20
GO:0043130	ubiquitin binding	0.74	>=0.20
GO:0000151	ubiquitin ligase complex	0.43	>=0.20
GO:0031625	ubiquitin protein ligase binding	0.16	>=0.20
GO:0004221	ubiquitin thiolesterase activity	0.87	>=0.20
ENSG00000135018	UBQLN1 PPI subnetwork	0.9	>=0.20
ENSG00000188021	UBQLN2 PPI subnetwork	0.41	>=0.20
ENSG00000160803	UBQLN4 PPI subnetwork	0.95	>=0.20
ENSG00000159459	UBR1 PPI subnetwork	0.32	>=0.20
ENSG00000024048	UBR2 PPI subnetwork	0.37	>=0.20
ENSG00000127481	UBR4 PPI subnetwork	0.62	>=0.20
ENSG00000104517	UBR5 PPI subnetwork	0.31	>=0.20

ENSG00000108312	UBTF PPI subnetwork	0.96	>=0.20
ENSG00000162191	UBXN1 PPI subnetwork	0.04	>=0.20
ENSG00000163960	UBXN7 PPI subnetwork	0.84	>=0.20
ENSG00000154277	UCHL1 PPI subnetwork	0.96	>=0.20
ENSG00000116750	UCHL5 PPI subnetwork	0.65	>=0.20
GO:0035250	UDP-galactosyltransferase activity	0.91	>=0.20
GO:0008194	UDP-glycosyltransferase activity	0.97	>=0.20
ENSG00000070010	UFD1L PPI subnetwork	0.07	>=0.20
ENSG00000109814	UGDH PPI subnetwork	0.66	>=0.20
ENSG00000136731	UGGT1 PPI subnetwork	0.66	>=0.20
ENSG00000147854	UHRF2 PPI subnetwork	0.67	>=0.20
ENSG00000109103	UNC119 PPI subnetwork	0.03	>=0.20
ENSG00000198722	UNC13B PPI subnetwork	0.97	>=0.20
GO:0051082	unfolded protein binding	0.81	>=0.20
ENSG00000076248	UNG PPI subnetwork	0.34	>=0.20
MP:0001491	unresponsive to tactile stimuli	0.98	>=0.20
GO:0006636	unsaturated fatty acid biosynthetic process	0.95	>=0.20
GO:0033559	unsaturated fatty acid metabolic process	0.93	>=0.20
ENSG00000005007	UPF1 PPI subnetwork	0.51	>=0.20
ENSG00000151461	UPF2 PPI subnetwork	0.55	>=0.20
ENSG00000169062	UPF3A PPI subnetwork	0.53	>=0.20
ENSG00000156467	UQCRB PPI subnetwork	0.97	>=0.20
ENSG00000010256	UQCRC1 PPI subnetwork	0.96	>=0.20
ENSG00000169021	UQCRFS1 PPI subnetwork	0.78	>=0.20
ENSG00000173660	UQCRH PPI subnetwork	0.99	>=0.20
GO:0046415	urate metabolic process	0.98	>=0.20
GO:0001657	ureteric bud development	1	>=0.20
GO:0060675	ureteric bud morphogenesis	1	>=0.20
ENSG00000105176	URI1 PPI subnetwork	0.36	>=0.20
GO:0001655	urogenital system development	0.93	>=0.20
ENSG00000103194	USP10 PPI subnetwork	0.24	>=0.20
ENSG00000102226	USP11 PPI subnetwork	0.15	>=0.20
ENSG00000101557	USP14 PPI subnetwork	0.54	>=0.20
ENSG00000124422	USP22 PPI subnetwork	0.09	>=0.20
ENSG00000134588	USP26 PPI subnetwork	0.09	>=0.20
ENSG00000187555	USP7 PPI subnetwork	0.83	>=0.20
GO:0060065	uterus development	0.95	>=0.20
ENSG00000156697	UTP14A PPI subnetwork	0.91	>=0.20
ENSG00000108651	UTP6 PPI subnetwork	0.23	>=0.20
ENSG00000152818	UTRN PPI subnetwork	0.51	>=0.20
GO:0033151	V(D)J recombination	0.82	>=0.20
ENSG00000103043	VAC14 PPI subnetwork	0.6	>=0.20
GO:0005774	vacuolar membrane	0.09	>=0.20
GO:0016471	vacuolar proton-transporting V-type ATPase complex	0.96	>=0.20
GO:0007034	vacuolar transport	0.18	>=0.20
GO:0007033	vacuole organization	0.43	>=0.20
ENSG00000139190	VAMP1 PPI subnetwork	0.99	>=0.20

ENSG00000049245	VAMP3 PPI subnetwork	0.69	>=0.20
ENSG00000117533	VAMP4 PPI subnetwork	0.64	>=0.20
ENSG00000124333	VAMP7 PPI subnetwork	0.78	>=0.20
ENSG00000118640	VAMP8 PPI subnetwork	0.41	>=0.20
ENSG00000101558	VAPA PPI subnetwork	0.56	>=0.20
ENSG00000124164	VAPB PPI subnetwork	0.79	>=0.20
MP:0002940	variable body spotting	0.73	>=0.20
ENSG00000096171	VARS PPI subnetwork	0.42	>=0.20
ENSG00000204394	VARS PPI subnetwork	0.42	>=0.20
GO:0010573	vascular endothelial growth factor production	0.24	>=0.20
GO:0048010	vascular endothelial growth factor receptor signaling pathwa	0.2	>=0.20
GO:0003018	vascular process in circulatory system	0.13	>=0.20
GO:0001570	vasculogenesis	0.49	>=0.20
GO:0042310	vasoconstriction	0.44	>=0.20
ENSG00000125753	VASP PPI subnetwork	0.13	>=0.20
ENSG00000108828	VAT1 PPI subnetwork	1	>=0.20
ENSG00000171724	VAT1L PPI subnetwork	1	>=0.20
ENSG00000160293	VAV2 PPI subnetwork	0.3	>=0.20
ENSG00000134215	VAV3 PPI subnetwork	0.06	>=0.20
ENSG00000155959	VBP1 PPI subnetwork	0.99	>=0.20
ENSG00000162692	VCAM1 PPI subnetwork	0.22	>=0.20
ENSG00000038427	VCAN PPI subnetwork	0.22	>=0.20
ENSG00000035403	VCL PPI subnetwork	0.18	>=0.20
ENSG00000175073	VCPIP1 PPI subnetwork	0.12	>=0.20
ENSG00000213585	VDAC1 PPI subnetwork	0.05	>=0.20
ENSG00000165637	VDAC2 PPI subnetwork	0.89	>=0.20
ENSG00000078668	VDAC3 PPI subnetwork	0.22	>=0.20
ENSG00000111424	VDR PPI subnetwork	0.35	>=0.20
ENSG00000112715	VEGFA PPI subnetwork	0.11	>=0.20
GO:0021517	ventral spinal cord development	1	>=0.20
GO:0055012	ventricular cardiac muscle cell differentiation	0.72	>=0.20
GO:0003229	ventricular cardiac muscle tissue development	0.98	>=0.20
GO:0055010	ventricular cardiac muscle tissue morphogenesis	0.99	>=0.20
MP:0000279	ventricular hypoplasia	0.28	>=0.20
MP:0010402	ventricular septal defect	0.44	>=0.20
GO:0003281	ventricular septum development	0.95	>=0.20
GO:0060412	ventricular septum morphogenesis	0.78	>=0.20
MP:0004609	vertebral fusion	0.41	>=0.20
MP:0003036	vertebral transformation	0.52	>=0.20
GO:0000038	very long-chain fatty acid metabolic process	0.48	>=0.20
GO:0006901	vesicle coating	0.3	>=0.20
GO:0048278	vesicle docking	0.74	>=0.20
GO:0006904	vesicle docking involved in exocytosis	0.84	>=0.20
GO:0006906	vesicle fusion	0.33	>=0.20
GO:0051648	vesicle localization	0.83	>=0.20
GO:0012506	vesicle membrane	0.87	>=0.20
GO:0016050	vesicle organization	0.22	>=0.20

GO:0006903	vesicle targeting	0.35	>=0.20
GO:0048199	vesicle targeting, to, from or within Golgi	0.38	>=0.20
GO:0047496	vesicle transport along microtubule	1	>=0.20
MP:0004324	vestibular hair cell degeneration	0.83	>=0.20
ENSG00000134086	VHL PPI subnetwork	0.07	>=0.20
ENSG00000026025	VIM PPI subnetwork	0.09	>=0.20
ENSG00000114812	VIPR1 PPI subnetwork	0.81	>=0.20
GO:0019080	viral genome expression	0.83	>=0.20
GO:0019079	viral genome replication	0.3	>=0.20
GO:0019058	viral infectious cycle	0.27	>=0.20
GO:0016032	viral reproduction	0.21	>=0.20
GO:0022415	viral reproductive process	0.19	>=0.20
GO:0019083	viral transcription	0.83	>=0.20
GO:0007632	visual behavior	1	>=0.20
GO:0008542	visual learning	1	>=0.20
GO:0007601	visual perception	1	>=0.20
GO:0006776	vitamin A metabolic process	0.48	>=0.20
GO:0042809	vitamin D receptor binding	0.57	>=0.20
GO:0005245	voltage-gated calcium channel activity	1	>=0.20
GO:0005891	voltage-gated calcium channel complex	1	>=0.20
GO:0022843	voltage-gated cation channel activity	1	>=0.20
GO:0022832	voltage-gated channel activity	1	>=0.20
GO:0005247	voltage-gated chloride channel activity	0.62	>=0.20
GO:0005244	voltage-gated ion channel activity	1	>=0.20
GO:0005249	voltage-gated potassium channel activity	1	>=0.20
GO:0008076	voltage-gated potassium channel complex	1	>=0.20
GO:0005248	voltage-gated sodium channel activity	1	>=0.20
GO:0001518	voltage-gated sodium channel complex	1	>=0.20
ENSG00000145041	VPRBP PPI subnetwork	0.97	>=0.20
ENSG00000197969	VPS13A PPI subnetwork	0.55	>=0.20
ENSG00000215305	VPS16 PPI subnetwork	0.27	>=0.20
ENSG00000104142	VPS18 PPI subnetwork	0.12	>=0.20
ENSG00000069329	VPS35 PPI subnetwork	0.39	>=0.20
ENSG00000136631	VPS45 PPI subnetwork	0.11	>=0.20
ENSG00000141252	VPS53 PPI subnetwork	0.12	>=0.20
ENSG00000163159	VPS72 PPI subnetwork	0.74	>=0.20
ENSG00000156931	VPS8 PPI subnetwork	0.27	>=0.20
ENSG00000163032	VSNL1 PPI subnetwork	0.66	>=0.20
ENSG00000151532	VTI1A PPI subnetwork	0.12	>=0.20
ENSG00000100568	VTI1B PPI subnetwork	0.74	>=0.20
ENSG00000110799	VWF PPI subnetwork	0.11	>=0.20
ENSG00000015285	WAS PPI subnetwork	0.03	>=0.20
ENSG00000112290	WASF1 PPI subnetwork	0.11	>=0.20
ENSG00000158195	WASF2 PPI subnetwork	0.15	>=0.20
ENSG00000106299	WASL PPI subnetwork	0.1	>=0.20
GO:0005372	water transmembrane transporter activity	0.27	>=0.20
GO:0006833	water transport	0.88	>=0.20

MP:0000410	waved hair	0.75	>=0.20
ENSG00000084463	WBP11 PPI subnetwork	0.44	>=0.20
ENSG00000120688	WBP4 PPI subnetwork	0.07	>=0.20
ENSG00000198554	WDHD1 PPI subnetwork	1	>=0.20
ENSG00000071127	WDR1 PPI subnetwork	0.22	>=0.20
ENSG00000120008	WDR11 PPI subnetwork	0.74	>=0.20
ENSG00000138442	WDR12 PPI subnetwork	0.34	>=0.20
ENSG00000162923	WDR26 PPI subnetwork	0.94	>=0.20
ENSG00000136709	WDR33 PPI subnetwork	0.09	>=0.20
ENSG00000118965	WDR35 PPI subnetwork	0.31	>=0.20
ENSG00000047056	WDR37 PPI subnetwork	0.99	>=0.20
ENSG00000163811	WDR43 PPI subnetwork	0.78	>=0.20
ENSG00000196363	WDR5 PPI subnetwork	0.05	>=0.20
ENSG00000196981	WDR5B PPI subnetwork	0.89	>=0.20
ENSG00000133316	WDR74 PPI subnetwork	0.57	>=0.20
ENSG00000092470	WDR76 PPI subnetwork	0.92	>=0.20
ENSG00000116455	WDR77 PPI subnetwork	0.31	>=0.20
ENSG00000164091	WDR82 PPI subnetwork	0.81	>=0.20
MP:0000746	weakness	0.71	>=0.20
ENSG00000166483	WEE1 PPI subnetwork	0.54	>=0.20
MP:0002938	white spotting	0.77	>=0.20
ENSG00000185049	WHSC2 PPI subnetwork	0.19	>=0.20
ENSG00000156076	WIF1 PPI subnetwork	1	>=0.20
ENSG00000115935	WIPF1 PPI subnetwork	0.98	>=0.20
ENSG00000171475	WIPF2 PPI subnetwork	0.17	>=0.20
ENSG00000126562	WNK4 PPI subnetwork	0.48	>=0.20
GO:0017147	Wnt-protein binding	0.22	>=0.20
GO:0016055	Wnt receptor signaling pathway	0.99	>=0.20
GO:0007223	Wnt receptor signaling pathway, calcium modulating pathwa	1	>=0.20
GO:0060071	Wnt receptor signaling pathway, planar cell polarity pathway	0.97	>=0.20
ENSG00000125084	WNT1 PPI subnetwork	0.28	>=0.20
ENSG00000135925	WNT10A PPI subnetwork	0.52	>=0.20
ENSG00000169884	WNT10B PPI subnetwork	0.52	>=0.20
ENSG00000085741	WNT11 PPI subnetwork	0.52	>=0.20
ENSG00000002745	WNT16 PPI subnetwork	0.25	>=0.20
ENSG00000105989	WNT2 PPI subnetwork	0.52	>=0.20
ENSG00000134245	WNT2B PPI subnetwork	0.5	>=0.20
ENSG00000108379	WNT3 PPI subnetwork	0.66	>=0.20
ENSG00000154342	WNT3A PPI subnetwork	0.57	>=0.20
ENSG00000162552	WNT4 PPI subnetwork	0.35	>=0.20
ENSG00000114251	WNT5A PPI subnetwork	0.76	>=0.20
ENSG00000111186	WNT5B PPI subnetwork	0.69	>=0.20
ENSG00000115596	WNT6 PPI subnetwork	0.6	>=0.20
ENSG00000154764	WNT7A PPI subnetwork	0.48	>=0.20
ENSG00000188064	WNT7B PPI subnetwork	0.49	>=0.20
ENSG00000061492	WNT8A PPI subnetwork	0.52	>=0.20
ENSG00000075290	WNT8B PPI subnetwork	0.52	>=0.20

ENSG00000143816	WNT9A PPI subnetwork	0.52	>=0.20
ENSG00000158955	WNT9B PPI subnetwork	0.52	>=0.20
GO:0044319	wound healing, spreading of cells	1	>=0.20
GO:0035313	wound healing, spreading of epidermal cells	1	>=0.20
ENSG00000116213	WRAP73 PPI subnetwork	0.31	>=0.20
ENSG00000182093	WRB PPI subnetwork	0.11	>=0.20
ENSG00000165392	WRN PPI subnetwork	0.92	>=0.20
ENSG00000124535	WRNIP1 PPI subnetwork	0.38	>=0.20
ENSG00000184937	WT1 PPI subnetwork	0.66	>=0.20
ENSG00000186153	WWOX PPI subnetwork	0.33	>=0.20
ENSG00000123124	WWP1 PPI subnetwork	0.36	>=0.20
ENSG00000198373	WWP2 PPI subnetwork	0.58	>=0.20
ENSG00000018408	WWTR1 PPI subnetwork	0.44	>=0.20
ENSG00000082898	XPO1 PPI subnetwork	0.07	>=0.20
ENSG00000124571	XPO5 PPI subnetwork	0.29	>=0.20
ENSG00000073050	XRCC1 PPI subnetwork	1	>=0.20
ENSG00000126215	XRCC3 PPI subnetwork	0.95	>=0.20
ENSG00000196419	XRCC6 PPI subnetwork	0.23	>=0.20
ENSG00000114127	XRN1 PPI subnetwork	0.23	>=0.20
ENSG00000093217	XYLB PPI subnetwork	0.6	>=0.20
ENSG00000015153	YAF2 PPI subnetwork	0.4	>=0.20
ENSG00000137693	YAP1 PPI subnetwork	0.41	>=0.20
ENSG00000127337	YEATS4 PPI subnetwork	0.67	>=0.20
ENSG00000176105	YES1 PPI subnetwork	0.1	>=0.20
ENSG00000174851	YIF1A PPI subnetwork	0.05	>=0.20
ENSG00000167645	YIF1B PPI subnetwork	0.05	>=0.20
ENSG00000145817	YIPF5 PPI subnetwork	0.34	>=0.20
ENSG00000166793	YPEL4 PPI subnetwork	0.68	>=0.20
ENSG00000083896	YTHDC1 PPI subnetwork	0.13	>=0.20
ENSG00000128245	YWHAH PPI subnetwork	0.3	>=0.20
ENSG00000100811	YY1 PPI subnetwork	0.16	>=0.20
GO:0030018	Z disc	0.72	>=0.20
ENSG00000115085	ZAP70 PPI subnetwork	0.27	>=0.20
ENSG00000116809	ZBTB17 PPI subnetwork	0.42	>=0.20
ENSG00000177485	ZBTB33 PPI subnetwork	0.46	>=0.20
ENSG00000160062	ZBTB8A PPI subnetwork	0.58	>=0.20
ENSG00000213588	ZBTB9 PPI subnetwork	0.62	>=0.20
ENSG00000105939	ZC3HAV1 PPI subnetwork	0.17	>=0.20
ENSG00000155329	ZCCHC10 PPI subnetwork	0.5	>=0.20
ENSG00000103994	ZFP106 PPI subnetwork	0.05	>=0.20
ENSG00000152518	ZFP36L2 PPI subnetwork	0.13	>=0.20
ENSG00000039319	ZFYVE16 PPI subnetwork	0.68	>=0.20
ENSG00000131381	ZFYVE20 PPI subnetwork	0.1	>=0.20
ENSG00000165156	ZHX1 PPI subnetwork	0.41	>=0.20
ENSG00000043355	ZIC2 PPI subnetwork	0.23	>=0.20
GO:0071577	zinc ion transmembrane transport	0.98	>=0.20
GO:0006829	zinc ion transport	0.97	>=0.20

ENSG00000101040	ZMYND8 PPI subnetwork	0.38	>=0.20
ENSG00000197961	ZNF121 PPI subnetwork	0.13	>=0.20
ENSG00000166478	ZNF143 PPI subnetwork	0.72	>=0.20
ENSG00000010244	ZNF207 PPI subnetwork	0.03	>=0.20
ENSG00000170260	ZNF212 PPI subnetwork	0.04	>=0.20
ENSG00000109917	ZNF259 PPI subnetwork	0.3	>=0.20
ENSG00000162702	ZNF281 PPI subnetwork	0.04	>=0.20
ENSG00000169131	ZNF354A PPI subnetwork	0.86	>=0.20
ENSG00000180855	ZNF443 PPI subnetwork	0.36	>=0.20
ENSG00000196700	ZNF512B PPI subnetwork	0.07	>=0.20
ENSG00000142684	ZNF593 PPI subnetwork	0.81	>=0.20
ENSG00000173545	ZNF622 PPI subnetwork	0.72	>=0.20
ENSG00000186230	ZNF749 PPI subnetwork	0.98	>=0.20
ENSG00000106400	ZNHIT1 PPI subnetwork	0.57	>=0.20
ENSG00000066379	ZNRD1 PPI subnetwork	0.83	>=0.20
ENSG00000206502	ZNRD1 PPI subnetwork	0.83	>=0.20
ENSG00000132485	ZRANB2 PPI subnetwork	0.45	>=0.20
ENSG00000169249	ZRSR2 PPI subnetwork	0.44	>=0.20
ENSG00000086827	ZW10 PPI subnetwork	0.49	>=0.20
ENSG00000174442	ZWILCH PPI subnetwork	0.7	>=0.20
ENSG00000122952	ZWINT PPI subnetwork	0.75	>=0.20
GO:0042588	zymogen granule	0.08	>=0.20
ENSG00000159840	ZYX PPI subnetwork	0.71	>=0.20

nited to gene sets that showed significant

LDL-C		TG	
P-value	FDR	P-value	FDR
4.35E-08	<0.01	2.56E-07	<0.01
1.61E-06	<0.01	5.90E-05	<0.01
3.92E-10	<0.01	5.49E-08	<0.01
8.77E-09	<0.01	1.23E-08	<0.01
7.85E-05	<0.01	1.48E-05	<0.01
7.89E-09	<0.01	2.73E-05	<0.01
8.04E-07	<0.01	1.87E-06	<0.01
1.27E-09	<0.01	1.29E-09	<0.01
7.97E-07	<0.01	3.81E-06	<0.01
9.63E-05	<0.01	3.55E-05	<0.01
2.26E-09	<0.01	2.92E-06	<0.01
0.000274	<0.01	5.20E-06	<0.01
0.000402	<0.01	6.82E-06	<0.01
1.71E-05	<0.01	4.48E-07	<0.01
0.000487	<0.01	0.000143	<0.01
2.18E-06	<0.01	3.41E-07	<0.01
2.13E-09	<0.01	6.35E-08	<0.01
0.000314	<0.01	2.50E-05	<0.01
1.86E-06	<0.01	2.75E-06	<0.01
0.000241	<0.01	0.000118	<0.01
3.50E-08	<0.01	3.48E-06	<0.01
2.10E-06	<0.01	3.35E-05	<0.01
4.18E-09	<0.01	7.27E-07	<0.01
3.61E-06	<0.01	1.22E-08	<0.01
2.03E-06	<0.01	6.38E-05	<0.01
4.28E-06	<0.01	0.000103	<0.01
1.72E-05	<0.01	3.72E-07	<0.01
5.06E-06	<0.01	6.30E-08	<0.01
1.54E-06	<0.01	1.96E-05	<0.01
0.000195	<0.01	2.23E-05	<0.01
0.000312	<0.01	1.58E-06	<0.01
0.000688	<0.01	8.31E-06	<0.01
5.99E-06	<0.01	5.92E-07	<0.01
2.15E-07	<0.01	6.06E-05	<0.01
0.00028	<0.01	7.30E-05	<0.01
0.000243	<0.01	7.46E-05	<0.01
2.55E-05	<0.01	1.34E-06	<0.01
0.000395	<0.01	0.000202	<0.01
1.81E-05	<0.01	6.68E-06	<0.01
1.54E-05	<0.01	6.71E-06	<0.01
5.35E-06	<0.01	0.000176	<0.01

5.13E-07	<0.01	1.98E-06	<0.01
0.000301	<0.01	0.00014	<0.01
9.13E-06	<0.01	4.39E-05	<0.01
1.97E-05	<0.01	3.26E-05	<0.01
1.57E-07	<0.01	9.96E-10	<0.01
0.000597	<0.01	1.44E-06	<0.01
1.55E-05	<0.01	6.50E-05	<0.01
1.35E-07	<0.01	1.50E-08	<0.01
0.000137	<0.01	2.41E-05	<0.01
7.56E-05	<0.01	8.24E-06	<0.01
1.94E-06	<0.01	5.93E-07	<0.01
1.04E-06	<0.01	8.18E-05	<0.01
1.56E-08	<0.01	1.95E-05	<0.01
2.41E-05	<0.01	0.000113	<0.01
4.25E-06	<0.01	3.52E-06	<0.01
1.42E-05	<0.01	2.71E-05	<0.01
5.04E-06	<0.01	3.02E-05	<0.01
3.06E-06	<0.01	3.80E-07	<0.01
9.77E-09	<0.01	0.00014	<0.01
1.38E-07	<0.01	3.94E-06	<0.01
1.07E-08	<0.01	3.59E-07	<0.01
4.12E-07	<0.01	1.05E-07	<0.01
4.02E-07	<0.01	7.31E-08	<0.01
0.00037	<0.01	0.000167	<0.01
0.000121	<0.01	2.27E-06	<0.01
1.42E-05	<0.01	3.59E-05	<0.01
2.95E-07	<0.01	8.02E-05	<0.01
6.80E-06	<0.01	9.82E-07	<0.01
2.53E-06	<0.01	3.12E-06	<0.01
5.02E-05	<0.01	3.47E-05	<0.01
1.92E-05	<0.01	7.51E-07	<0.01
3.81E-06	<0.01	1.40E-07	<0.01
1.21E-06	<0.01	1.97E-06	<0.01
3.66E-05	<0.01	3.98E-05	<0.01
0.000188	<0.01	1.12E-05	<0.01
2.31E-06	<0.01	7.56E-06	<0.01
0.000637	<0.01	0.000198	<0.01
2.68E-06	<0.01	3.99E-05	<0.01
2.31E-06	<0.01	7.56E-06	<0.01
0.00037	<0.01	0.000167	<0.01
0.000687	<0.01	4.67E-06	<0.01
1.15E-07	<0.01	1.47E-05	<0.01
2.96E-06	<0.01	4.00E-06	<0.01
3.14E-05	<0.01	0.000106	<0.01
1.18E-07	<0.01	5.26E-09	<0.01
2.56E-08	<0.01	2.73E-07	<0.01
3.54E-09	<0.01	4.61E-09	<0.01

5.60E-07	<0.01	3.60E-05	<0.01
5.60E-07	<0.01	3.60E-05	<0.01
2.65E-06	<0.01	1.06E-05	<0.01
2.95E-06	<0.01	1.52E-05	<0.01
0.000183	<0.01	7.26E-05	<0.01
1.20E-05	<0.01	6.61E-05	<0.01
1.03E-05	<0.01	0.000109	<0.01
5.73E-06	<0.01	6.05E-05	<0.01
0.000183	<0.01	7.26E-05	<0.01
0.000207	<0.01	6.89E-05	<0.01
0.000116	<0.01	2.92E-05	<0.01
0.000109	<0.01	4.64E-05	<0.01
6.74E-05	<0.01	0.000218	<0.01
2.33E-05	<0.01	1.48E-05	<0.01
3.50E-08	<0.01	3.48E-06	<0.01
1.46E-06	<0.01	1.49E-05	<0.01
1.37E-07	<0.01	3.17E-05	<0.01
1.66E-08	<0.01	8.64E-05	<0.01
3.11E-05	<0.01	1.99E-06	<0.01
4.31E-07	<0.01	7.07E-05	<0.01
1.22E-07	<0.01	1.80E-05	<0.01
0.00017	<0.01	0.00233	<0.05
2.46E-05	<0.01	0.000399	<0.05
0.00021	<0.01	0.0026	<0.05
2.32E-05	<0.01	0.00209	<0.05
0.000589	<0.01	0.0022	<0.05
0.000166	<0.01	0.00042	<0.05
2.03E-05	<0.01	0.000959	<0.05
0.000464	<0.01	0.00153	<0.05
6.91E-05	<0.01	0.000832	<0.05
4.16E-06	<0.01	0.000258	<0.05
8.27E-06	<0.01	0.00056	<0.05
2.46E-05	<0.01	0.000399	<0.05
0.00015	<0.01	0.000284	<0.05
0.000104	<0.01	0.000251	<0.05
0.000251	<0.01	0.00102	<0.05
0.00013	<0.01	0.000589	<0.05
9.49E-05	<0.01	0.00137	<0.05
1.02E-05	<0.01	0.00312	<0.20
1.10E-05	<0.01	0.00783	<0.20
3.70E-05	<0.01	0.00469	<0.20
9.96E-05	<0.01	0.00332	<0.20
0.000221	<0.01	0.00318	<0.20
0.000413	<0.01	0.05	>=0.20
0.00038	<0.01	0.04	>=0.20
0.00308	<0.05	0.000243	<0.01
0.00507	<0.05	5.16E-05	<0.01

0.00152	<0.05	2.04E-05	<0.01
0.00131	<0.05	9.94E-07	<0.01
0.0045	<0.05	4.42E-05	<0.01
0.00143	<0.05	1.83E-05	<0.01
0.00473	<0.05	2.73E-05	<0.01
0.00375	<0.05	5.08E-05	<0.01
0.00507	<0.05	5.16E-05	<0.01
0.00444	<0.05	2.26E-05	<0.01
0.000994	<0.05	1.25E-06	<0.01
0.00176	<0.05	6.05E-06	<0.01
0.00336	<0.05	8.56E-06	<0.01
0.00196	<0.05	5.47E-05	<0.01
0.00133	<0.05	1.56E-05	<0.01
0.00568	<0.05	6.18E-06	<0.01
0.00337	<0.05	6.50E-05	<0.01
0.00104	<0.05	7.07E-06	<0.01
0.00507	<0.05	5.16E-05	<0.01
0.00273	<0.05	3.00E-05	<0.01
0.0035	<0.05	2.43E-06	<0.01
0.00398	<0.05	0.000178	<0.01
0.00283	<0.05	0.00164	<0.05
0.00171	<0.05	0.00124	<0.05
0.00537	<0.05	0.00093	<0.05
0.00113	<0.05	0.000663	<0.05
0.00153	<0.05	0.000328	<0.05
0.00109	<0.05	0.00082	<0.05
0.00312	<0.05	0.000615	<0.05
0.00251	<0.05	0.00123	<0.05
0.00231	<0.05	0.00142	<0.05
0.00144	<0.05	0.00172	<0.05
0.00154	<0.05	0.0052	<0.20
0.000822	<0.05	0.00844	<0.20
0.00327	<0.05	0.00383	<0.20
0.00116	<0.05	0.00542	<0.20
0.00164	<0.05	0.00466	<0.20
0.00336	<0.05	0.02	<0.20
0.00299	<0.05	0.00389	<0.20
0.00137	<0.05	0.02	<0.20
0.00238	<0.05	0.02	<0.20
0.00206	<0.05	0.00622	<0.20
0.00196	<0.05	0.00925	<0.20
0.0051	<0.05	0.17	>=0.20
0.00149	<0.05	0.04	>=0.20
0.0055	<0.05	0.09	>=0.20
0.00127	<0.05	0.04	>=0.20
0.00352	<0.05	0.03	>=0.20
0.00379	<0.05	0.04	>=0.20

0.03	<0.20	0.00023	<0.01
0.01	<0.20	8.85E-08	<0.01
0.01	<0.20	2.51E-05	<0.01
0.04	<0.20	6.71E-05	<0.01
0.00963	<0.20	1.77E-06	<0.01
0.00791	<0.20	6.82E-05	<0.01
0.0083	<0.20	3.53E-05	<0.01
0.03	<0.20	0.000119	<0.01
0.02	<0.20	1.76E-05	<0.01
0.00725	<0.20	6.25E-05	<0.01
0.02	<0.20	0.000258	<0.05
0.03	<0.20	0.00205	<0.05
0.00919	<0.20	0.000887	<0.05
0.00869	<0.20	0.000266	<0.05
0.0065	<0.20	0.00197	<0.05
0.01	<0.20	0.00103	<0.05
0.03	<0.20	0.00173	<0.05
0.03	<0.20	0.00247	<0.05
0.03	<0.20	0.00113	<0.05
0.00899	<0.20	0.000954	<0.05
0.03	<0.20	0.000545	<0.05
0.03	<0.20	0.00102	<0.05
0.02	<0.20	0.000503	<0.05
0.00613	<0.20	0.00175	<0.05
0.00839	<0.20	0.000808	<0.05
0.00993	<0.20	0.00231	<0.05
0.02	<0.20	5.00E-04	<0.05
0.0078	<0.20	0.001	<0.05
0.01	<0.20	0.000313	<0.05
0.03	<0.20	0.00205	<0.05
0.02	<0.20	0.00544	<0.20
0.00773	<0.20	0.00273	<0.20
0.03	<0.20	0.02	<0.20
0.02	<0.20	0.00825	<0.20
0.01	<0.20	0.00414	<0.20
0.00773	<0.20	0.00273	<0.20
0.02	<0.20	0.00605	<0.20
0.03	<0.20	0.01	<0.20
0.01	<0.20	0.01	<0.20
0.02	<0.20	0.02	<0.20
0.02	<0.20	0.05	>=0.20
0.02	<0.20	0.03	>=0.20
0.04	<0.20	0.04	>=0.20
0.02	<0.20	0.41	>=0.20
0.01	<0.20	0.08	>=0.20
0.00637	<0.20	0.06	>=0.20
0.00782	<0.20	0.05	>=0.20

0.03	<0.20	0.03	>=0.20
0.02	<0.20	0.08	>=0.20
0.19	>=0.20	0.000242	<0.01
0.32	>=0.20	0.000243	<0.01
0.15	>=0.20	0.000631	<0.05
0.13	>=0.20	0.00258	<0.05
0.29	>=0.20	0.000861	<0.05
0.1	>=0.20	0.00152	<0.05
0.1	>=0.20	0.000338	<0.05
0.47	>=0.20	0.00134	<0.05
0.07	>=0.20	0.00134	<0.05
0.15	>=0.20	0.00146	<0.05
0.09	>=0.20	0.00118	<0.05
0.13	>=0.20	0.00026	<0.05
0.04	>=0.20	0.000932	<0.05
0.07	>=0.20	0.00134	<0.05
0.06	>=0.20	0.000681	<0.05
0.06	>=0.20	0.000589	<0.05
0.09	>=0.20	0.02	<0.20
0.04	>=0.20	0.00288	<0.20
0.69	>=0.20	0.00729	<0.20
0.11	>=0.20	0.02	<0.20
0.5	>=0.20	0.02	<0.20
0.21	>=0.20	0.00379	<0.20
0.06	>=0.20	0.00401	<0.20
0.12	>=0.20	0.00495	<0.20
0.18	>=0.20	0.00497	<0.20
0.42	>=0.20	0.00325	<0.20
0.18	>=0.20	0.00979	<0.20
0.05	>=0.20	0.00294	<0.20
0.06	>=0.20	0.00736	<0.20
0.51	>=0.20	0.01	<0.20
0.06	>=0.20	0.02	<0.20
0.17	>=0.20	0.02	<0.20
0.06	>=0.20	0.00734	<0.20
0.25	>=0.20	0.01	<0.20
0.53	>=0.20	0.00449	<0.20
0.73	>=0.20	0.00806	<0.20
0.04	>=0.20	0.00476	<0.20
0.29	>=0.20	0.01	<0.20
0.74	>=0.20	0.11	>=0.20
0.19	>=0.20	0.16	>=0.20
0.05	>=0.20	0.07	>=0.20
0.14	>=0.20	0.04	>=0.20
0.69	>=0.20	0.03	>=0.20
0.69	>=0.20	0.05	>=0.20
0.06	>=0.20	0.09	>=0.20

0.06	>=0.20	0.1	>=0.20
0.8	>=0.20	0.08	>=0.20
0.22	>=0.20	0.03	>=0.20
0.05	>=0.20	0.09	>=0.20
0.46	>=0.20	0.18	>=0.20
0.42	>=0.20	0.03	>=0.20
0.06	>=0.20	0.08	>=0.20
0.52	>=0.20	0.03	>=0.20
0.98	>=0.20	0.06	>=0.20
0.56	>=0.20	0.04	>=0.20
0.52	>=0.20	0.03	>=0.20
0.12	>=0.20	0.05	>=0.20
0.43	>=0.20	0.05	>=0.20
0.21	>=0.20	0.03	>=0.20
0.93	>=0.20	0.23	>=0.20
0.22	>=0.20	0.21	>=0.20
0.27	>=0.20	0.05	>=0.20
0.9	>=0.20	0.05	>=0.20
0.54	>=0.20	0.1	>=0.20
0.12	>=0.20	0.04	>=0.20
0.45	>=0.20	0.02	>=0.20
0.06	>=0.20	0.02	>=0.20
0.06	>=0.20	0.06	>=0.20
0.08	>=0.20	0.03	>=0.20
0.49	>=0.20	0.12	>=0.20
0.49	>=0.20	0.09	>=0.20
0.82	>=0.20	0.19	>=0.20
3.98E-06	<0.01	0.000243	<0.01
5.59E-05	<0.01	0.00017	<0.01
0.000313	<0.01	0.000114	<0.01
0.000548	<0.01	0.000121	<0.01
1.36E-05	<0.01	0.000186	<0.01
4.83E-06	<0.01	2.95E-05	<0.01
1.18E-05	<0.01	3.33E-05	<0.01
3.54E-06	<0.01	6.23E-05	<0.01
1.04E-06	<0.01	3.15E-06	<0.01
1.43E-05	<0.01	3.26E-05	<0.01
3.61E-05	<0.01	1.29E-06	<0.01
1.26E-05	<0.01	6.49E-06	<0.01
1.40E-05	<0.01	0.000152	<0.01
1.56E-05	<0.01	5.00E-07	<0.01
0.000222	<0.01	6.89E-05	<0.01
1.58E-05	<0.01	8.99E-05	<0.01
3.71E-06	<0.01	4.78E-05	<0.01
1.27E-05	<0.01	2.93E-05	<0.01
1.35E-05	<0.01	8.75E-05	<0.01
4.80E-06	<0.01	0.000166	<0.01

1.08E-07	<0.01	7.28E-05	<0.01
3.38E-05	<0.01	1.69E-05	<0.01
2.39E-05	<0.01	3.00E-05	<0.01
0.000287	<0.01	2.95E-05	<0.01
7.19E-06	<0.01	0.000209	<0.01
7.19E-06	<0.01	0.000209	<0.01
7.09E-06	<0.01	2.09E-05	<0.01
3.89E-06	<0.01	2.62E-05	<0.01
3.74E-05	<0.01	7.65E-05	<0.01
3.63E-06	<0.01	8.67E-06	<0.01
4.44E-06	<0.01	0.000125	<0.01
5.18E-05	<0.01	8.71E-05	<0.01
1.53E-06	<0.01	2.82E-06	<0.01
5.18E-05	<0.01	8.71E-05	<0.01
6.81E-06	<0.01	0.000239	<0.01
1.77E-06	<0.01	0.000668	<0.05
0.000311	<0.01	0.000827	<0.05
0.000305	<0.01	0.00047	<0.05
9.30E-06	<0.01	0.00208	<0.05
1.55E-07	<0.01	0.000919	<0.05
6.35E-05	<0.01	0.0015	<0.05
4.06E-05	<0.01	0.0011	<0.05
2.40E-05	<0.01	0.000803	<0.05
5.13E-05	<0.01	0.00069	<0.05
5.20E-05	<0.01	0.00188	<0.05
2.09E-05	<0.01	0.000357	<0.05
1.94E-05	<0.01	0.000331	<0.05
0.000367	<0.01	0.00103	<0.05
6.65E-05	<0.01	0.00178	<0.05
6.06E-05	<0.01	0.000341	<0.05
7.56E-05	<0.01	0.00104	<0.05
0.000155	<0.01	0.000293	<0.05
4.99E-05	<0.01	0.00196	<0.05
4.31E-05	<0.01	0.00215	<0.05
6.06E-05	<0.01	0.000341	<0.05
6.06E-05	<0.01	0.000341	<0.05
0.000275	<0.01	0.000287	<0.05
8.68E-05	<0.01	0.00132	<0.05
9.49E-05	<0.01	0.00189	<0.05
0.000597	<0.01	0.00223	<0.05
0.000233	<0.01	0.00105	<0.05
2.34E-06	<0.01	0.00212	<0.05
8.38E-08	<0.01	0.000352	<0.05
1.02E-07	<0.01	0.00167	<0.05
0.000289	<0.01	0.00141	<0.05
1.63E-05	<0.01	0.00519	<0.20
6.26E-05	<0.01	0.02	<0.20

0.000461	<0.01	0.01	<0.20
0.000231	<0.01	0.00885	<0.20
0.000316	<0.01	0.00453	<0.20
0.000295	<0.01	0.01	<0.20
0.000425	<0.01	0.00866	<0.20
7.76E-06	<0.01	0.00852	<0.20
0.000447	<0.01	0.00739	<0.20
0.000582	<0.01	0.00422	<0.20
0.000637	<0.01	0.00787	<0.20
1.38E-05	<0.01	0.01	<0.20
0.000123	<0.01	0.00763	<0.20
2.66E-06	<0.01	0.01	<0.20
0.000399	<0.01	0.00551	<0.20
2.86E-05	<0.01	0.01	<0.20
4.31E-05	<0.01	0.02	<0.20
1.31E-06	<0.01	0.01	<0.20
0.000323	<0.01	0.02	<0.20
0.00017	<0.01	0.12	>=0.20
0.000459	<0.01	0.03	>=0.20
0.000636	<0.01	0.06	>=0.20
0.000323	<0.01	0.03	>=0.20
0.00212	<0.05	0.000158	<0.01
0.000903	<0.05	1.74E-05	<0.01
0.00194	<0.05	2.94E-05	<0.01
0.000732	<0.05	9.59E-05	<0.01
0.00188	<0.05	7.06E-05	<0.01
0.00171	<0.05	0.00011	<0.01
0.00243	<0.05	4.47E-05	<0.01
0.00113	<0.05	6.39E-05	<0.01
0.00388	<0.05	0.000156	<0.01
0.000927	<0.05	0.00158	<0.05
0.000858	<0.05	0.000821	<0.05
0.000994	<0.05	0.00134	<0.05
0.00371	<0.05	0.00129	<0.05
0.00578	<0.05	0.00257	<0.05
0.00602	<0.05	0.00148	<0.05
0.00445	<0.05	0.000708	<0.05
0.00137	<0.05	0.00102	<0.05
0.00304	<0.05	0.00143	<0.05
0.0017	<0.05	0.000602	<0.05
0.000882	<0.05	0.00163	<0.05
0.00114	<0.05	0.00775	<0.20
0.00474	<0.05	0.0054	<0.20
0.00182	<0.05	0.00839	<0.20
0.00194	<0.05	0.00531	<0.20
0.00219	<0.05	0.00728	<0.20
0.0039	<0.05	0.01	<0.20

0.00261	<0.05	0.01	<0.20
0.00467	<0.05	0.00963	<0.20
0.00506	<0.05	0.00956	<0.20
0.00326	<0.05	0.00319	<0.20
0.000888	<0.05	0.02	<0.20
0.00169	<0.05	0.01	<0.20
0.00426	<0.05	0.56	>=0.20
0.00225	<0.05	0.03	>=0.20
0.00185	<0.05	0.03	>=0.20
0.00238	<0.05	0.06	>=0.20
0.00446	<0.05	0.11	>=0.20
0.000949	<0.05	0.15	>=0.20
0.00279	<0.05	0.14	>=0.20
0.00275	<0.05	0.03	>=0.20
0.00642	<0.20	0.000189	<0.01
0.03	<0.20	0.00106	<0.05
0.02	<0.20	0.00121	<0.05
0.01	<0.20	0.000341	<0.05
0.02	<0.20	0.000317	<0.05
0.00803	<0.20	0.00152	<0.05
0.02	<0.20	0.00255	<0.05
0.04	<0.20	0.00195	<0.05
0.01	<0.20	0.000924	<0.05
0.02	<0.20	0.00262	<0.05
0.00656	<0.20	0.00213	<0.05
0.01	<0.20	0.00174	<0.05
0.03	<0.20	0.00399	<0.20
0.01	<0.20	0.02	<0.20
0.02	<0.20	0.01	<0.20
0.00641	<0.20	0.0041	<0.20
0.00983	<0.20	0.02	<0.20
0.03	<0.20	0.00982	<0.20
0.03	<0.20	0.02	<0.20
0.01	<0.20	0.02	<0.20
0.02	<0.20	0.02	<0.20
0.00641	<0.20	0.0041	<0.20
0.00612	<0.20	0.00503	<0.20
0.03	<0.20	0.02	<0.20
0.03	<0.20	0.00458	<0.20
0.03	<0.20	0.02	<0.20
0.02	<0.20	0.00903	<0.20
0.01	<0.20	0.00531	<0.20
0.01	<0.20	0.00828	<0.20
0.00751	<0.20	0.00707	<0.20
0.01	<0.20	0.02	<0.20
0.02	<0.20	0.00461	<0.20
0.01	<0.20	0.02	<0.20

0.02	<0.20	0.00439	<0.20
0.02	<0.20	0.02	<0.20
0.01	<0.20	0.01	<0.20
0.01	<0.20	0.02	<0.20
0.02	<0.20	0.00612	<0.20
0.02	<0.20	0.00415	<0.20
0.00652	<0.20	0.00692	<0.20
0.01	<0.20	0.01	<0.20
0.00749	<0.20	0.00826	<0.20
0.01	<0.20	0.02	<0.20
0.00618	<0.20	0.02	<0.20
0.04	<0.20	0.05	>=0.20
0.00706	<0.20	0.03	>=0.20
0.01	<0.20	0.03	>=0.20
0.01	<0.20	0.23	>=0.20
0.00632	<0.20	0.04	>=0.20
0.01	<0.20	0.03	>=0.20
0.03	<0.20	0.15	>=0.20
0.04	<0.20	0.04	>=0.20
0.03	<0.20	0.09	>=0.20
0.02	<0.20	0.09	>=0.20
0.03	<0.20	0.05	>=0.20
0.02	<0.20	0.12	>=0.20
0.00616	<0.20	0.06	>=0.20
0.03	<0.20	0.05	>=0.20
0.01	<0.20	0.04	>=0.20
0.03	<0.20	0.03	>=0.20
0.03	<0.20	0.06	>=0.20
0.02	<0.20	0.14	>=0.20
0.00628	<0.20	0.07	>=0.20
0.00695	<0.20	0.03	>=0.20
0.00715	<0.20	0.11	>=0.20
0.02	<0.20	0.39	>=0.20
0.02	<0.20	0.09	>=0.20
0.04	<0.20	0.05	>=0.20
0.3	>=0.20	0.000139	<0.01
0.06	>=0.20	0.000209	<0.01
0.11	>=0.20	5.75E-05	<0.01
0.48	>=0.20	0.000182	<0.01
0.37	>=0.20	0.00156	<0.05
0.17	>=0.20	0.00102	<0.05
0.3	>=0.20	0.00227	<0.05
0.05	>=0.20	0.00194	<0.05
0.17	>=0.20	0.000535	<0.05
0.34	>=0.20	0.000327	<0.05
0.04	>=0.20	0.00104	<0.05
0.09	>=0.20	0.00198	<0.05

0.87	>=0.20	0.00263	<0.05
0.54	>=0.20	0.00481	<0.20
0.14	>=0.20	0.00463	<0.20
0.14	>=0.20	0.0042	<0.20
0.13	>=0.20	0.0055	<0.20
0.13	>=0.20	0.01	<0.20
0.74	>=0.20	0.01	<0.20
0.24	>=0.20	0.00362	<0.20
0.11	>=0.20	0.009	<0.20
0.2	>=0.20	0.01	<0.20
0.09	>=0.20	0.00981	<0.20
0.18	>=0.20	0.02	<0.20
0.73	>=0.20	0.01	<0.20
0.51	>=0.20	0.00739	<0.20
0.12	>=0.20	0.02	<0.20
0.69	>=0.20	0.00495	<0.20
0.1	>=0.20	0.01	<0.20
0.19	>=0.20	0.02	<0.20
0.4	>=0.20	0.02	<0.20
0.15	>=0.20	0.01	<0.20
0.15	>=0.20	0.00737	<0.20
0.08	>=0.20	0.00278	<0.20
0.11	>=0.20	0.02	<0.20
0.19	>=0.20	0.02	<0.20
0.06	>=0.20	0.02	<0.20
0.11	>=0.20	0.00714	<0.20
0.17	>=0.20	0.02	<0.20
0.17	>=0.20	0.00751	<0.20
0.39	>=0.20	0.02	<0.20
0.32	>=0.20	0.01	<0.20
0.17	>=0.20	0.0096	<0.20
0.28	>=0.20	0.00528	<0.20
0.46	>=0.20	0.00293	<0.20
0.06	>=0.20	0.00792	<0.20
0.39	>=0.20	0.00311	<0.20
0.51	>=0.20	0.00657	<0.20
0.06	>=0.20	0.00344	<0.20
0.2	>=0.20	0.02	<0.20
0.06	>=0.20	0.02	<0.20
0.07	>=0.20	0.00511	<0.20
0.14	>=0.20	0.02	<0.20
0.1	>=0.20	0.02	<0.20
0.65	>=0.20	0.02	<0.20
0.5	>=0.20	0.00447	<0.20
0.07	>=0.20	0.00559	<0.20
0.14	>=0.20	0.01	<0.20
0.19	>=0.20	0.00337	<0.20

0.18 >=0.20	0.03 >=0.20
0.28 >=0.20	0.17 >=0.20
0.37 >=0.20	0.12 >=0.20
0.51 >=0.20	0.34 >=0.20
0.2 >=0.20	0.06 >=0.20
0.05 >=0.20	0.03 >=0.20
0.29 >=0.20	0.04 >=0.20
0.32 >=0.20	0.04 >=0.20
0.28 >=0.20	0.08 >=0.20
0.12 >=0.20	0.07 >=0.20
0.35 >=0.20	0.03 >=0.20
0.09 >=0.20	0.1 >=0.20
0.05 >=0.20	0.16 >=0.20
0.09 >=0.20	0.03 >=0.20
0.14 >=0.20	0.08 >=0.20
0.42 >=0.20	0.03 >=0.20
0.16 >=0.20	0.08 >=0.20
0.06 >=0.20	0.1 >=0.20
0.35 >=0.20	0.13 >=0.20
0.29 >=0.20	0.35 >=0.20
0.7 >=0.20	0.45 >=0.20
0.16 >=0.20	0.04 >=0.20
0.27 >=0.20	0.06 >=0.20
0.19 >=0.20	0.1 >=0.20
0.73 >=0.20	0.04 >=0.20
0.81 >=0.20	0.14 >=0.20
0.09 >=0.20	0.6 >=0.20
0.23 >=0.20	0.09 >=0.20
0.08 >=0.20	0.03 >=0.20
0.79 >=0.20	0.57 >=0.20
0.79 >=0.20	0.57 >=0.20
0.11 >=0.20	0.21 >=0.20
0.06 >=0.20	0.04 >=0.20
0.42 >=0.20	0.16 >=0.20
0.44 >=0.20	0.09 >=0.20
0.27 >=0.20	0.07 >=0.20
0.79 >=0.20	0.57 >=0.20
0.66 >=0.20	0.06 >=0.20
0.99 >=0.20	0.62 >=0.20
0.3 >=0.20	0.07 >=0.20
0.77 >=0.20	0.63 >=0.20
0.2 >=0.20	0.03 >=0.20
0.38 >=0.20	0.04 >=0.20
0.04 >=0.20	0.22 >=0.20
0.38 >=0.20	0.32 >=0.20
0.37 >=0.20	0.06 >=0.20
0.05 >=0.20	0.17 >=0.20

0.39 >=0.20	0.18 >=0.20
0.86 >=0.20	0.05 >=0.20
0.65 >=0.20	0.06 >=0.20
0.47 >=0.20	0.04 >=0.20
0.09 >=0.20	0.06 >=0.20
0.98 >=0.20	0.68 >=0.20
0.59 >=0.20	0.18 >=0.20
0.56 >=0.20	0.19 >=0.20
0.08 >=0.20	0.06 >=0.20
0.11 >=0.20	0.39 >=0.20
0.68 >=0.20	0.11 >=0.20
0.08 >=0.20	0.09 >=0.20
0.25 >=0.20	0.09 >=0.20
0.09 >=0.20	0.04 >=0.20
0.23 >=0.20	0.12 >=0.20
0.81 >=0.20	0.13 >=0.20
0.27 >=0.20	0.27 >=0.20
0.14 >=0.20	0.03 >=0.20
1 >=0.20	0.25 >=0.20
0.53 >=0.20	0.26 >=0.20
0.71 >=0.20	0.04 >=0.20
0.6 >=0.20	0.07 >=0.20
0.18 >=0.20	0.11 >=0.20
0.14 >=0.20	0.1 >=0.20
0.26 >=0.20	0.38 >=0.20
0.23 >=0.20	0.36 >=0.20
0.23 >=0.20	0.19 >=0.20
0.07 >=0.20	0.03 >=0.20
0.76 >=0.20	0.14 >=0.20
0.16 >=0.20	0.11 >=0.20
0.08 >=0.20	0.15 >=0.20
0.13 >=0.20	0.18 >=0.20
0.05 >=0.20	0.03 >=0.20
0.56 >=0.20	0.06 >=0.20
0.3 >=0.20	0.04 >=0.20
0.11 >=0.20	0.04 >=0.20
0.67 >=0.20	0.17 >=0.20
0.2 >=0.20	0.07 >=0.20
0.2 >=0.20	0.03 >=0.20
0.45 >=0.20	0.18 >=0.20
0.06 >=0.20	0.04 >=0.20
0.84 >=0.20	0.42 >=0.20
0.67 >=0.20	0.27 >=0.20
0.05 >=0.20	0.07 >=0.20
0.16 >=0.20	0.03 >=0.20
0.66 >=0.20	0.03 >=0.20
0.07 >=0.20	0.03 >=0.20

0.49	>=0.20	0.03	>=0.20
0.22	>=0.20	0.25	>=0.20
0.15	>=0.20	0.35	>=0.20
0.48	>=0.20	0.14	>=0.20
5.53E-07	<0.01	8.60E-05	<0.01
1.38E-05	<0.01	6.14E-05	<0.01
3.22E-05	<0.01	2.15E-05	<0.01
9.11E-05	<0.01	0.000102	<0.01
0.000102	<0.01	0.00016	<0.01
0.000139	<0.01	0.000199	<0.01
7.67E-05	<0.01	0.000135	<0.01
9.11E-05	<0.01	0.000102	<0.01
1.38E-05	<0.01	6.14E-05	<0.01
0.000265	<0.01	1.18E-05	<0.01
1.17E-07	<0.01	6.24E-05	<0.01
2.07E-05	<0.01	1.41E-05	<0.01
0.000689	<0.01	1.96E-05	<0.01
0.000405	<0.01	6.61E-05	<0.01
5.19E-06	<0.01	3.15E-05	<0.01
7.51E-06	<0.01	0.000101	<0.01
0.000178	<0.01	0.00012	<0.01
0.000102	<0.01	0.00016	<0.01
0.000178	<0.01	0.00012	<0.01
3.71E-05	<0.01	4.92E-05	<0.01
1.59E-05	<0.01	8.55E-05	<0.01
3.50E-06	<0.01	0.000222	<0.01
5.93E-06	<0.01	0.000154	<0.01
0.000281	<0.01	0.000644	<0.05
0.000421	<0.01	0.00147	<0.05
4.67E-05	<0.01	0.00253	<0.05
6.00E-04	<0.01	0.000738	<0.05
0.000433	<0.01	0.000629	<0.05
0.000531	<0.01	0.000646	<0.05
2.07E-09	<0.01	0.000976	<0.05
1.12E-05	<0.01	0.00153	<0.05
0.000132	<0.01	0.00222	<0.05
4.02E-05	<0.01	0.00053	<0.05
1.12E-05	<0.01	0.00153	<0.05
2.64E-05	<0.01	0.00146	<0.05
0.000218	<0.01	0.000413	<0.05
3.38E-05	<0.01	0.00206	<0.05
1.60E-06	<0.01	0.00136	<0.05
0.000313	<0.01	0.00243	<0.05
0.000251	<0.01	0.000643	<0.05
0.000132	<0.01	0.000389	<0.05
0.000477	<0.01	0.00248	<0.05
6.58E-06	<0.01	0.000592	<0.05

7.00E-06	<0.01	0.000437	<0.05
0.000143	<0.01	0.000441	<0.05
4.95E-05	<0.01	0.000606	<0.05
0.000664	<0.01	0.000297	<0.05
7.76E-05	<0.01	0.000903	<0.05
0.000154	<0.01	0.0025	<0.05
4.95E-05	<0.01	0.000606	<0.05
0.000143	<0.01	0.000441	<0.05
2.81E-06	<0.01	0.00041	<0.05
0.000157	<0.01	0.000617	<0.05
1.00E-05	<0.01	0.000428	<0.05
2.70E-06	<0.01	0.00202	<0.05
0.000139	<0.01	0.00101	<0.05
8.53E-05	<0.01	0.00054	<0.05
2.00E-06	<0.01	0.000451	<0.05
0.000717	<0.01	0.00155	<0.05
6.16E-05	<0.01	0.00095	<0.05
1.92E-05	<0.01	0.00198	<0.05
0.000539	<0.01	0.000795	<0.05
0.000498	<0.01	0.000407	<0.05
1.25E-05	<0.01	0.000534	<0.05
3.59E-05	<0.01	0.00176	<0.05
4.14E-06	<0.01	0.000259	<0.05
7.35E-05	<0.01	0.00192	<0.05
2.96E-05	<0.01	0.00089	<0.05
2.81E-05	<0.01	0.00443	<0.20
4.57E-05	<0.01	0.00497	<0.20
0.000661	<0.01	0.01	<0.20
5.82E-05	<0.01	0.00344	<0.20
0.000653	<0.01	0.01	<0.20
2.10E-06	<0.01	0.00435	<0.20
1.58E-05	<0.01	0.00351	<0.20
3.18E-05	<0.01	0.0072	<0.20
2.52E-06	<0.01	0.01	<0.20
2.05E-05	<0.01	0.00397	<0.20
0.000109	<0.01	0.00379	<0.20
0.000351	<0.01	0.00293	<0.20
6.32E-05	<0.01	0.00785	<0.20
3.23E-05	<0.01	0.00441	<0.20
9.04E-05	<0.01	0.0057	<0.20
0.000178	<0.01	0.02	<0.20
1.57E-05	<0.01	0.00418	<0.20
3.53E-05	<0.01	0.00878	<0.20
4.39E-05	<0.01	0.00542	<0.20
0.000412	<0.01	0.01	<0.20
4.64E-05	<0.01	0.01	<0.20
3.20E-05	<0.01	0.00488	<0.20

6.71E-06	<0.01	0.00446	<0.20
5.14E-05	<0.01	0.00524	<0.20
4.26E-06	<0.01	0.00527	<0.20
0.000173	<0.01	0.00279	<0.20
2.25E-05	<0.01	0.00284	<0.20
2.00E-04	<0.01	0.00454	<0.20
5.01E-05	<0.01	0.00521	<0.20
3.28E-05	<0.01	0.0072	<0.20
2.51E-05	<0.01	0.01	<0.20
0.000233	<0.01	0.01	<0.20
0.000336	<0.01	0.02	<0.20
0.000314	<0.01	0.00813	<0.20
0.000487	<0.01	0.00631	<0.20
3.05E-05	<0.01	0.0042	<0.20
0.000323	<0.01	0.00462	<0.20
2.10E-06	<0.01	0.00435	<0.20
4.74E-05	<0.01	0.00604	<0.20
3.23E-05	<0.01	0.00441	<0.20
3.14E-05	<0.01	0.00489	<0.20
0.000413	<0.01	0.00276	<0.20
2.06E-05	<0.01	0.00343	<0.20
3.83E-07	<0.01	0.00417	<0.20
1.17E-06	<0.01	0.02	<0.20
7.10E-06	<0.01	0.00321	<0.20
4.59E-05	<0.01	0.00542	<0.20
5.24E-06	<0.01	0.01	<0.20
0.000256	<0.01	0.00845	<0.20
0.000471	<0.01	0.01	<0.20
3.51E-05	<0.01	0.00466	<0.20
0.000418	<0.01	0.22	>=0.20
0.000626	<0.01	0.03	>=0.20
3.75E-05	<0.01	0.04	>=0.20
2.82E-05	<0.01	0.16	>=0.20
5.82E-06	<0.01	0.11	>=0.20
0.000257	<0.01	0.31	>=0.20
0.000585	<0.01	0.03	>=0.20
8.77E-05	<0.01	0.03	>=0.20
0.000157	<0.01	0.03	>=0.20
0.00092	<0.05	3.46E-05	<0.01
0.000933	<0.05	1.76E-06	<0.01
0.00125	<0.05	0.000128	<0.01
0.00081	<0.05	5.00E-05	<0.01
0.00302	<0.05	9.20E-05	<0.01
0.000833	<0.05	0.000184	<0.01
0.00255	<0.05	0.00238	<0.05
0.00247	<0.05	0.00178	<0.05
0.000785	<0.05	0.00114	<0.05

0.00127	<0.05	0.00119	<0.05
0.00259	<0.05	0.00209	<0.05
0.0051	<0.05	0.000415	<0.05
0.00438	<0.05	0.000753	<0.05
0.0022	<0.05	0.000921	<0.05
0.000998	<0.05	0.00106	<0.05
0.00548	<0.05	0.00219	<0.05
0.00127	<0.05	0.00235	<0.05
0.00206	<0.05	0.00196	<0.05
0.00542	<0.05	0.000269	<0.05
0.00103	<0.05	0.00138	<0.05
0.00419	<0.05	0.00236	<0.05
0.00481	<0.05	0.00197	<0.05
0.000865	<0.05	0.00213	<0.05
0.0014	<0.05	0.01	<0.20
0.00337	<0.05	0.02	<0.20
0.00296	<0.05	0.02	<0.20
0.00299	<0.05	0.01	<0.20
0.000758	<0.05	0.01	<0.20
0.000735	<0.05	0.01	<0.20
0.00296	<0.05	0.00654	<0.20
0.00247	<0.05	0.02	<0.20
0.00382	<0.05	0.00573	<0.20
0.00132	<0.05	0.01	<0.20
0.00407	<0.05	0.01	<0.20
0.00467	<0.05	0.00403	<0.20
0.000843	<0.05	0.00683	<0.20
0.00114	<0.05	0.00827	<0.20
0.00262	<0.05	0.00892	<0.20
0.00262	<0.05	0.00892	<0.20
0.00262	<0.05	0.02	<0.20
0.000906	<0.05	0.01	<0.20
0.00484	<0.05	0.00414	<0.20
0.00207	<0.05	0.02	<0.20
0.00082	<0.05	0.01	<0.20
0.00169	<0.05	0.00426	<0.20
0.00422	<0.05	0.02	<0.20
0.00291	<0.05	0.02	<0.20
0.000873	<0.05	0.00294	<0.20
0.000939	<0.05	0.01	<0.20
0.0041	<0.05	0.01	<0.20
0.00145	<0.05	0.00649	<0.20
0.00188	<0.05	0.00942	<0.20
0.00237	<0.05	0.00968	<0.20
0.00107	<0.05	0.01	<0.20
0.00204	<0.05	0.02	<0.20
0.00138	<0.05	0.01	<0.20

0.00369	<0.05	0.18	>=0.20
0.0018	<0.05	0.04	>=0.20
0.00308	<0.05	0.02	>=0.20
0.00313	<0.05	0.24	>=0.20
0.00348	<0.05	0.14	>=0.20
0.00159	<0.05	0.04	>=0.20
0.00271	<0.05	0.09	>=0.20
0.00527	<0.05	0.03	>=0.20
0.00219	<0.05	0.04	>=0.20
0.00219	<0.05	0.04	>=0.20
0.00335	<0.05	0.12	>=0.20
0.00343	<0.05	0.07	>=0.20
0.00315	<0.05	0.05	>=0.20
0.00511	<0.05	0.05	>=0.20
0.00209	<0.05	0.05	>=0.20
0.00493	<0.05	0.05	>=0.20
0.00364	<0.05	0.2	>=0.20
0.00289	<0.05	0.07	>=0.20
0.00339	<0.05	0.05	>=0.20
0.00106	<0.05	0.23	>=0.20
0.00298	<0.05	0.03	>=0.20
0.00415	<0.05	0.13	>=0.20
0.0014	<0.05	0.05	>=0.20
0.00461	<0.05	0.02	>=0.20
0.00157	<0.05	0.04	>=0.20
0.00285	<0.05	0.06	>=0.20
0.00406	<0.05	0.05	>=0.20
0.03	<0.20	0.000105	<0.01
0.02	<0.20	2.91E-06	<0.01
0.02	<0.20	0.000105	<0.01
0.03	<0.20	0.00157	<0.05
0.03	<0.20	0.000706	<0.05
0.00667	<0.20	0.00152	<0.05
0.03	<0.20	0.00212	<0.05
0.02	<0.20	0.00107	<0.05
0.03	<0.20	0.0024	<0.05
0.02	<0.20	0.000935	<0.05
0.00855	<0.20	0.00275	<0.20
0.01	<0.20	0.00583	<0.20
0.03	<0.20	0.02	<0.20
0.02	<0.20	0.0051	<0.20
0.01	<0.20	0.01	<0.20
0.00886	<0.20	0.00578	<0.20
0.04	<0.20	0.02	<0.20
0.02	<0.20	0.02	<0.20
0.01	<0.20	0.0045	<0.20
0.03	<0.20	0.00685	<0.20

0.00755	<0.20	0.00298	<0.20
0.02	<0.20	0.00869	<0.20
0.00917	<0.20	0.00646	<0.20
0.01	<0.20	0.00639	<0.20
0.03	<0.20	0.00307	<0.20
0.00789	<0.20	0.00556	<0.20
0.03	<0.20	0.02	<0.20
0.03	<0.20	0.00986	<0.20
0.03	<0.20	0.00386	<0.20
0.02	<0.20	0.00808	<0.20
0.00703	<0.20	0.01	<0.20
0.02	<0.20	0.00991	<0.20
0.03	<0.20	0.02	<0.20
0.00984	<0.20	0.00354	<0.20
0.02	<0.20	0.02	<0.20
0.02	<0.20	0.02	<0.20
0.04	<0.20	0.02	<0.20
0.01	<0.20	0.00882	<0.20
0.00711	<0.20	0.00633	<0.20
0.02	<0.20	0.02	<0.20
0.02	<0.20	0.02	<0.20
0.03	<0.20	0.19	>=0.20
0.03	<0.20	0.03	>=0.20
0.03	<0.20	0.09	>=0.20
0.02	<0.20	0.39	>=0.20
0.02	<0.20	0.05	>=0.20
0.00735	<0.20	0.09	>=0.20
0.01	<0.20	0.06	>=0.20
0.01	<0.20	0.15	>=0.20
0.00973	<0.20	0.12	>=0.20
0.02	<0.20	0.42	>=0.20
0.03	<0.20	0.09	>=0.20
0.04	<0.20	0.15	>=0.20
0.00901	<0.20	0.19	>=0.20
0.03	<0.20	0.17	>=0.20
0.00754	<0.20	0.25	>=0.20
0.02	<0.20	0.05	>=0.20
0.02	<0.20	0.19	>=0.20
0.04	<0.20	0.03	>=0.20
0.04	<0.20	0.03	>=0.20
0.01	<0.20	0.06	>=0.20
0.00666	<0.20	0.13	>=0.20
0.03	<0.20	0.06	>=0.20
0.01	<0.20	0.22	>=0.20
0.02	<0.20	0.19	>=0.20
0.02	<0.20	0.07	>=0.20
0.00823	<0.20	0.04	>=0.20

0.03	<0.20	0.04	>=0.20
0.00967	<0.20	0.07	>=0.20
0.03	<0.20	0.12	>=0.20
0.01	<0.20	0.23	>=0.20
0.01	<0.20	0.06	>=0.20
0.01	<0.20	0.1	>=0.20
0.04	<0.20	0.04	>=0.20
0.03	<0.20	0.09	>=0.20
0.01	<0.20	0.06	>=0.20
0.01	<0.20	0.06	>=0.20
0.01	<0.20	0.1	>=0.20
0.00848	<0.20	0.09	>=0.20
0.03	<0.20	0.05	>=0.20
0.02	<0.20	0.08	>=0.20
0.02	<0.20	0.03	>=0.20
0.01	<0.20	0.09	>=0.20
0.03	<0.20	0.03	>=0.20
0.02	<0.20	0.05	>=0.20
0.00961	<0.20	0.04	>=0.20
0.02	<0.20	0.23	>=0.20
0.00749	<0.20	0.03	>=0.20
0.02	<0.20	0.23	>=0.20
0.00677	<0.20	0.05	>=0.20
0.02	<0.20	0.16	>=0.20
0.03	<0.20	0.23	>=0.20
0.03	<0.20	0.06	>=0.20
0.03	<0.20	0.06	>=0.20
0.00779	<0.20	0.07	>=0.20
0.00905	<0.20	0.07	>=0.20
0.02	<0.20	0.07	>=0.20
0.02	<0.20	0.21	>=0.20
0.16	>=0.20	0.000178	<0.01
0.06	>=0.20	3.41E-05	<0.01
0.34	>=0.20	0.00189	<0.05
0.37	>=0.20	0.00266	<0.05
0.24	>=0.20	0.00138	<0.05
0.66	>=0.20	0.00266	<0.05
0.74	>=0.20	0.002	<0.05
0.17	>=0.20	0.000673	<0.05
0.08	>=0.20	0.00239	<0.05
0.09	>=0.20	0.00162	<0.05
0.25	>=0.20	0.00228	<0.05
0.04	>=0.20	0.00211	<0.05
0.12	>=0.20	0.00144	<0.05
0.15	>=0.20	0.00174	<0.05
0.19	>=0.20	0.00112	<0.05
0.59	>=0.20	0.0023	<0.05

0.07	>=0.20	0.00312	<0.20
0.24	>=0.20	0.02	<0.20
0.89	>=0.20	0.00397	<0.20
0.31	>=0.20	0.00528	<0.20
0.53	>=0.20	0.02	<0.20
0.06	>=0.20	0.00301	<0.20
0.05	>=0.20	0.01	<0.20
0.12	>=0.20	0.00795	<0.20
0.05	>=0.20	0.00398	<0.20
0.56	>=0.20	0.00731	<0.20
0.76	>=0.20	0.02	<0.20
0.09	>=0.20	0.02	<0.20
0.11	>=0.20	0.01	<0.20
0.48	>=0.20	0.00645	<0.20
0.3	>=0.20	0.02	<0.20
0.05	>=0.20	0.02	<0.20
0.24	>=0.20	0.00294	<0.20
0.23	>=0.20	0.00312	<0.20
0.57	>=0.20	0.00954	<0.20
0.21	>=0.20	0.01	<0.20
0.04	>=0.20	0.00702	<0.20
0.51	>=0.20	0.01	<0.20
0.14	>=0.20	0.01	<0.20
0.14	>=0.20	0.01	<0.20
0.05	>=0.20	0.00273	<0.20
0.05	>=0.20	0.00273	<0.20
0.48	>=0.20	0.01	<0.20
0.18	>=0.20	0.00343	<0.20
0.04	>=0.20	0.01	<0.20
0.86	>=0.20	0.02	<0.20
0.5	>=0.20	0.01	<0.20
0.04	>=0.20	0.01	<0.20
0.08	>=0.20	0.02	<0.20
0.1	>=0.20	0.00493	<0.20
0.17	>=0.20	0.02	<0.20
0.07	>=0.20	0.02	<0.20
0.1	>=0.20	0.02	<0.20
0.11	>=0.20	0.02	<0.20
0.05	>=0.20	0.01	<0.20
0.06	>=0.20	0.02	<0.20
0.05	>=0.20	0.00814	<0.20
0.12	>=0.20	0.02	<0.20
0.09	>=0.20	0.0071	<0.20
0.05	>=0.20	0.02	<0.20
0.25	>=0.20	0.01	<0.20
0.1	>=0.20	0.01	<0.20
0.13	>=0.20	0.02	<0.20

0.1	>=0.20	0.01	<0.20
0.12	>=0.20	0.00684	<0.20
0.33	>=0.20	0.00659	<0.20
0.48	>=0.20	0.02	<0.20
0.19	>=0.20	0.02	<0.20
0.04	>=0.20	0.02	<0.20
0.12	>=0.20	0.02	<0.20
0.78	>=0.20	0.02	<0.20
0.04	>=0.20	0.02	<0.20
0.04	>=0.20	0.02	<0.20
0.78	>=0.20	0.02	<0.20
0.65	>=0.20	0.02	<0.20
0.64	>=0.20	0.00856	<0.20
0.59	>=0.20	0.00768	<0.20
0.19	>=0.20	0.02	<0.20
0.17	>=0.20	0.02	<0.20
0.23	>=0.20	0.00994	<0.20
0.2	>=0.20	0.0098	<0.20
0.6	>=0.20	0.00996	<0.20
0.07	>=0.20	0.00435	<0.20
0.44	>=0.20	0.00399	<0.20
0.42	>=0.20	0.00513	<0.20
0.08	>=0.20	0.00364	<0.20
0.18	>=0.20	0.06	>=0.20
0.68	>=0.20	0.1	>=0.20
0.87	>=0.20	0.13	>=0.20
0.95	>=0.20	0.08	>=0.20
0.21	>=0.20	0.04	>=0.20
0.29	>=0.20	0.17	>=0.20
0.81	>=0.20	0.29	>=0.20
0.46	>=0.20	0.08	>=0.20
0.05	>=0.20	0.7	>=0.20
0.69	>=0.20	0.2	>=0.20
0.15	>=0.20	0.03	>=0.20
0.94	>=0.20	0.32	>=0.20
0.05	>=0.20	0.11	>=0.20
0.19	>=0.20	0.39	>=0.20
0.07	>=0.20	0.06	>=0.20
0.14	>=0.20	0.3	>=0.20
0.6	>=0.20	0.12	>=0.20
0.44	>=0.20	0.3	>=0.20
0.32	>=0.20	0.26	>=0.20
0.51	>=0.20	0.04	>=0.20
0.61	>=0.20	0.1	>=0.20
0.04	>=0.20	0.08	>=0.20
0.42	>=0.20	0.1	>=0.20
0.56	>=0.20	0.03	>=0.20

0.15 >=0.20	0.29 >=0.20
0.18 >=0.20	0.09 >=0.20
0.78 >=0.20	0.07 >=0.20
0.9 >=0.20	0.18 >=0.20
0.83 >=0.20	0.03 >=0.20
0.1 >=0.20	0.04 >=0.20
0.78 >=0.20	0.09 >=0.20
0.06 >=0.20	0.08 >=0.20
0.61 >=0.20	0.2 >=0.20
0.21 >=0.20	0.06 >=0.20
0.16 >=0.20	0.26 >=0.20
0.77 >=0.20	0.03 >=0.20
0.86 >=0.20	0.06 >=0.20
0.8 >=0.20	0.38 >=0.20
0.31 >=0.20	0.06 >=0.20
0.85 >=0.20	0.14 >=0.20
0.06 >=0.20	0.12 >=0.20
0.86 >=0.20	0.24 >=0.20
0.16 >=0.20	0.13 >=0.20
0.21 >=0.20	0.13 >=0.20
0.83 >=0.20	0.53 >=0.20
0.28 >=0.20	0.17 >=0.20
0.36 >=0.20	0.34 >=0.20
0.9 >=0.20	0.29 >=0.20
0.18 >=0.20	0.03 >=0.20
0.83 >=0.20	0.2 >=0.20
0.56 >=0.20	0.81 >=0.20
0.66 >=0.20	0.34 >=0.20
0.94 >=0.20	0.25 >=0.20
0.65 >=0.20	0.06 >=0.20
0.87 >=0.20	0.05 >=0.20
0.2 >=0.20	0.33 >=0.20
0.55 >=0.20	0.04 >=0.20
0.72 >=0.20	0.64 >=0.20
0.07 >=0.20	0.04 >=0.20
0.53 >=0.20	0.08 >=0.20
0.57 >=0.20	0.2 >=0.20
0.05 >=0.20	0.29 >=0.20
0.18 >=0.20	0.33 >=0.20
0.26 >=0.20	0.03 >=0.20
0.55 >=0.20	0.07 >=0.20
0.16 >=0.20	0.04 >=0.20
0.6 >=0.20	0.34 >=0.20
0.82 >=0.20	0.19 >=0.20
0.27 >=0.20	0.07 >=0.20
0.18 >=0.20	0.2 >=0.20
0.77 >=0.20	0.38 >=0.20

0.88 >=0.20	0.04 >=0.20
0.31 >=0.20	0.22 >=0.20
0.22 >=0.20	0.18 >=0.20
0.35 >=0.20	0.41 >=0.20
0.66 >=0.20	0.03 >=0.20
0.78 >=0.20	0.23 >=0.20
0.38 >=0.20	0.11 >=0.20
0.1 >=0.20	0.35 >=0.20
0.94 >=0.20	0.31 >=0.20
0.35 >=0.20	0.07 >=0.20
0.05 >=0.20	0.21 >=0.20
0.06 >=0.20	0.18 >=0.20
0.5 >=0.20	0.07 >=0.20
0.23 >=0.20	0.14 >=0.20
0.15 >=0.20	0.09 >=0.20
0.55 >=0.20	0.08 >=0.20
0.1 >=0.20	0.05 >=0.20
0.17 >=0.20	0.13 >=0.20
0.9 >=0.20	0.47 >=0.20
0.65 >=0.20	0.16 >=0.20
0.6 >=0.20	0.04 >=0.20
0.78 >=0.20	0.04 >=0.20
0.43 >=0.20	0.06 >=0.20
0.49 >=0.20	0.03 >=0.20
0.22 >=0.20	0.1 >=0.20
0.43 >=0.20	0.32 >=0.20
0.33 >=0.20	0.03 >=0.20
0.64 >=0.20	0.1 >=0.20
0.5 >=0.20	0.05 >=0.20
0.14 >=0.20	0.09 >=0.20
0.06 >=0.20	0.03 >=0.20
0.24 >=0.20	0.03 >=0.20
0.89 >=0.20	0.28 >=0.20
0.72 >=0.20	0.09 >=0.20
0.43 >=0.20	0.3 >=0.20
0.9 >=0.20	0.16 >=0.20
0.74 >=0.20	0.04 >=0.20
0.16 >=0.20	0.08 >=0.20
0.99 >=0.20	0.53 >=0.20
0.06 >=0.20	0.17 >=0.20
0.6 >=0.20	0.03 >=0.20
0.89 >=0.20	0.18 >=0.20
0.18 >=0.20	0.13 >=0.20
0.98 >=0.20	0.44 >=0.20
0.04 >=0.20	0.61 >=0.20
0.04 >=0.20	0.44 >=0.20
0.37 >=0.20	0.04 >=0.20

0.05 >=0.20	0.03 >=0.20
0.2 >=0.20	0.07 >=0.20
0.32 >=0.20	0.17 >=0.20
0.13 >=0.20	0.16 >=0.20
0.12 >=0.20	0.1 >=0.20
0.28 >=0.20	0.1 >=0.20
0.11 >=0.20	0.19 >=0.20
0.11 >=0.20	0.19 >=0.20
0.76 >=0.20	0.45 >=0.20
0.29 >=0.20	0.19 >=0.20
0.29 >=0.20	0.09 >=0.20
0.8 >=0.20	0.41 >=0.20
0.07 >=0.20	0.05 >=0.20
0.04 >=0.20	0.09 >=0.20
0.06 >=0.20	0.12 >=0.20
0.91 >=0.20	0.19 >=0.20
0.66 >=0.20	0.02 >=0.20
0.81 >=0.20	0.12 >=0.20
0.23 >=0.20	0.23 >=0.20
0.14 >=0.20	0.1 >=0.20
0.41 >=0.20	0.03 >=0.20
0.13 >=0.20	0.05 >=0.20
0.11 >=0.20	0.57 >=0.20
0.05 >=0.20	0.35 >=0.20
0.13 >=0.20	0.1 >=0.20
0.35 >=0.20	0.17 >=0.20
0.69 >=0.20	0.07 >=0.20
0.52 >=0.20	0.16 >=0.20
0.52 >=0.20	0.31 >=0.20
0.88 >=0.20	0.15 >=0.20
0.8 >=0.20	0.24 >=0.20
0.47 >=0.20	0.3 >=0.20
0.56 >=0.20	0.22 >=0.20
0.97 >=0.20	0.2 >=0.20
0.33 >=0.20	0.06 >=0.20
0.52 >=0.20	0.03 >=0.20
0.08 >=0.20	0.09 >=0.20
0.38 >=0.20	0.04 >=0.20
0.36 >=0.20	0.08 >=0.20
0.81 >=0.20	0.4 >=0.20
0.21 >=0.20	0.2 >=0.20
0.17 >=0.20	0.07 >=0.20
0.73 >=0.20	0.45 >=0.20
0.1 >=0.20	0.08 >=0.20
0.22 >=0.20	0.05 >=0.20
0.14 >=0.20	0.09 >=0.20
0.11 >=0.20	0.19 >=0.20

0.25 >=0.20	0.26 >=0.20
0.11 >=0.20	0.19 >=0.20
0.11 >=0.20	0.19 >=0.20
0.12 >=0.20	0.1 >=0.20
0.16 >=0.20	0.17 >=0.20
0.11 >=0.20	0.23 >=0.20
0.18 >=0.20	0.08 >=0.20
0.87 >=0.20	0.25 >=0.20
0.06 >=0.20	0.28 >=0.20
0.42 >=0.20	0.53 >=0.20
0.08 >=0.20	0.16 >=0.20
0.06 >=0.20	0.06 >=0.20
0.13 >=0.20	0.13 >=0.20
0.66 >=0.20	0.11 >=0.20
0.36 >=0.20	0.37 >=0.20
0.12 >=0.20	0.23 >=0.20
0.24 >=0.20	0.03 >=0.20
0.88 >=0.20	0.29 >=0.20
0.18 >=0.20	0.13 >=0.20
0.71 >=0.20	0.03 >=0.20
0.05 >=0.20	0.15 >=0.20
0.27 >=0.20	0.08 >=0.20
0.04 >=0.20	0.05 >=0.20
0.04 >=0.20	0.03 >=0.20
0.32 >=0.20	0.05 >=0.20
0.66 >=0.20	0.94 >=0.20
0.29 >=0.20	0.08 >=0.20
0.14 >=0.20	0.03 >=0.20
0.34 >=0.20	0.11 >=0.20
0.89 >=0.20	0.32 >=0.20
0.16 >=0.20	0.03 >=0.20
0.55 >=0.20	0.27 >=0.20
0.7 >=0.20	0.15 >=0.20
0.94 >=0.20	0.13 >=0.20
0.26 >=0.20	0.2 >=0.20
0.89 >=0.20	0.2 >=0.20
0.73 >=0.20	0.08 >=0.20
0.46 >=0.20	0.08 >=0.20
0.12 >=0.20	0.06 >=0.20
0.29 >=0.20	0.08 >=0.20
0.36 >=0.20	0.03 >=0.20
0.7 >=0.20	0.11 >=0.20
0.21 >=0.20	0.27 >=0.20
0.12 >=0.20	0.1 >=0.20
0.4 >=0.20	0.5 >=0.20
0.05 >=0.20	0.05 >=0.20
0.74 >=0.20	0.35 >=0.20

0.44 >=0.20	0.13 >=0.20
0.59 >=0.20	0.43 >=0.20
0.08 >=0.20	0.29 >=0.20
0.24 >=0.20	0.02 >=0.20
0.08 >=0.20	0.19 >=0.20
0.36 >=0.20	0.08 >=0.20
0.04 >=0.20	0.27 >=0.20
0.37 >=0.20	0.03 >=0.20
0.18 >=0.20	0.13 >=0.20
0.1 >=0.20	0.09 >=0.20
0.54 >=0.20	0.17 >=0.20
0.92 >=0.20	0.35 >=0.20
0.15 >=0.20	0.03 >=0.20
0.43 >=0.20	0.03 >=0.20
0.12 >=0.20	0.04 >=0.20
0.72 >=0.20	0.08 >=0.20
0.12 >=0.20	0.17 >=0.20
0.47 >=0.20	0.05 >=0.20
0.07 >=0.20	0.09 >=0.20
0.32 >=0.20	0.15 >=0.20
0.49 >=0.20	0.03 >=0.20
0.2 >=0.20	0.13 >=0.20
0.43 >=0.20	0.08 >=0.20
0.46 >=0.20	0.15 >=0.20
0.37 >=0.20	0.04 >=0.20
0.17 >=0.20	0.05 >=0.20
0.36 >=0.20	0.25 >=0.20
0.37 >=0.20	0.27 >=0.20
0.61 >=0.20	0.12 >=0.20
0.28 >=0.20	0.15 >=0.20
0.43 >=0.20	0.27 >=0.20
0.35 >=0.20	0.34 >=0.20
0.91 >=0.20	0.26 >=0.20
0.09 >=0.20	0.13 >=0.20
0.08 >=0.20	0.19 >=0.20
0.49 >=0.20	0.23 >=0.20
0.35 >=0.20	0.17 >=0.20
0.33 >=0.20	0.12 >=0.20
0.41 >=0.20	0.26 >=0.20
0.08 >=0.20	0.18 >=0.20
0.17 >=0.20	0.34 >=0.20
0.48 >=0.20	0.07 >=0.20
0.97 >=0.20	0.56 >=0.20
0.49 >=0.20	0.19 >=0.20
0.63 >=0.20	0.46 >=0.20
0.07 >=0.20	0.55 >=0.20
0.22 >=0.20	0.04 >=0.20

0.06 >=0.20	0.08 >=0.20
0.65 >=0.20	0.24 >=0.20
0.04 >=0.20	0.08 >=0.20
0.69 >=0.20	0.12 >=0.20
0.1 >=0.20	0.29 >=0.20
0.28 >=0.20	0.1 >=0.20
0.28 >=0.20	0.1 >=0.20
0.2 >=0.20	0.32 >=0.20
0.1 >=0.20	0.05 >=0.20
0.23 >=0.20	0.16 >=0.20
0.27 >=0.20	0.3 >=0.20
0.4 >=0.20	0.09 >=0.20
0.31 >=0.20	0.35 >=0.20
0.4 >=0.20	0.5 >=0.20
0.33 >=0.20	0.09 >=0.20
0.77 >=0.20	0.16 >=0.20
0.87 >=0.20	0.34 >=0.20
0.82 >=0.20	0.18 >=0.20
0.48 >=0.20	0.11 >=0.20
0.56 >=0.20	0.05 >=0.20
0.65 >=0.20	0.17 >=0.20
0.98 >=0.20	0.44 >=0.20
0.76 >=0.20	0.09 >=0.20
0.16 >=0.20	0.09 >=0.20
0.32 >=0.20	0.1 >=0.20
0.82 >=0.20	0.28 >=0.20
0.2 >=0.20	0.08 >=0.20
0.17 >=0.20	0.04 >=0.20
0.37 >=0.20	0.24 >=0.20
0.17 >=0.20	0.2 >=0.20
0.16 >=0.20	0.03 >=0.20
0.3 >=0.20	0.23 >=0.20
0.06 >=0.20	0.06 >=0.20
0.72 >=0.20	0.03 >=0.20
0.07 >=0.20	0.14 >=0.20
0.08 >=0.20	0.05 >=0.20
0.04 >=0.20	0.04 >=0.20
0.07 >=0.20	0.04 >=0.20
0.96 >=0.20	0.47 >=0.20
0.48 >=0.20	0.27 >=0.20
0.54 >=0.20	0.18 >=0.20
0.41 >=0.20	0.08 >=0.20
0.56 >=0.20	0.56 >=0.20
0.29 >=0.20	0.08 >=0.20
0.61 >=0.20	0.1 >=0.20
0.08 >=0.20	0.07 >=0.20
0.94 >=0.20	0.26 >=0.20

0.04 >=0.20	0.04 >=0.20
0.08 >=0.20	0.05 >=0.20
0.08 >=0.20	0.04 >=0.20
0.04 >=0.20	0.04 >=0.20
0.04 >=0.20	0.04 >=0.20
0.1 >=0.20	0.05 >=0.20
0.17 >=0.20	0.2 >=0.20
0.05 >=0.20	0.08 >=0.20
0.65 >=0.20	0.39 >=0.20
0.22 >=0.20	0.22 >=0.20
0.17 >=0.20	0.04 >=0.20
0.99 >=0.20	0.4 >=0.20
0.11 >=0.20	0.22 >=0.20
0.86 >=0.20	0.06 >=0.20
0.08 >=0.20	0.5 >=0.20
0.6 >=0.20	0.46 >=0.20
0.09 >=0.20	0.06 >=0.20
0.44 >=0.20	0.04 >=0.20
0.1 >=0.20	0.19 >=0.20
0.16 >=0.20	0.14 >=0.20
0.47 >=0.20	0.59 >=0.20
0.25 >=0.20	0.36 >=0.20
0.11 >=0.20	0.03 >=0.20
0.77 >=0.20	0.06 >=0.20
0.05 >=0.20	0.04 >=0.20
0.06 >=0.20	0.13 >=0.20
0.08 >=0.20	0.03 >=0.20
0.71 >=0.20	0.36 >=0.20
0.42 >=0.20	0.17 >=0.20
0.95 >=0.20	0.47 >=0.20
0.79 >=0.20	0.04 >=0.20
0.42 >=0.20	0.33 >=0.20
0.08 >=0.20	0.08 >=0.20
0.47 >=0.20	0.44 >=0.20
0.06 >=0.20	0.05 >=0.20
0.07 >=0.20	0.06 >=0.20
0.06 >=0.20	0.2 >=0.20
0.46 >=0.20	0.48 >=0.20
0.08 >=0.20	0.09 >=0.20
0.3 >=0.20	0.29 >=0.20
0.91 >=0.20	0.58 >=0.20
0.84 >=0.20	0.6 >=0.20
0.14 >=0.20	0.19 >=0.20
0.48 >=0.20	0.09 >=0.20
0.12 >=0.20	0.47 >=0.20
0.2 >=0.20	0.37 >=0.20
0.82 >=0.20	0.03 >=0.20

0.7 >=0.20	0.25 >=0.20
0.91 >=0.20	0.15 >=0.20
0.16 >=0.20	0.04 >=0.20
0.37 >=0.20	0.51 >=0.20
0.41 >=0.20	0.41 >=0.20
0.72 >=0.20	0.47 >=0.20
0.75 >=0.20	0.34 >=0.20
0.23 >=0.20	0.04 >=0.20
0.97 >=0.20	0.32 >=0.20
0.21 >=0.20	0.14 >=0.20
0.26 >=0.20	0.07 >=0.20
0.97 >=0.20	0.32 >=0.20
0.65 >=0.20	0.06 >=0.20
0.51 >=0.20	0.58 >=0.20
0.14 >=0.20	0.27 >=0.20
0.49 >=0.20	0.41 >=0.20
0.79 >=0.20	0.17 >=0.20
0.99 >=0.20	0.49 >=0.20
0.34 >=0.20	0.11 >=0.20
0.98 >=0.20	0.17 >=0.20
0.94 >=0.20	0.06 >=0.20
0.67 >=0.20	0.29 >=0.20
0.84 >=0.20	0.27 >=0.20
0.82 >=0.20	0.2 >=0.20
0.36 >=0.20	0.09 >=0.20
0.78 >=0.20	0.39 >=0.20
0.19 >=0.20	0.26 >=0.20
0.47 >=0.20	0.59 >=0.20
0.54 >=0.20	0.68 >=0.20
0.93 >=0.20	0.39 >=0.20
0.25 >=0.20	0.13 >=0.20
0.26 >=0.20	0.28 >=0.20
0.11 >=0.20	0.11 >=0.20
0.9 >=0.20	0.03 >=0.20
0.8 >=0.20	0.11 >=0.20
0.59 >=0.20	0.18 >=0.20
0.68 >=0.20	0.05 >=0.20
0.7 >=0.20	0.12 >=0.20
0.9 >=0.20	0.35 >=0.20
0.44 >=0.20	0.41 >=0.20
0.49 >=0.20	0.1 >=0.20
0.31 >=0.20	0.12 >=0.20
0.34 >=0.20	0.09 >=0.20
0.29 >=0.20	0.11 >=0.20
0.35 >=0.20	0.13 >=0.20
0.24 >=0.20	0.15 >=0.20
0.18 >=0.20	0.2 >=0.20

0.26	>=0.20	0.08	>=0.20
0.000167	<0.01	0.000128	<0.01
1.58E-06	<0.01	0.000209	<0.01
2.12E-07	<0.01	1.81E-05	<0.01
1.14E-06	<0.01	0.0027	<0.05
0.000529	<0.01	0.00151	<0.05
1.72E-05	<0.01	0.000414	<0.05
4.60E-06	<0.01	0.00115	<0.05
0.000513	<0.01	0.00161	<0.05
0.000288	<0.01	0.00228	<0.05
0.000373	<0.01	0.00148	<0.05
0.000198	<0.01	0.000744	<0.05
0.000347	<0.01	0.000315	<0.05
0.000279	<0.01	0.00214	<0.05
0.000193	<0.01	0.00202	<0.05
2.19E-05	<0.01	0.00256	<0.05
0.00055	<0.01	0.00235	<0.05
5.17E-05	<0.01	0.00111	<0.05
8.82E-06	<0.01	0.00194	<0.05
0.00015	<0.01	0.00211	<0.05
2.18E-05	<0.01	0.00179	<0.05
4.37E-05	<0.01	0.00107	<0.05
0.000408	<0.01	0.001	<0.05
3.13E-06	<0.01	0.00239	<0.05
0.000182	<0.01	0.00366	<0.20
4.08E-05	<0.01	0.00866	<0.20
0.000449	<0.01	0.00828	<0.20
3.68E-05	<0.01	0.02	<0.20
2.20E-06	<0.01	0.00824	<0.20
0.000265	<0.01	0.00691	<0.20
0.000712	<0.01	0.00286	<0.20
1.19E-07	<0.01	0.00486	<0.20
4.76E-05	<0.01	0.01	<0.20
2.69E-06	<0.01	0.02	<0.20
0.000179	<0.01	0.00695	<0.20
0.000149	<0.01	0.00869	<0.20
3.23E-06	<0.01	0.01	<0.20
0.000376	<0.01	0.00912	<0.20
1.55E-06	<0.01	0.00924	<0.20
9.78E-05	<0.01	0.02	<0.20
0.000182	<0.01	0.00353	<0.20
0.000449	<0.01	0.00661	<0.20
0.000334	<0.01	0.02	<0.20
0.000286	<0.01	0.02	<0.20
0.000526	<0.01	0.02	<0.20
0.000192	<0.01	0.00988	<0.20
0.000252	<0.01	0.00346	<0.20

2.10E-06	<0.01	0.00509	<0.20
3.82E-05	<0.01	0.01	<0.20
2.49E-05	<0.01	0.00449	<0.20
0.000228	<0.01	0.02	<0.20
2.01E-05	<0.01	0.00302	<0.20
0.000718	<0.01	0.0045	<0.20
0.000526	<0.01	0.00441	<0.20
1.02E-05	<0.01	0.02	<0.20
0.000119	<0.01	0.02	<0.20
4.98E-06	<0.01	0.0032	<0.20
0.000482	<0.01	0.02	<0.20
3.00E-04	<0.01	0.00403	<0.20
1.19E-06	<0.01	0.01	<0.20
3.00E-04	<0.01	0.00403	<0.20
4.54E-06	<0.01	0.00834	<0.20
0.000384	<0.01	0.00533	<0.20
0.000557	<0.01	0.00528	<0.20
4.96E-05	<0.01	0.01	<0.20
4.91E-05	<0.01	0.02	<0.20
0.000282	<0.01	0.00298	<0.20
1.78E-05	<0.01	0.00988	<0.20
0.000145	<0.01	0.0068	<0.20
0.000132	<0.01	0.00281	<0.20
3.59E-05	<0.01	0.02	<0.20
0.000686	<0.01	0.00567	<0.20
4.55E-05	<0.01	0.00719	<0.20
2.98E-05	<0.01	0.02	<0.20
6.19E-05	<0.01	0.01	<0.20
4.54E-06	<0.01	0.00834	<0.20
0.000589	<0.01	0.02	<0.20
0.000228	<0.01	0.07	>=0.20
0.000312	<0.01	0.11	>=0.20
0.000318	<0.01	0.05	>=0.20
1.26E-05	<0.01	0.08	>=0.20
0.00051	<0.01	0.07	>=0.20
0.00032	<0.01	0.22	>=0.20
0.000472	<0.01	0.06	>=0.20
0.000267	<0.01	0.04	>=0.20
0.000627	<0.01	0.03	>=0.20
0.000104	<0.01	0.1	>=0.20
0.000256	<0.01	0.05	>=0.20
0.000162	<0.01	0.07	>=0.20
0.000245	<0.01	0.08	>=0.20
0.000182	<0.01	0.05	>=0.20
0.000605	<0.01	0.1	>=0.20
0.000315	<0.01	0.08	>=0.20
9.06E-05	<0.01	0.45	>=0.20

0.00033	<0.01	0.05	>=0.20
0.000189	<0.01	0.12	>=0.20
0.000687	<0.01	0.02	>=0.20
0.000183	<0.01	0.26	>=0.20
0.000272	<0.01	0.08	>=0.20
0.000386	<0.01	0.14	>=0.20
5.36E-06	<0.01	0.17	>=0.20
0.000566	<0.01	0.18	>=0.20
9.23E-06	<0.01	0.04	>=0.20
2.85E-05	<0.01	0.15	>=0.20
0.000275	<0.01	0.17	>=0.20
0.000148	<0.01	0.07	>=0.20
0.000355	<0.01	0.1	>=0.20
9.23E-06	<0.01	0.04	>=0.20
3.77E-05	<0.01	0.07	>=0.20
0.000463	<0.01	0.06	>=0.20
0.000239	<0.01	0.07	>=0.20
0.000382	<0.01	0.09	>=0.20
0.000627	<0.01	0.03	>=0.20
4.83E-05	<0.01	0.07	>=0.20
0.000567	<0.01	0.08	>=0.20
0.000586	<0.01	0.82	>=0.20
0.000484	<0.01	0.18	>=0.20
7.08E-06	<0.01	0.03	>=0.20
9.58E-05	<0.01	0.08	>=0.20
9.29E-05	<0.01	0.1	>=0.20
0.000647	<0.01	0.03	>=0.20
0.00121	<0.05	5.32E-05	<0.01
0.00152	<0.05	0.000127	<0.01
0.00191	<0.05	0.000189	<0.01
0.00233	<0.05	0.00151	<0.05
0.00252	<0.05	0.00244	<0.05
0.00429	<0.05	0.00238	<0.05
0.00467	<0.05	0.00209	<0.05
0.00197	<0.05	0.00191	<0.05
0.00463	<0.05	0.00206	<0.05
0.00281	<0.05	0.00267	<0.05
0.00119	<0.05	0.00166	<0.05
0.00114	<0.05	0.00161	<0.05
0.00403	<0.05	0.00185	<0.05
0.00439	<0.05	0.00201	<0.05
0.00461	<0.05	0.00434	<0.20
0.00291	<0.05	0.01	<0.20
0.000895	<0.05	0.02	<0.20
0.00436	<0.05	0.01	<0.20
0.0023	<0.05	0.00419	<0.20
0.00157	<0.05	0.02	<0.20

0.00144	<0.05	0.00295	<0.20
0.00139	<0.05	0.00485	<0.20
0.00207	<0.05	0.00921	<0.20
0.00168	<0.05	0.00663	<0.20
0.00405	<0.05	0.00508	<0.20
0.005	<0.05	0.01	<0.20
0.000911	<0.05	0.0046	<0.20
0.00168	<0.05	0.00523	<0.20
0.00546	<0.05	0.00742	<0.20
0.00474	<0.05	0.00536	<0.20
0.00438	<0.05	0.02	<0.20
0.0014	<0.05	0.02	<0.20
0.00262	<0.05	0.0068	<0.20
0.00162	<0.05	0.01	<0.20
0.00209	<0.05	0.00558	<0.20
0.000763	<0.05	0.01	<0.20
0.00116	<0.05	0.01	<0.20
0.00573	<0.05	0.02	<0.20
0.00201	<0.05	0.00686	<0.20
0.00494	<0.05	0.02	<0.20
0.00377	<0.05	0.00369	<0.20
0.00316	<0.05	0.02	<0.20
0.00174	<0.05	0.02	<0.20
0.00336	<0.05	0.02	<0.20
0.00292	<0.05	0.00365	<0.20
0.00165	<0.05	0.00433	<0.20
0.00564	<0.05	0.02	<0.20
0.00436	<0.05	0.02	<0.20
0.000765	<0.05	0.00501	<0.20
0.00144	<0.05	0.00531	<0.20
0.00303	<0.05	0.02	<0.20
0.00417	<0.05	0.02	<0.20
0.00372	<0.05	0.01	<0.20
0.000925	<0.05	0.00523	<0.20
0.00136	<0.05	0.00523	<0.20
0.00459	<0.05	0.02	<0.20
0.000888	<0.05	0.00559	<0.20
0.00365	<0.05	0.00437	<0.20
0.0053	<0.05	0.01	<0.20
0.00572	<0.05	0.02	<0.20
0.00235	<0.05	0.02	<0.20
0.00562	<0.05	0.00743	<0.20
0.00146	<0.05	0.02	<0.20
0.00402	<0.05	0.00729	<0.20
0.00261	<0.05	0.00696	<0.20
0.00262	<0.05	0.02	<0.20
0.00281	<0.05	0.02	<0.20

0.000754	<0.05	0.01	<0.20
0.000811	<0.05	0.2	>=0.20
0.0035	<0.05	0.03	>=0.20
0.00564	<0.05	0.08	>=0.20
0.00265	<0.05	0.16	>=0.20
0.0038	<0.05	0.14	>=0.20
0.00391	<0.05	0.11	>=0.20
0.00422	<0.05	0.08	>=0.20
0.00365	<0.05	0.03	>=0.20
0.00278	<0.05	0.25	>=0.20
0.000818	<0.05	0.05	>=0.20
0.0058	<0.05	0.09	>=0.20
0.0027	<0.05	0.14	>=0.20
0.00491	<0.05	0.05	>=0.20
0.00371	<0.05	0.06	>=0.20
0.00162	<0.05	0.05	>=0.20
0.000839	<0.05	0.03	>=0.20
0.0026	<0.05	0.15	>=0.20
0.00331	<0.05	0.04	>=0.20
0.00211	<0.05	0.07	>=0.20
0.0048	<0.05	0.17	>=0.20
0.00123	<0.05	0.09	>=0.20
0.000828	<0.05	0.23	>=0.20
0.00397	<0.05	0.07	>=0.20
0.00153	<0.05	0.14	>=0.20
0.00568	<0.05	0.18	>=0.20
0.00105	<0.05	0.03	>=0.20
0.00351	<0.05	0.06	>=0.20
0.00183	<0.05	0.03	>=0.20
0.00388	<0.05	0.22	>=0.20
0.00148	<0.05	0.14	>=0.20
0.00464	<0.05	0.09	>=0.20
0.00302	<0.05	0.09	>=0.20
0.00428	<0.05	0.05	>=0.20
0.00325	<0.05	0.1	>=0.20
0.0029	<0.05	0.08	>=0.20
0.00314	<0.05	0.08	>=0.20
0.00314	<0.05	0.08	>=0.20
0.00601	<0.05	0.03	>=0.20
0.00446	<0.05	0.05	>=0.20
0.00091	<0.05	0.33	>=0.20
0.000815	<0.05	0.19	>=0.20
0.00325	<0.05	0.27	>=0.20
0.00388	<0.05	0.04	>=0.20
0.00601	<0.05	0.16	>=0.20
0.00426	<0.05	0.1	>=0.20
0.0017	<0.05	0.37	>=0.20

0.00331	<0.05	0.08	>=0.20
0.0026	<0.05	0.12	>=0.20
0.00314	<0.05	0.08	>=0.20
0.00303	<0.05	0.03	>=0.20
0.000904	<0.05	0.1	>=0.20
0.00461	<0.05	0.08	>=0.20
0.0029	<0.05	0.54	>=0.20
0.00198	<0.05	0.48	>=0.20
0.00213	<0.05	0.04	>=0.20
0.00107	<0.05	0.04	>=0.20
0.00473	<0.05	0.1	>=0.20
0.00559	<0.05	0.15	>=0.20
0.000833	<0.05	0.05	>=0.20
0.0031	<0.05	0.14	>=0.20
0.00159	<0.05	0.04	>=0.20
0.00125	<0.05	0.03	>=0.20
0.00569	<0.05	0.03	>=0.20
0.00152	<0.05	0.11	>=0.20
0.00394	<0.05	0.27	>=0.20
0.00405	<0.05	0.03	>=0.20
0.00296	<0.05	0.2	>=0.20
0.00534	<0.05	0.03	>=0.20
0.00227	<0.05	0.1	>=0.20
0.00227	<0.05	0.1	>=0.20
0.00297	<0.05	0.05	>=0.20
0.00166	<0.05	0.07	>=0.20
0.0045	<0.05	0.05	>=0.20
0.00214	<0.05	0.56	>=0.20
0.00561	<0.05	0.07	>=0.20
0.00368	<0.05	0.07	>=0.20
0.00423	<0.05	0.35	>=0.20
0.00264	<0.05	0.03	>=0.20
0.00119	<0.05	0.06	>=0.20
0.00287	<0.05	0.09	>=0.20
0.00194	<0.05	0.29	>=0.20
0.0036	<0.05	0.32	>=0.20
0.000996	<0.05	0.07	>=0.20
0.00384	<0.05	0.24	>=0.20
0.00167	<0.05	0.04	>=0.20
0.00199	<0.05	0.03	>=0.20
0.00185	<0.05	0.57	>=0.20
0.0053	<0.05	0.06	>=0.20
0.000945	<0.05	0.72	>=0.20
0.0048	<0.05	0.42	>=0.20
0.00277	<0.05	0.11	>=0.20
0.00531	<0.05	0.04	>=0.20
0.00137	<0.05	0.05	>=0.20

0.00153	<0.05	0.11	>=0.20
0.00332	<0.05	0.26	>=0.20
0.00128	<0.05	0.04	>=0.20
0.00487	<0.05	0.17	>=0.20
0.00116	<0.05	0.05	>=0.20
0.000758	<0.05	0.06	>=0.20
0.0035	<0.05	0.22	>=0.20
0.00213	<0.05	0.16	>=0.20
0.00581	<0.05	0.2	>=0.20
0.00285	<0.05	0.43	>=0.20
0.0039	<0.05	0.67	>=0.20
0.00366	<0.05	0.19	>=0.20
0.00587	<0.05	0.59	>=0.20
0.00383	<0.05	0.34	>=0.20
0.00161	<0.05	0.03	>=0.20
0.00246	<0.05	0.07	>=0.20
0.00189	<0.05	0.25	>=0.20
0.00158	<0.05	0.12	>=0.20
0.00483	<0.05	0.24	>=0.20
0.0047	<0.05	0.21	>=0.20
0.0035	<0.05	0.06	>=0.20
0.000973	<0.05	0.43	>=0.20
0.00374	<0.05	0.28	>=0.20
0.0044	<0.05	0.29	>=0.20
0.00406	<0.05	0.23	>=0.20
0.00123	<0.05	0.23	>=0.20
0.00402	<0.05	0.11	>=0.20
0.00211	<0.05	0.08	>=0.20
0.00202	<0.05	0.03	>=0.20
0.00202	<0.05	0.03	>=0.20
0.0012	<0.05	0.15	>=0.20
0.00172	<0.05	0.39	>=0.20
0.00365	<0.05	0.17	>=0.20
0.00426	<0.05	0.17	>=0.20
0.00551	<0.05	0.03	>=0.20
0.0052	<0.05	0.08	>=0.20
0.00233	<0.05	0.14	>=0.20
0.000993	<0.05	0.06	>=0.20
0.00258	<0.05	0.03	>=0.20
0.0052	<0.05	0.08	>=0.20
0.00227	<0.05	0.09	>=0.20
0.00208	<0.05	0.04	>=0.20
0.0052	<0.05	0.08	>=0.20
0.00409	<0.05	0.19	>=0.20
0.00547	<0.05	0.11	>=0.20
0.00232	<0.05	0.16	>=0.20
0.00255	<0.05	0.65	>=0.20

0.000807	<0.05	0.04	>=0.20
0.00477	<0.05	0.23	>=0.20
0.00178	<0.05	0.06	>=0.20
0.00371	<0.05	0.32	>=0.20
0.000774	<0.05	0.04	>=0.20
0.00185	<0.05	0.11	>=0.20
0.00323	<0.05	0.07	>=0.20
0.00474	<0.05	0.2	>=0.20
0.00339	<0.05	0.18	>=0.20
0.00407	<0.05	0.17	>=0.20
0.00163	<0.05	0.2	>=0.20
0.00584	<0.05	0.12	>=0.20
0.00162	<0.05	0.16	>=0.20
0.00316	<0.05	0.18	>=0.20
0.00545	<0.05	0.06	>=0.20
0.0039	<0.05	0.67	>=0.20
0.00313	<0.05	0.21	>=0.20
0.00237	<0.05	0.03	>=0.20
0.00176	<0.05	0.15	>=0.20
0.00256	<0.05	0.35	>=0.20
0.00575	<0.05	0.11	>=0.20
0.00303	<0.05	0.03	>=0.20
0.00528	<0.05	0.09	>=0.20
0.00391	<0.05	0.44	>=0.20
0.00227	<0.05	0.1	>=0.20
0.00468	<0.05	0.12	>=0.20
0.00486	<0.05	0.87	>=0.20
0.00459	<0.05	0.03	>=0.20
0.02	<0.20	0.000225	<0.01
0.01	<0.20	0.0027	<0.05
0.04	<0.20	0.000876	<0.05
0.04	<0.20	0.00181	<0.05
0.03	<0.20	0.00224	<0.05
0.03	<0.20	0.000828	<0.05
0.03	<0.20	0.00189	<0.05
0.00706	<0.20	0.0026	<0.05
0.02	<0.20	0.00135	<0.05
0.01	<0.20	0.00098	<0.05
0.00892	<0.20	0.00238	<0.05
0.02	<0.20	0.00218	<0.05
0.01	<0.20	0.000622	<0.05
0.01	<0.20	0.00678	<0.20
0.00913	<0.20	0.00384	<0.20
0.03	<0.20	0.00273	<0.20
0.00941	<0.20	0.02	<0.20
0.03	<0.20	0.00776	<0.20
0.00974	<0.20	0.00602	<0.20

0.00816	<0.20	0.00809	<0.20
0.00801	<0.20	0.02	<0.20
0.00831	<0.20	0.00925	<0.20
0.00689	<0.20	0.00691	<0.20
0.00937	<0.20	0.01	<0.20
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0.02	<0.20	0.02	<0.20
0.02	<0.20	0.02	<0.20
0.00651	<0.20	0.02	<0.20
0.02	<0.20	0.01	<0.20
0.00698	<0.20	0.02	<0.20
0.00858	<0.20	0.00889	<0.20
0.03	<0.20	0.01	<0.20
0.03	<0.20	0.00369	<0.20
0.01	<0.20	0.00993	<0.20
0.00957	<0.20	0.00305	<0.20
0.01	<0.20	0.00625	<0.20
0.04	<0.20	0.01	<0.20
0.02	<0.20	0.00496	<0.20
0.00782	<0.20	0.01	<0.20
0.02	<0.20	0.02	<0.20
0.04	<0.20	0.00928	<0.20
0.01	<0.20	0.02	<0.20
0.03	<0.20	0.00699	<0.20
0.00616	<0.20	0.01	<0.20
0.00752	<0.20	0.01	<0.20
0.00912	<0.20	0.02	<0.20
0.00967	<0.20	0.00525	<0.20
0.03	<0.20	0.02	<0.20
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0.00846	<0.20	0.00326	<0.20
0.01	<0.20	0.02	<0.20
0.00689	<0.20	0.00691	<0.20
0.00689	<0.20	0.00691	<0.20
0.03	<0.20	0.01	<0.20
0.02	<0.20	0.00589	<0.20
0.02	<0.20	0.01	<0.20
0.01	<0.20	0.02	<0.20
0.03	<0.20	0.00334	<0.20
0.00793	<0.20	0.01	<0.20
0.01	<0.20	0.00853	<0.20
0.03	<0.20	0.01	<0.20
0.03	<0.20	0.45	>=0.20
0.02	<0.20	0.31	>=0.20
0.01	<0.20	0.27	>=0.20
0.02	<0.20	0.06	>=0.20
0.00771	<0.20	0.69	>=0.20

0.02	<0.20	0.07	>=0.20
0.00881	<0.20	0.1	>=0.20
0.01	<0.20	0.24	>=0.20
0.02	<0.20	0.85	>=0.20
0.01	<0.20	0.16	>=0.20
0.03	<0.20	0.28	>=0.20
0.01	<0.20	0.73	>=0.20
0.02	<0.20	0.11	>=0.20
0.0097	<0.20	0.12	>=0.20
0.00897	<0.20	0.25	>=0.20
0.01	<0.20	0.28	>=0.20
0.00985	<0.20	0.25	>=0.20
0.03	<0.20	0.05	>=0.20
0.01	<0.20	0.13	>=0.20
0.00843	<0.20	0.06	>=0.20
0.02	<0.20	0.13	>=0.20
0.03	<0.20	0.29	>=0.20
0.00655	<0.20	0.1	>=0.20
0.01	<0.20	0.33	>=0.20
0.03	<0.20	0.16	>=0.20
0.03	<0.20	0.13	>=0.20
0.03	<0.20	0.05	>=0.20
0.02	<0.20	0.41	>=0.20
0.02	<0.20	0.04	>=0.20
0.03	<0.20	0.59	>=0.20
0.03	<0.20	0.64	>=0.20
0.00829	<0.20	0.11	>=0.20
0.01	<0.20	0.09	>=0.20
0.02	<0.20	0.41	>=0.20
0.01	<0.20	0.43	>=0.20
0.02	<0.20	0.69	>=0.20
0.03	<0.20	0.27	>=0.20
0.01	<0.20	0.2	>=0.20
0.03	<0.20	0.16	>=0.20
0.04	<0.20	0.26	>=0.20
0.00684	<0.20	0.33	>=0.20
0.00981	<0.20	0.17	>=0.20
0.00642	<0.20	0.07	>=0.20
0.03	<0.20	0.13	>=0.20
0.03	<0.20	0.37	>=0.20
0.02	<0.20	0.06	>=0.20
0.02	<0.20	0.06	>=0.20
0.02	<0.20	0.03	>=0.20
0.02	<0.20	0.03	>=0.20
0.01	<0.20	0.31	>=0.20
0.03	<0.20	0.59	>=0.20
0.03	<0.20	0.14	>=0.20

0.02	<0.20	0.3	>=0.20
0.02	<0.20	0.12	>=0.20
0.02	<0.20	0.18	>=0.20
0.01	<0.20	0.08	>=0.20
0.02	<0.20	0.39	>=0.20
0.03	<0.20	0.21	>=0.20
0.01	<0.20	0.03	>=0.20
0.00805	<0.20	0.13	>=0.20
0.02	<0.20	0.03	>=0.20
0.03	<0.20	0.25	>=0.20
0.03	<0.20	0.81	>=0.20
0.04	<0.20	0.29	>=0.20
0.00957	<0.20	0.44	>=0.20
0.01	<0.20	0.03	>=0.20
0.01	<0.20	0.2	>=0.20
0.02	<0.20	0.38	>=0.20
0.03	<0.20	0.9	>=0.20
0.03	<0.20	0.17	>=0.20
0.01	<0.20	0.77	>=0.20
0.03	<0.20	0.07	>=0.20
0.03	<0.20	0.29	>=0.20
0.01	<0.20	0.12	>=0.20
0.02	<0.20	0.19	>=0.20
0.02	<0.20	0.19	>=0.20
0.03	<0.20	0.15	>=0.20
0.03	<0.20	0.18	>=0.20
0.00985	<0.20	0.11	>=0.20
0.02	<0.20	0.15	>=0.20
0.01	<0.20	0.66	>=0.20
0.02	<0.20	0.76	>=0.20
0.03	<0.20	0.56	>=0.20
0.01	<0.20	0.22	>=0.20
0.04	<0.20	0.57	>=0.20
0.02	<0.20	0.13	>=0.20
0.03	<0.20	0.1	>=0.20
0.02	<0.20	0.17	>=0.20
0.02	<0.20	0.1	>=0.20
0.01	<0.20	0.13	>=0.20
0.00939	<0.20	0.16	>=0.20
0.02	<0.20	0.1	>=0.20
0.03	<0.20	0.09	>=0.20
0.02	<0.20	0.07	>=0.20
0.03	<0.20	0.15	>=0.20
0.03	<0.20	0.7	>=0.20
0.03	<0.20	0.07	>=0.20
0.01	<0.20	0.03	>=0.20
0.04	<0.20	0.04	>=0.20

0.00897	<0.20	0.24	>=0.20
0.02	<0.20	0.04	>=0.20
0.02	<0.20	0.09	>=0.20
0.01	<0.20	0.11	>=0.20
0.02	<0.20	0.51	>=0.20
0.01	<0.20	0.43	>=0.20
0.02	<0.20	0.1	>=0.20
0.01	<0.20	0.04	>=0.20
0.02	<0.20	0.42	>=0.20
0.0086	<0.20	0.3	>=0.20
0.02	<0.20	0.38	>=0.20
0.04	<0.20	0.32	>=0.20
0.00819	<0.20	0.31	>=0.20
0.01	<0.20	0.3	>=0.20
0.02	<0.20	0.18	>=0.20
0.01	<0.20	0.09	>=0.20
0.01	<0.20	0.36	>=0.20
0.02	<0.20	0.21	>=0.20
0.03	<0.20	0.05	>=0.20
0.01	<0.20	0.2	>=0.20
0.03	<0.20	0.1	>=0.20
0.03	<0.20	0.26	>=0.20
0.02	<0.20	0.39	>=0.20
0.02	<0.20	0.11	>=0.20
0.03	<0.20	0.28	>=0.20
0.01	<0.20	0.13	>=0.20
0.03	<0.20	0.29	>=0.20
0.02	<0.20	0.08	>=0.20
0.01	<0.20	0.05	>=0.20
0.01	<0.20	0.17	>=0.20
0.00612	<0.20	0.16	>=0.20
0.00896	<0.20	0.09	>=0.20
0.01	<0.20	0.07	>=0.20
0.04	<0.20	0.1	>=0.20
0.01	<0.20	0.57	>=0.20
0.02	<0.20	0.43	>=0.20
0.03	<0.20	0.36	>=0.20
0.01	<0.20	0.27	>=0.20
0.03	<0.20	0.07	>=0.20
0.02	<0.20	0.39	>=0.20
0.00985	<0.20	0.06	>=0.20
0.02	<0.20	0.03	>=0.20
0.03	<0.20	0.7	>=0.20
0.00626	<0.20	0.32	>=0.20
0.01	<0.20	0.06	>=0.20
0.03	<0.20	0.04	>=0.20
0.03	<0.20	0.09	>=0.20

0.02	<0.20	0.2	>=0.20
0.03	<0.20	0.71	>=0.20
0.03	<0.20	0.29	>=0.20
0.03	<0.20	0.52	>=0.20
0.00853	<0.20	0.35	>=0.20
0.01	<0.20	0.11	>=0.20
0.02	<0.20	0.08	>=0.20
0.01	<0.20	0.16	>=0.20
0.01	<0.20	0.03	>=0.20
0.03	<0.20	0.11	>=0.20
0.03	<0.20	0.24	>=0.20
0.04	<0.20	0.12	>=0.20
0.01	<0.20	0.59	>=0.20
0.03	<0.20	0.26	>=0.20
0.01	<0.20	0.36	>=0.20
0.02	<0.20	0.37	>=0.20
0.03	<0.20	0.27	>=0.20
0.03	<0.20	0.22	>=0.20
0.03	<0.20	0.66	>=0.20
0.02	<0.20	0.23	>=0.20
0.02	<0.20	0.07	>=0.20
0.00623	<0.20	0.05	>=0.20
0.00953	<0.20	0.03	>=0.20
0.00916	<0.20	0.79	>=0.20
0.02	<0.20	0.11	>=0.20
0.03	<0.20	0.41	>=0.20
0.03	<0.20	0.03	>=0.20
0.01	<0.20	0.13	>=0.20
0.00761	<0.20	0.09	>=0.20
0.02	<0.20	0.24	>=0.20
0.02	<0.20	0.2	>=0.20
0.02	<0.20	0.05	>=0.20
0.03	<0.20	0.12	>=0.20
0.02	<0.20	0.07	>=0.20
0.02	<0.20	0.16	>=0.20
0.02	<0.20	0.09	>=0.20
0.02	<0.20	0.32	>=0.20
0.03	<0.20	0.3	>=0.20
0.03	<0.20	0.3	>=0.20
0.00889	<0.20	0.08	>=0.20
0.03	<0.20	0.76	>=0.20
0.03	<0.20	0.03	>=0.20
0.03	<0.20	0.16	>=0.20
0.03	<0.20	0.61	>=0.20
0.02	<0.20	0.25	>=0.20
0.03	<0.20	0.31	>=0.20
0.03	<0.20	0.04	>=0.20

0.00654	<0.20	0.08	>=0.20
0.01	<0.20	0.74	>=0.20
0.00845	<0.20	0.07	>=0.20
0.03	<0.20	0.34	>=0.20
0.00932	<0.20	0.04	>=0.20
0.02	<0.20	0.67	>=0.20
0.03	<0.20	0.41	>=0.20
0.02	<0.20	0.03	>=0.20
0.04	<0.20	0.2	>=0.20
0.03	<0.20	0.31	>=0.20
0.00795	<0.20	0.44	>=0.20
0.02	<0.20	0.3	>=0.20
0.03	<0.20	0.26	>=0.20
0.03	<0.20	0.12	>=0.20
0.00758	<0.20	0.04	>=0.20
0.01	<0.20	0.19	>=0.20
0.02	<0.20	0.06	>=0.20
0.03	<0.20	0.33	>=0.20
0.01	<0.20	0.18	>=0.20
0.01	<0.20	0.19	>=0.20
0.03	<0.20	0.06	>=0.20
0.03	<0.20	0.26	>=0.20
0.03	<0.20	0.26	>=0.20
0.02	<0.20	0.91	>=0.20
0.01	<0.20	0.63	>=0.20
0.00897	<0.20	0.29	>=0.20
0.03	<0.20	0.05	>=0.20
0.0094	<0.20	0.33	>=0.20
0.02	<0.20	0.08	>=0.20
0.00733	<0.20	0.36	>=0.20
0.02	<0.20	0.11	>=0.20
0.02	<0.20	0.15	>=0.20
0.02	<0.20	0.25	>=0.20
0.00912	<0.20	0.03	>=0.20
0.01	<0.20	0.15	>=0.20
0.00657	<0.20	0.07	>=0.20
0.02	<0.20	0.21	>=0.20
0.00698	<0.20	0.1	>=0.20
0.03	<0.20	0.03	>=0.20
0.02	<0.20	0.35	>=0.20
0.02	<0.20	0.19	>=0.20
0.02	<0.20	0.41	>=0.20
0.03	<0.20	0.1	>=0.20
0.03	<0.20	0.39	>=0.20
0.02	<0.20	0.12	>=0.20
0.03	<0.20	0.17	>=0.20
0.03	<0.20	0.11	>=0.20

0.03	<0.20	0.06	>=0.20
0.00987	<0.20	0.07	>=0.20
0.01	<0.20	0.05	>=0.20
0.01	<0.20	0.16	>=0.20
0.01	<0.20	0.21	>=0.20
0.01	<0.20	0.19	>=0.20
0.01	<0.20	0.09	>=0.20
0.03	<0.20	0.18	>=0.20
0.03	<0.20	0.15	>=0.20
0.01	<0.20	0.66	>=0.20
0.01	<0.20	0.51	>=0.20
0.00615	<0.20	0.11	>=0.20
0.00922	<0.20	0.24	>=0.20
0.03	<0.20	0.37	>=0.20
0.02	<0.20	0.06	>=0.20
0.03	<0.20	0.18	>=0.20
0.01	<0.20	0.13	>=0.20
0.00821	<0.20	0.04	>=0.20
0.02	<0.20	0.65	>=0.20
0.03	<0.20	0.28	>=0.20
0.01	<0.20	0.1	>=0.20
0.01	<0.20	0.13	>=0.20
0.02	<0.20	0.12	>=0.20
0.01	<0.20	0.17	>=0.20
0.00719	<0.20	0.05	>=0.20
0.02	<0.20	0.13	>=0.20
0.01	<0.20	0.22	>=0.20
0.02	<0.20	0.83	>=0.20
0.02	<0.20	0.81	>=0.20
0.02	<0.20	0.92	>=0.20
0.02	<0.20	0.58	>=0.20
0.01	<0.20	0.21	>=0.20
0.00847	<0.20	0.45	>=0.20
0.02	<0.20	0.17	>=0.20
0.02	<0.20	0.79	>=0.20
0.01	<0.20	0.34	>=0.20
0.00956	<0.20	0.27	>=0.20
0.02	<0.20	0.39	>=0.20
0.00843	<0.20	0.31	>=0.20
0.02	<0.20	0.08	>=0.20
0.02	<0.20	0.22	>=0.20
0.02	<0.20	0.22	>=0.20
0.02	<0.20	0.48	>=0.20
0.01	<0.20	0.57	>=0.20
0.00998	<0.20	0.11	>=0.20
0.00654	<0.20	0.07	>=0.20
0.02	<0.20	0.15	>=0.20

0.01	<0.20	0.06	>=0.20
0.03	<0.20	0.23	>=0.20
0.04	<0.20	0.11	>=0.20
0.03	<0.20	0.51	>=0.20
0.02	<0.20	0.17	>=0.20
0.02	<0.20	0.09	>=0.20
0.04	<0.20	0.52	>=0.20
0.01	<0.20	0.13	>=0.20
0.04	<0.20	0.13	>=0.20
0.03	<0.20	0.92	>=0.20
0.00657	<0.20	0.07	>=0.20
0.02	<0.20	0.18	>=0.20
0.02	<0.20	0.46	>=0.20
0.03	<0.20	0.25	>=0.20
0.01	<0.20	0.31	>=0.20
0.02	<0.20	0.09	>=0.20
0.02	<0.20	0.45	>=0.20
0.00697	<0.20	0.82	>=0.20
0.01	<0.20	0.07	>=0.20
0.00762	<0.20	0.12	>=0.20
0.02	<0.20	0.36	>=0.20
0.02	<0.20	0.23	>=0.20
0.03	<0.20	0.24	>=0.20
0.00848	<0.20	0.25	>=0.20
0.02	<0.20	0.3	>=0.20
0.00738	<0.20	0.17	>=0.20
0.02	<0.20	0.26	>=0.20
0.01	<0.20	0.22	>=0.20
0.03	<0.20	0.34	>=0.20
0.02	<0.20	0.05	>=0.20
0.02	<0.20	0.07	>=0.20
0.02	<0.20	0.12	>=0.20
0.01	<0.20	0.12	>=0.20
0.02	<0.20	0.74	>=0.20
0.02	<0.20	0.74	>=0.20
0.01	<0.20	0.64	>=0.20
0.00774	<0.20	0.1	>=0.20
0.03	<0.20	0.2	>=0.20
0.03	<0.20	0.44	>=0.20
0.03	<0.20	0.44	>=0.20
0.04	<0.20	0.2	>=0.20
0.02	<0.20	0.49	>=0.20
0.02	<0.20	0.67	>=0.20
0.02	<0.20	0.39	>=0.20
0.03	<0.20	0.12	>=0.20
0.02	<0.20	0.1	>=0.20
0.03	<0.20	0.19	>=0.20

0.02	<0.20	0.14	>=0.20
0.02	<0.20	0.39	>=0.20
0.02	<0.20	0.09	>=0.20
0.02	<0.20	0.25	>=0.20
0.02	<0.20	0.19	>=0.20
0.01	<0.20	0.06	>=0.20
0.02	<0.20	0.11	>=0.20
0.03	<0.20	0.64	>=0.20
0.02	<0.20	0.58	>=0.20
0.02	<0.20	0.51	>=0.20
0.00793	<0.20	0.34	>=0.20
0.02	<0.20	0.22	>=0.20
0.02	<0.20	0.28	>=0.20
0.04	<0.20	0.59	>=0.20
0.01	<0.20	0.3	>=0.20
0.02	<0.20	0.41	>=0.20
0.00796	<0.20	0.23	>=0.20
0.00655	<0.20	0.29	>=0.20
0.02	<0.20	0.39	>=0.20
0.03	<0.20	0.48	>=0.20
0.02	<0.20	0.08	>=0.20
0.01	<0.20	0.03	>=0.20
0.02	<0.20	0.43	>=0.20
0.02	<0.20	0.43	>=0.20
0.02	<0.20	0.19	>=0.20
0.03	<0.20	0.8	>=0.20
0.02	<0.20	0.44	>=0.20
0.03	<0.20	0.17	>=0.20
0.03	<0.20	0.07	>=0.20
0.01	<0.20	0.09	>=0.20
0.02	<0.20	0.14	>=0.20
0.03	<0.20	0.19	>=0.20
0.02	<0.20	0.26	>=0.20
0.03	<0.20	0.77	>=0.20
0.04	<0.20	0.55	>=0.20
0.01	<0.20	0.15	>=0.20
0.00898	<0.20	0.84	>=0.20
0.02	<0.20	0.29	>=0.20
0.00811	<0.20	0.12	>=0.20
0.02	<0.20	0.91	>=0.20
0.03	<0.20	0.49	>=0.20
0.04	<0.20	0.44	>=0.20
0.02	<0.20	0.24	>=0.20
0.02	<0.20	0.39	>=0.20
0.03	<0.20	0.04	>=0.20
0.03	<0.20	0.3	>=0.20
0.03	<0.20	0.83	>=0.20

0.03	<0.20	0.73	>=0.20
0.02	<0.20	0.05	>=0.20
0.02	<0.20	0.91	>=0.20
0.02	<0.20	0.08	>=0.20
0.02	<0.20	0.08	>=0.20
0.02	<0.20	0.26	>=0.20
0.03	<0.20	0.22	>=0.20
0.02	<0.20	0.36	>=0.20
0.02	<0.20	0.29	>=0.20
0.04	<0.20	0.69	>=0.20
0.04	<0.20	0.69	>=0.20
0.02	<0.20	0.05	>=0.20
0.02	<0.20	0.2	>=0.20
0.00634	<0.20	0.09	>=0.20
0.02	<0.20	0.2	>=0.20
0.02	<0.20	0.83	>=0.20
0.00898	<0.20	0.84	>=0.20
0.02	<0.20	0.83	>=0.20
0.01	<0.20	0.42	>=0.20
0.02	<0.20	0.25	>=0.20
0.00785	<0.20	0.03	>=0.20
0.04	<0.20	0.44	>=0.20
0.00995	<0.20	0.14	>=0.20
0.02	<0.20	0.18	>=0.20
0.03	<0.20	0.21	>=0.20
0.00972	<0.20	0.11	>=0.20
0.03	<0.20	0.22	>=0.20
0.03	<0.20	0.29	>=0.20
0.04	<0.20	0.69	>=0.20
0.01	<0.20	0.06	>=0.20
0.02	<0.20	0.43	>=0.20
0.02	<0.20	0.75	>=0.20
0.04	<0.20	0.65	>=0.20
0.03	<0.20	0.36	>=0.20
0.01	<0.20	0.11	>=0.20
0.02	<0.20	0.55	>=0.20
0.02	<0.20	0.05	>=0.20
0.02	<0.20	0.14	>=0.20
0.02	<0.20	0.14	>=0.20
0.03	<0.20	0.3	>=0.20
0.02	<0.20	0.07	>=0.20
0.00977	<0.20	0.08	>=0.20
0.02	<0.20	0.25	>=0.20
0.04	<0.20	0.41	>=0.20
0.00723	<0.20	0.15	>=0.20
0.02	<0.20	0.14	>=0.20
0.04	<0.20	0.09	>=0.20

0.03	<0.20	0.29	>=0.20
0.03	<0.20	0.13	>=0.20
0.02	<0.20	0.06	>=0.20
0.01	<0.20	0.13	>=0.20
0.02	<0.20	0.07	>=0.20
0.01	<0.20	0.15	>=0.20
0.02	<0.20	0.19	>=0.20
0.02	<0.20	0.1	>=0.20
0.01	<0.20	0.19	>=0.20
0.03	<0.20	0.1	>=0.20
0.02	<0.20	0.14	>=0.20
0.02	<0.20	0.34	>=0.20
0.02	<0.20	0.2	>=0.20
0.02	<0.20	0.27	>=0.20
0.03	<0.20	0.31	>=0.20
0.03	<0.20	0.47	>=0.20
0.00964	<0.20	0.07	>=0.20
0.00856	<0.20	0.08	>=0.20
0.01	<0.20	0.09	>=0.20
0.02	<0.20	0.19	>=0.20
0.02	<0.20	0.79	>=0.20
0.03	<0.20	0.19	>=0.20
0.03	<0.20	0.1	>=0.20
0.03	<0.20	0.29	>=0.20
0.03	<0.20	0.36	>=0.20
0.01	<0.20	0.04	>=0.20
0.02	<0.20	0.06	>=0.20
0.00886	<0.20	0.14	>=0.20
0.00872	<0.20	0.36	>=0.20
0.00642	<0.20	0.84	>=0.20
0.03	<0.20	0.29	>=0.20
0.02	<0.20	0.17	>=0.20
0.02	<0.20	0.17	>=0.20
0.01	<0.20	0.08	>=0.20
0.03	<0.20	0.25	>=0.20
0.04	<0.20	0.22	>=0.20
0.01	<0.20	0.24	>=0.20
0.04	<0.20	0.26	>=0.20
0.02	<0.20	0.13	>=0.20
0.01	<0.20	0.13	>=0.20
0.02	<0.20	0.8	>=0.20
0.04	<0.20	0.58	>=0.20
0.03	<0.20	0.04	>=0.20
0.03	<0.20	0.08	>=0.20
0.02	<0.20	0.59	>=0.20
0.02	<0.20	0.04	>=0.20
0.01	<0.20	0.56	>=0.20

0.02	<0.20	0.11	>=0.20
0.02	<0.20	0.14	>=0.20
0.02	<0.20	0.08	>=0.20
0.03	<0.20	0.07	>=0.20
0.03	<0.20	0.06	>=0.20
0.02	<0.20	0.09	>=0.20
0.03	<0.20	0.08	>=0.20
0.01	<0.20	0.35	>=0.20
0.03	<0.20	0.16	>=0.20
0.04	<0.20	0.11	>=0.20
0.03	<0.20	0.1	>=0.20
0.00659	<0.20	0.1	>=0.20
0.02	<0.20	0.1	>=0.20
0.02	<0.20	0.02	>=0.20
0.00897	<0.20	0.25	>=0.20
0.04	<0.20	0.67	>=0.20
0.02	<0.20	0.35	>=0.20
0.02	<0.20	0.87	>=0.20
0.03	<0.20	0.13	>=0.20
0.03	<0.20	0.13	>=0.20
0.00649	<0.20	0.22	>=0.20
0.02	<0.20	0.33	>=0.20
0.00949	<0.20	0.06	>=0.20
0.02	<0.20	0.21	>=0.20
0.02	<0.20	0.17	>=0.20
0.02	<0.20	0.16	>=0.20
0.03	<0.20	0.43	>=0.20
0.02	<0.20	0.29	>=0.20
0.02	<0.20	0.26	>=0.20
0.02	<0.20	0.15	>=0.20
0.01	<0.20	0.26	>=0.20
0.02	<0.20	0.66	>=0.20
0.00696	<0.20	0.62	>=0.20
0.02	<0.20	0.27	>=0.20
0.01	<0.20	0.09	>=0.20
0.03	<0.20	0.57	>=0.20
0.03	<0.20	0.09	>=0.20
0.03	<0.20	0.19	>=0.20
0.02	<0.20	0.2	>=0.20
0.02	<0.20	0.07	>=0.20
0.02	<0.20	0.19	>=0.20
0.01	<0.20	0.47	>=0.20
0.02	<0.20	0.18	>=0.20
0.03	<0.20	0.31	>=0.20
0.00831	<0.20	0.1	>=0.20
0.00892	<0.20	0.15	>=0.20
0.01	<0.20	0.31	>=0.20

0.04	<0.20	0.45	>=0.20
0.02	<0.20	0.08	>=0.20
0.02	<0.20	0.07	>=0.20
0.01	<0.20	0.09	>=0.20
0.0084	<0.20	0.12	>=0.20
0.01	<0.20	0.11	>=0.20
0.02	<0.20	0.22	>=0.20
0.02	<0.20	0.22	>=0.20
0.03	<0.20	0.48	>=0.20
0.02	<0.20	0.04	>=0.20
0.01	<0.20	0.25	>=0.20
0.03	<0.20	0.26	>=0.20
0.03	<0.20	0.82	>=0.20
0.01	<0.20	0.92	>=0.20
0.01	<0.20	0.23	>=0.20
0.03	<0.20	0.07	>=0.20
0.03	<0.20	0.27	>=0.20
0.03	<0.20	0.6	>=0.20
0.03	<0.20	0.2	>=0.20
0.03	<0.20	0.28	>=0.20
0.01	<0.20	0.19	>=0.20
0.11	>=0.20	0.000243	<0.01
0.66	>=0.20	0.000164	<0.01
0.11	>=0.20	0.00163	<0.05
0.5	>=0.20	0.00134	<0.05
0.54	>=0.20	0.000645	<0.05
0.29	>=0.20	0.000848	<0.05
0.04	>=0.20	0.000348	<0.05
0.06	>=0.20	0.00172	<0.05
0.37	>=0.20	0.00165	<0.05
0.07	>=0.20	0.000708	<0.05
0.11	>=0.20	0.0014	<0.05
0.05	>=0.20	0.00108	<0.05
0.7	>=0.20	0.00189	<0.05
0.04	>=0.20	0.00233	<0.05
0.07	>=0.20	0.000975	<0.05
0.07	>=0.20	0.000975	<0.05
0.33	>=0.20	0.00818	<0.20
0.21	>=0.20	0.02	<0.20
0.21	>=0.20	0.02	<0.20
0.11	>=0.20	0.02	<0.20
0.45	>=0.20	0.00693	<0.20
0.26	>=0.20	0.02	<0.20
0.28	>=0.20	0.00635	<0.20
0.33	>=0.20	0.01	<0.20
0.12	>=0.20	0.01	<0.20
0.29	>=0.20	0.02	<0.20

0.16	>=0.20	0.02	<0.20
0.31	>=0.20	0.00886	<0.20
0.07	>=0.20	0.02	<0.20
0.15	>=0.20	0.02	<0.20
0.05	>=0.20	0.01	<0.20
0.67	>=0.20	0.0042	<0.20
0.3	>=0.20	0.02	<0.20
0.15	>=0.20	0.00469	<0.20
0.17	>=0.20	0.00935	<0.20
0.74	>=0.20	0.02	<0.20
0.86	>=0.20	0.02	<0.20
0.27	>=0.20	0.01	<0.20
0.11	>=0.20	0.00493	<0.20
0.04	>=0.20	0.02	<0.20
0.33	>=0.20	0.00827	<0.20
0.53	>=0.20	0.02	<0.20
0.23	>=0.20	0.00737	<0.20
0.34	>=0.20	0.00957	<0.20
0.28	>=0.20	0.00444	<0.20
0.36	>=0.20	0.02	<0.20
0.35	>=0.20	0.02	<0.20
0.37	>=0.20	0.00832	<0.20
0.11	>=0.20	0.00273	<0.20
0.77	>=0.20	0.00696	<0.20
0.37	>=0.20	0.0033	<0.20
0.52	>=0.20	0.02	<0.20
0.25	>=0.20	0.02	<0.20
0.61	>=0.20	0.02	<0.20
0.17	>=0.20	0.0046	<0.20
0.35	>=0.20	0.02	<0.20
0.15	>=0.20	0.02	<0.20
0.39	>=0.20	0.02	<0.20
0.07	>=0.20	0.00369	<0.20
0.78	>=0.20	0.02	<0.20
0.06	>=0.20	0.02	<0.20
0.2	>=0.20	0.00503	<0.20
0.12	>=0.20	0.00847	<0.20
0.06	>=0.20	0.01	<0.20
0.62	>=0.20	0.02	<0.20
0.17	>=0.20	0.02	<0.20
0.1	>=0.20	0.00485	<0.20
0.08	>=0.20	0.02	<0.20
0.09	>=0.20	0.00674	<0.20
0.16	>=0.20	0.01	<0.20
0.62	>=0.20	0.02	<0.20
0.62	>=0.20	0.02	<0.20
0.1	>=0.20	0.02	<0.20

0.11	>=0.20	0.02	<0.20
0.05	>=0.20	0.02	<0.20
0.34	>=0.20	0.01	<0.20
0.29	>=0.20	0.01	<0.20
0.21	>=0.20	0.02	<0.20
0.09	>=0.20	0.02	<0.20
0.3	>=0.20	0.02	<0.20
0.88	>=0.20	0.02	<0.20
0.54	>=0.20	0.00373	<0.20
0.17	>=0.20	0.00344	<0.20
0.19	>=0.20	0.02	<0.20
0.77	>=0.20	0.01	<0.20
0.68	>=0.20	0.00778	<0.20
0.04	>=0.20	0.01	<0.20
0.5	>=0.20	0.02	<0.20
0.24	>=0.20	0.01	<0.20
0.2	>=0.20	0.00503	<0.20
0.12	>=0.20	0.01	<0.20
0.12	>=0.20	0.02	<0.20
0.04	>=0.20	0.02	<0.20
0.07	>=0.20	0.02	<0.20
0.08	>=0.20	0.00982	<0.20
0.73	>=0.20	0.00574	<0.20
0.77	>=0.20	0.02	<0.20
0.76	>=0.20	0.00588	<0.20
0.23	>=0.20	0.02	<0.20
0.32	>=0.20	0.02	<0.20
0.04	>=0.20	0.01	<0.20
0.08	>=0.20	0.02	<0.20
0.06	>=0.20	0.00409	<0.20
0.67	>=0.20	0.02	<0.20
0.08	>=0.20	0.00435	<0.20
0.05	>=0.20	0.01	<0.20
0.15	>=0.20	0.02	<0.20
0.18	>=0.20	0.01	<0.20
0.28	>=0.20	0.00583	<0.20
0.14	>=0.20	0.01	<0.20
0.08	>=0.20	0.02	<0.20
0.12	>=0.20	0.00501	<0.20
0.05	>=0.20	0.02	<0.20
0.07	>=0.20	0.02	<0.20
0.05	>=0.20	0.02	<0.20
0.12	>=0.20	0.00971	<0.20
0.24	>=0.20	0.01	<0.20
0.28	>=0.20	0.02	<0.20
0.38	>=0.20	0.00395	<0.20
0.07	>=0.20	0.02	<0.20

0.26	>=0.20	0.00697	<0.20
0.38	>=0.20	0.01	<0.20
0.12	>=0.20	0.02	<0.20
0.86	>=0.20	0.02	<0.20
0.69	>=0.20	0.98	>=0.20
0.66	>=0.20	0.98	>=0.20
0.51	>=0.20	0.55	>=0.20
0.09	>=0.20	0.44	>=0.20
0.08	>=0.20	0.44	>=0.20
0.32	>=0.20	0.98	>=0.20
0.71	>=0.20	0.98	>=0.20
1	>=0.20	0.4	>=0.20
0.66	>=0.20	0.88	>=0.20
0.92	>=0.20	0.53	>=0.20
0.11	>=0.20	0.47	>=0.20
0.88	>=0.20	0.94	>=0.20
0.04	>=0.20	0.49	>=0.20
0.83	>=0.20	0.7	>=0.20
0.35	>=0.20	0.63	>=0.20
0.14	>=0.20	0.14	>=0.20
0.07	>=0.20	0.39	>=0.20
0.52	>=0.20	0.17	>=0.20
0.41	>=0.20	0.32	>=0.20
0.61	>=0.20	0.26	>=0.20
0.79	>=0.20	0.56	>=0.20
0.93	>=0.20	0.64	>=0.20
0.99	>=0.20	0.46	>=0.20
0.84	>=0.20	0.75	>=0.20
0.94	>=0.20	0.83	>=0.20
0.15	>=0.20	0.5	>=0.20
0.97	>=0.20	1	>=0.20
1	>=0.20	0.78	>=0.20
1	>=0.20	1	>=0.20
0.82	>=0.20	0.86	>=0.20
0.06	>=0.20	0.77	>=0.20
0.99	>=0.20	0.79	>=0.20
0.85	>=0.20	0.2	>=0.20
0.89	>=0.20	0.68	>=0.20
0.85	>=0.20	0.97	>=0.20
0.63	>=0.20	0.86	>=0.20
0.91	>=0.20	0.79	>=0.20
0.98	>=0.20	1	>=0.20
0.21	>=0.20	0.16	>=0.20
0.81	>=0.20	0.96	>=0.20
0.98	>=0.20	0.08	>=0.20
0.85	>=0.20	0.29	>=0.20
0.79	>=0.20	0.55	>=0.20

0.88	>=0.20	0.47	>=0.20
0.86	>=0.20	0.91	>=0.20
0.71	>=0.20	0.21	>=0.20
0.99	>=0.20	0.84	>=0.20
1	>=0.20	0.66	>=0.20
0.68	>=0.20	0.9	>=0.20
0.37	>=0.20	0.24	>=0.20
0.92	>=0.20	1	>=0.20
0.31	>=0.20	0.19	>=0.20
0.63	>=0.20	0.04	>=0.20
0.98	>=0.20	0.71	>=0.20
0.61	>=0.20	0.08	>=0.20
0.47	>=0.20	0.62	>=0.20
0.86	>=0.20	0.97	>=0.20
0.56	>=0.20	0.24	>=0.20
0.99	>=0.20	0.75	>=0.20
0.95	>=0.20	0.71	>=0.20
1	>=0.20	0.93	>=0.20
0.79	>=0.20	0.11	>=0.20
0.94	>=0.20	1	>=0.20
0.33	>=0.20	0.38	>=0.20
0.14	>=0.20	0.22	>=0.20
0.67	>=0.20	0.49	>=0.20
0.76	>=0.20	0.07	>=0.20
0.99	>=0.20	0.44	>=0.20
0.3	>=0.20	0.03	>=0.20
0.86	>=0.20	0.27	>=0.20
0.78	>=0.20	0.07	>=0.20
0.98	>=0.20	0.89	>=0.20
0.51	>=0.20	0.07	>=0.20
0.7	>=0.20	0.86	>=0.20
0.8	>=0.20	0.45	>=0.20
1	>=0.20	1	>=0.20
0.8	>=0.20	0.24	>=0.20
0.46	>=0.20	0.39	>=0.20
0.88	>=0.20	0.96	>=0.20
0.88	>=0.20	0.26	>=0.20
0.91	>=0.20	0.55	>=0.20
0.59	>=0.20	0.31	>=0.20
0.76	>=0.20	0.51	>=0.20
0.96	>=0.20	0.1	>=0.20
0.88	>=0.20	0.95	>=0.20
0.2	>=0.20	0.52	>=0.20
0.74	>=0.20	0.78	>=0.20
1	>=0.20	0.74	>=0.20
0.63	>=0.20	0.19	>=0.20
1	>=0.20	0.22	>=0.20

0.99 >=0.20	1 >=0.20
0.96 >=0.20	0.82 >=0.20
0.92 >=0.20	0.24 >=0.20
0.86 >=0.20	0.45 >=0.20
0.61 >=0.20	0.92 >=0.20
0.34 >=0.20	0.42 >=0.20
0.82 >=0.20	0.99 >=0.20
0.39 >=0.20	0.97 >=0.20
0.7 >=0.20	0.52 >=0.20
0.51 >=0.20	0.55 >=0.20
0.04 >=0.20	0.23 >=0.20
0.89 >=0.20	0.93 >=0.20
0.13 >=0.20	0.78 >=0.20
0.9 >=0.20	0.92 >=0.20
0.67 >=0.20	0.7 >=0.20
0.72 >=0.20	0.81 >=0.20
0.82 >=0.20	0.99 >=0.20
0.95 >=0.20	0.94 >=0.20
0.94 >=0.20	0.99 >=0.20
0.6 >=0.20	0.96 >=0.20
0.33 >=0.20	0.43 >=0.20
0.45 >=0.20	0.39 >=0.20
0.99 >=0.20	0.63 >=0.20
0.87 >=0.20	0.86 >=0.20
1 >=0.20	0.53 >=0.20
0.99 >=0.20	1 >=0.20
0.56 >=0.20	0.3 >=0.20
0.12 >=0.20	0.15 >=0.20
0.78 >=0.20	0.96 >=0.20
0.08 >=0.20	0.21 >=0.20
0.93 >=0.20	0.86 >=0.20
0.54 >=0.20	0.45 >=0.20
1 >=0.20	1 >=0.20
0.17 >=0.20	0.08 >=0.20
0.07 >=0.20	0.13 >=0.20
0.95 >=0.20	0.72 >=0.20
0.85 >=0.20	0.13 >=0.20
0.83 >=0.20	0.98 >=0.20
0.99 >=0.20	0.65 >=0.20
0.99 >=0.20	0.57 >=0.20
0.05 >=0.20	0.26 >=0.20
0.75 >=0.20	0.55 >=0.20
0.43 >=0.20	0.19 >=0.20
0.46 >=0.20	0.87 >=0.20
1 >=0.20	1 >=0.20
0.91 >=0.20	0.82 >=0.20
0.76 >=0.20	0.54 >=0.20

0.79 >=0.20	0.26 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
0.83 >=0.20	0.75 >=0.20
0.99 >=0.20	0.73 >=0.20
0.78 >=0.20	0.81 >=0.20
1 >=0.20	0.84 >=0.20
0.99 >=0.20	0.96 >=0.20
0.87 >=0.20	0.33 >=0.20
0.97 >=0.20	0.84 >=0.20
0.83 >=0.20	0.92 >=0.20
1 >=0.20	1 >=0.20
0.49 >=0.20	0.9 >=0.20
0.15 >=0.20	0.53 >=0.20
0.09 >=0.20	0.84 >=0.20
0.95 >=0.20	0.08 >=0.20
0.13 >=0.20	0.28 >=0.20
0.41 >=0.20	0.84 >=0.20
0.72 >=0.20	0.92 >=0.20
0.08 >=0.20	0.51 >=0.20
1 >=0.20	0.88 >=0.20
0.93 >=0.20	0.94 >=0.20
0.55 >=0.20	0.7 >=0.20
0.55 >=0.20	0.2 >=0.20
0.26 >=0.20	0.41 >=0.20
0.93 >=0.20	0.92 >=0.20
0.85 >=0.20	0.28 >=0.20
0.94 >=0.20	0.95 >=0.20
0.62 >=0.20	0.07 >=0.20
0.93 >=0.20	0.81 >=0.20
0.97 >=0.20	0.87 >=0.20
0.97 >=0.20	0.89 >=0.20
0.67 >=0.20	0.28 >=0.20
0.88 >=0.20	0.77 >=0.20
0.69 >=0.20	0.62 >=0.20
0.08 >=0.20	0.62 >=0.20
0.74 >=0.20	0.73 >=0.20
0.84 >=0.20	0.99 >=0.20
0.84 >=0.20	0.86 >=0.20
0.67 >=0.20	0.55 >=0.20
0.99 >=0.20	0.91 >=0.20
0.54 >=0.20	0.37 >=0.20
1 >=0.20	0.99 >=0.20
0.16 >=0.20	0.39 >=0.20
0.37 >=0.20	0.04 >=0.20
0.64 >=0.20	0.08 >=0.20
0.56 >=0.20	0.26 >=0.20

0.92 >=0.20	0.97 >=0.20
0.99 >=0.20	0.95 >=0.20
0.56 >=0.20	0.11 >=0.20
0.64 >=0.20	0.41 >=0.20
0.56 >=0.20	0.17 >=0.20
0.95 >=0.20	0.9 >=0.20
0.88 >=0.20	1 >=0.20
0.93 >=0.20	0.22 >=0.20
0.95 >=0.20	0.68 >=0.20
0.88 >=0.20	0.88 >=0.20
1 >=0.20	0.98 >=0.20
0.42 >=0.20	0.6 >=0.20
0.8 >=0.20	0.98 >=0.20
0.64 >=0.20	0.11 >=0.20
0.19 >=0.20	0.23 >=0.20
0.73 >=0.20	0.69 >=0.20
0.2 >=0.20	0.24 >=0.20
0.05 >=0.20	0.16 >=0.20
0.21 >=0.20	0.38 >=0.20
0.39 >=0.20	0.68 >=0.20
0.05 >=0.20	0.05 >=0.20
0.16 >=0.20	0.17 >=0.20
0.97 >=0.20	1 >=0.20
0.67 >=0.20	0.61 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
0.95 >=0.20	0.89 >=0.20
0.94 >=0.20	0.7 >=0.20
0.67 >=0.20	0.9 >=0.20
0.94 >=0.20	0.99 >=0.20
0.36 >=0.20	0.14 >=0.20
0.72 >=0.20	0.98 >=0.20
0.37 >=0.20	0.6 >=0.20
0.68 >=0.20	0.35 >=0.20
0.99 >=0.20	0.87 >=0.20
0.6 >=0.20	0.68 >=0.20
0.55 >=0.20	0.83 >=0.20
0.69 >=0.20	0.24 >=0.20
0.94 >=0.20	0.91 >=0.20
1 >=0.20	0.52 >=0.20
0.99 >=0.20	0.98 >=0.20
0.62 >=0.20	0.66 >=0.20
0.75 >=0.20	0.16 >=0.20
0.85 >=0.20	0.64 >=0.20
0.9 >=0.20	0.9 >=0.20
0.27 >=0.20	0.81 >=0.20
0.74 >=0.20	0.16 >=0.20

0.56 >=0.20	0.91 >=0.20
0.05 >=0.20	0.04 >=0.20
0.17 >=0.20	0.04 >=0.20
0.9 >=0.20	0.83 >=0.20
0.98 >=0.20	1 >=0.20
0.95 >=0.20	0.86 >=0.20
0.14 >=0.20	0.08 >=0.20
0.98 >=0.20	0.57 >=0.20
0.96 >=0.20	0.77 >=0.20
0.88 >=0.20	0.03 >=0.20
0.67 >=0.20	0.73 >=0.20
0.24 >=0.20	0.44 >=0.20
0.4 >=0.20	0.37 >=0.20
0.8 >=0.20	0.47 >=0.20
0.95 >=0.20	0.98 >=0.20
0.98 >=0.20	0.68 >=0.20
0.18 >=0.20	0.03 >=0.20
0.29 >=0.20	0.28 >=0.20
0.44 >=0.20	0.23 >=0.20
0.96 >=0.20	0.79 >=0.20
1 >=0.20	0.98 >=0.20
0.99 >=0.20	0.54 >=0.20
0.72 >=0.20	0.14 >=0.20
0.99 >=0.20	0.55 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.78 >=0.20
0.83 >=0.20	0.31 >=0.20
1 >=0.20	0.99 >=0.20
0.87 >=0.20	0.22 >=0.20
1 >=0.20	0.69 >=0.20
0.72 >=0.20	0.47 >=0.20
0.7 >=0.20	0.11 >=0.20
0.6 >=0.20	0.35 >=0.20
0.74 >=0.20	0.88 >=0.20
0.58 >=0.20	0.56 >=0.20
0.85 >=0.20	0.57 >=0.20
1 >=0.20	0.27 >=0.20
1 >=0.20	0.97 >=0.20
0.99 >=0.20	1 >=0.20
0.19 >=0.20	0.34 >=0.20
0.62 >=0.20	0.32 >=0.20
0.96 >=0.20	0.97 >=0.20
0.98 >=0.20	0.59 >=0.20
0.48 >=0.20	0.09 >=0.20
0.96 >=0.20	0.86 >=0.20
0.74 >=0.20	0.52 >=0.20
0.88 >=0.20	0.94 >=0.20

1 >=0.20	0.72 >=0.20
0.84 >=0.20	0.93 >=0.20
0.77 >=0.20	0.31 >=0.20
0.06 >=0.20	0.11 >=0.20
0.57 >=0.20	0.16 >=0.20
0.19 >=0.20	0.16 >=0.20
0.96 >=0.20	0.6 >=0.20
0.52 >=0.20	0.65 >=0.20
1 >=0.20	0.99 >=0.20
0.87 >=0.20	0.75 >=0.20
0.37 >=0.20	0.69 >=0.20
0.83 >=0.20	0.59 >=0.20
0.34 >=0.20	0.28 >=0.20
0.95 >=0.20	0.23 >=0.20
0.45 >=0.20	0.17 >=0.20
0.71 >=0.20	0.38 >=0.20
0.22 >=0.20	0.56 >=0.20
0.98 >=0.20	0.9 >=0.20
0.04 >=0.20	0.06 >=0.20
0.26 >=0.20	0.11 >=0.20
0.25 >=0.20	0.04 >=0.20
0.88 >=0.20	0.82 >=0.20
0.74 >=0.20	0.71 >=0.20
1 >=0.20	1 >=0.20
0.87 >=0.20	0.42 >=0.20
0.49 >=0.20	0.44 >=0.20
0.6 >=0.20	0.6 >=0.20
0.53 >=0.20	0.33 >=0.20
0.71 >=0.20	0.92 >=0.20
0.55 >=0.20	0.15 >=0.20
1 >=0.20	0.77 >=0.20
0.39 >=0.20	0.43 >=0.20
0.32 >=0.20	0.18 >=0.20
0.35 >=0.20	0.62 >=0.20
0.31 >=0.20	0.98 >=0.20
1 >=0.20	0.76 >=0.20
0.95 >=0.20	0.85 >=0.20
0.72 >=0.20	0.72 >=0.20
0.5 >=0.20	0.26 >=0.20
0.98 >=0.20	0.87 >=0.20
0.47 >=0.20	0.14 >=0.20
0.66 >=0.20	0.51 >=0.20
0.12 >=0.20	0.18 >=0.20
0.07 >=0.20	0.1 >=0.20
0.89 >=0.20	0.38 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.78 >=0.20

0.9 >=0.20	0.95 >=0.20
0.7 >=0.20	0.97 >=0.20
0.83 >=0.20	0.45 >=0.20
1 >=0.20	1 >=0.20
0.59 >=0.20	0.06 >=0.20
0.83 >=0.20	0.68 >=0.20
0.51 >=0.20	0.23 >=0.20
0.65 >=0.20	0.59 >=0.20
0.89 >=0.20	0.93 >=0.20
0.93 >=0.20	0.39 >=0.20
0.99 >=0.20	0.94 >=0.20
0.94 >=0.20	0.4 >=0.20
0.94 >=0.20	0.09 >=0.20
0.77 >=0.20	0.14 >=0.20
0.97 >=0.20	0.27 >=0.20
0.93 >=0.20	0.92 >=0.20
0.66 >=0.20	0.69 >=0.20
0.72 >=0.20	0.38 >=0.20
0.67 >=0.20	0.32 >=0.20
0.74 >=0.20	0.28 >=0.20
0.4 >=0.20	0.23 >=0.20
0.39 >=0.20	0.34 >=0.20
0.07 >=0.20	0.25 >=0.20
0.54 >=0.20	0.93 >=0.20
0.92 >=0.20	0.69 >=0.20
1 >=0.20	0.98 >=0.20
0.3 >=0.20	0.18 >=0.20
0.35 >=0.20	0.71 >=0.20
0.82 >=0.20	0.61 >=0.20
0.98 >=0.20	1 >=0.20
0.95 >=0.20	0.91 >=0.20
0.95 >=0.20	0.94 >=0.20
0.9 >=0.20	0.67 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.81 >=0.20	0.94 >=0.20
0.3 >=0.20	0.04 >=0.20
0.24 >=0.20	0.8 >=0.20
0.97 >=0.20	0.84 >=0.20
0.77 >=0.20	0.58 >=0.20
0.15 >=0.20	0.11 >=0.20
0.54 >=0.20	0.41 >=0.20
1 >=0.20	0.81 >=0.20
0.97 >=0.20	0.95 >=0.20
0.73 >=0.20	0.66 >=0.20
0.39 >=0.20	0.73 >=0.20
0.9 >=0.20	0.73 >=0.20

0.99 >=0.20	0.92 >=0.20
0.98 >=0.20	0.94 >=0.20
0.73 >=0.20	0.73 >=0.20
0.99 >=0.20	0.99 >=0.20
0.59 >=0.20	0.92 >=0.20
0.46 >=0.20	0.64 >=0.20
0.38 >=0.20	0.84 >=0.20
0.97 >=0.20	0.36 >=0.20
0.51 >=0.20	0.94 >=0.20
0.97 >=0.20	1 >=0.20
0.99 >=0.20	0.98 >=0.20
0.78 >=0.20	0.61 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	1 >=0.20
0.99 >=0.20	0.55 >=0.20
0.91 >=0.20	0.96 >=0.20
0.96 >=0.20	0.96 >=0.20
0.37 >=0.20	0.49 >=0.20
0.67 >=0.20	0.96 >=0.20
0.9 >=0.20	0.31 >=0.20
0.98 >=0.20	0.99 >=0.20
0.96 >=0.20	0.2 >=0.20
0.9 >=0.20	0.96 >=0.20
0.84 >=0.20	0.6 >=0.20
0.19 >=0.20	0.66 >=0.20
0.55 >=0.20	0.69 >=0.20
1 >=0.20	0.28 >=0.20
0.97 >=0.20	0.56 >=0.20
0.98 >=0.20	0.46 >=0.20
0.99 >=0.20	0.99 >=0.20
0.99 >=0.20	0.98 >=0.20
0.9 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
0.92 >=0.20	1 >=0.20
0.71 >=0.20	0.09 >=0.20
1 >=0.20	1 >=0.20
0.16 >=0.20	0.08 >=0.20
0.94 >=0.20	0.61 >=0.20
0.95 >=0.20	0.39 >=0.20
0.47 >=0.20	0.15 >=0.20
0.74 >=0.20	0.33 >=0.20
1 >=0.20	0.78 >=0.20
0.88 >=0.20	0.96 >=0.20
0.99 >=0.20	0.98 >=0.20
0.15 >=0.20	0.16 >=0.20
0.82 >=0.20	0.83 >=0.20
0.98 >=0.20	0.98 >=0.20

0.97	>=0.20	0.83	>=0.20
1	>=0.20	0.99	>=0.20
0.84	>=0.20	0.98	>=0.20
0.26	>=0.20	0.91	>=0.20
0.28	>=0.20	0.44	>=0.20
1	>=0.20	0.99	>=0.20
0.85	>=0.20	0.77	>=0.20
0.55	>=0.20	0.74	>=0.20
0.96	>=0.20	0.71	>=0.20
0.74	>=0.20	0.62	>=0.20
0.72	>=0.20	0.88	>=0.20
0.98	>=0.20	0.99	>=0.20
0.98	>=0.20	0.95	>=0.20
1	>=0.20	0.98	>=0.20
1	>=0.20	0.78	>=0.20
1	>=0.20	0.99	>=0.20
0.15	>=0.20	0.13	>=0.20
0.4	>=0.20	0.3	>=0.20
0.99	>=0.20	0.81	>=0.20
0.9	>=0.20	0.6	>=0.20
0.78	>=0.20	0.78	>=0.20
0.51	>=0.20	0.06	>=0.20
0.2	>=0.20	0.1	>=0.20
0.44	>=0.20	0.04	>=0.20
0.16	>=0.20	0.14	>=0.20
0.08	>=0.20	0.1	>=0.20
0.88	>=0.20	0.89	>=0.20
0.94	>=0.20	0.76	>=0.20
0.58	>=0.20	0.3	>=0.20
0.7	>=0.20	0.08	>=0.20
0.94	>=0.20	0.16	>=0.20
0.95	>=0.20	0.91	>=0.20
1	>=0.20	0.75	>=0.20
1	>=0.20	0.94	>=0.20
0.81	>=0.20	0.3	>=0.20
0.71	>=0.20	0.49	>=0.20
0.43	>=0.20	0.69	>=0.20
0.09	>=0.20	0.25	>=0.20
0.48	>=0.20	0.33	>=0.20
0.51	>=0.20	0.3	>=0.20
0.98	>=0.20	1	>=0.20
0.88	>=0.20	0.34	>=0.20
0.65	>=0.20	0.86	>=0.20
0.8	>=0.20	0.24	>=0.20
0.9	>=0.20	0.79	>=0.20
0.93	>=0.20	0.99	>=0.20
0.45	>=0.20	0.8	>=0.20

0.93 >=0.20	0.4 >=0.20
0.97 >=0.20	0.64 >=0.20
0.56 >=0.20	0.05 >=0.20
0.76 >=0.20	0.55 >=0.20
0.77 >=0.20	0.59 >=0.20
0.79 >=0.20	0.98 >=0.20
0.77 >=0.20	0.32 >=0.20
0.13 >=0.20	0.1 >=0.20
0.95 >=0.20	1 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	0.88 >=0.20
0.99 >=0.20	0.92 >=0.20
0.87 >=0.20	0.97 >=0.20
0.99 >=0.20	0.78 >=0.20
0.95 >=0.20	0.19 >=0.20
0.99 >=0.20	0.6 >=0.20
0.98 >=0.20	1 >=0.20
0.57 >=0.20	0.05 >=0.20
0.7 >=0.20	0.14 >=0.20
0.97 >=0.20	0.76 >=0.20
1 >=0.20	0.47 >=0.20
1 >=0.20	0.54 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.95 >=0.20
0.65 >=0.20	0.65 >=0.20
0.68 >=0.20	0.84 >=0.20
0.99 >=0.20	0.77 >=0.20
0.1 >=0.20	0.31 >=0.20
0.25 >=0.20	0.2 >=0.20
0.27 >=0.20	0.33 >=0.20
0.98 >=0.20	0.53 >=0.20
0.63 >=0.20	0.66 >=0.20
0.74 >=0.20	0.08 >=0.20
0.14 >=0.20	0.57 >=0.20
0.45 >=0.20	0.19 >=0.20
0.54 >=0.20	0.36 >=0.20
0.66 >=0.20	0.32 >=0.20
0.93 >=0.20	0.97 >=0.20
0.6 >=0.20	0.99 >=0.20
0.98 >=0.20	0.77 >=0.20
0.79 >=0.20	0.64 >=0.20
0.11 >=0.20	0.11 >=0.20
0.58 >=0.20	0.04 >=0.20
0.82 >=0.20	0.98 >=0.20
0.09 >=0.20	0.15 >=0.20
0.59 >=0.20	0.93 >=0.20
0.56 >=0.20	0.77 >=0.20

0.53	>=0.20	0.84	>=0.20
0.33	>=0.20	0.42	>=0.20
0.31	>=0.20	0.49	>=0.20
0.39	>=0.20	0.88	>=0.20
0.35	>=0.20	0.98	>=0.20
0.68	>=0.20	0.39	>=0.20
0.98	>=0.20	0.87	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	0.93	>=0.20
0.6	>=0.20	0.97	>=0.20
0.88	>=0.20	0.34	>=0.20
0.99	>=0.20	0.82	>=0.20
0.79	>=0.20	0.83	>=0.20
0.96	>=0.20	0.58	>=0.20
0.62	>=0.20	0.8	>=0.20
0.73	>=0.20	0.7	>=0.20
0.69	>=0.20	0.03	>=0.20
1	>=0.20	0.27	>=0.20
0.99	>=0.20	0.8	>=0.20
0.81	>=0.20	0.26	>=0.20
0.98	>=0.20	0.55	>=0.20
0.55	>=0.20	0.2	>=0.20
0.97	>=0.20	0.76	>=0.20
1	>=0.20	0.95	>=0.20
0.85	>=0.20	0.42	>=0.20
0.26	>=0.20	0.34	>=0.20
0.57	>=0.20	0.44	>=0.20
0.95	>=0.20	0.62	>=0.20
0.16	>=0.20	0.25	>=0.20
0.97	>=0.20	0.79	>=0.20
0.86	>=0.20	0.45	>=0.20
0.91	>=0.20	0.87	>=0.20
0.62	>=0.20	0.14	>=0.20
0.12	>=0.20	0.69	>=0.20
0.18	>=0.20	0.32	>=0.20
0.66	>=0.20	0.62	>=0.20
0.46	>=0.20	0.62	>=0.20
0.93	>=0.20	0.7	>=0.20
0.56	>=0.20	0.56	>=0.20
0.99	>=0.20	0.99	>=0.20
0.08	>=0.20	0.04	>=0.20
0.99	>=0.20	1	>=0.20
0.72	>=0.20	0.05	>=0.20
0.75	>=0.20	0.06	>=0.20
0.98	>=0.20	0.94	>=0.20
1	>=0.20	0.87	>=0.20
0.42	>=0.20	0.56	>=0.20

0.19 >=0.20	0.85 >=0.20
0.13 >=0.20	0.3 >=0.20
0.36 >=0.20	0.93 >=0.20
0.38 >=0.20	0.31 >=0.20
0.83 >=0.20	0.99 >=0.20
0.42 >=0.20	0.39 >=0.20
0.55 >=0.20	0.17 >=0.20
1 >=0.20	0.96 >=0.20
0.92 >=0.20	0.84 >=0.20
1 >=0.20	0.99 >=0.20
0.79 >=0.20	0.73 >=0.20
0.79 >=0.20	0.65 >=0.20
0.97 >=0.20	0.97 >=0.20
0.19 >=0.20	0.11 >=0.20
0.24 >=0.20	0.12 >=0.20
0.11 >=0.20	0.1 >=0.20
0.45 >=0.20	0.44 >=0.20
0.1 >=0.20	0.17 >=0.20
0.49 >=0.20	0.49 >=0.20
0.81 >=0.20	0.69 >=0.20
0.92 >=0.20	0.9 >=0.20
0.97 >=0.20	0.6 >=0.20
0.97 >=0.20	0.45 >=0.20
1 >=0.20	0.68 >=0.20
0.95 >=0.20	0.85 >=0.20
0.96 >=0.20	1 >=0.20
0.66 >=0.20	0.38 >=0.20
0.85 >=0.20	0.36 >=0.20
0.66 >=0.20	0.55 >=0.20
0.99 >=0.20	0.87 >=0.20
0.93 >=0.20	0.81 >=0.20
0.78 >=0.20	0.81 >=0.20
0.5 >=0.20	0.52 >=0.20
0.87 >=0.20	0.9 >=0.20
0.96 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
0.91 >=0.20	0.92 >=0.20
1 >=0.20	1 >=0.20
0.81 >=0.20	0.94 >=0.20
0.53 >=0.20	0.08 >=0.20
0.44 >=0.20	0.77 >=0.20
0.15 >=0.20	0.22 >=0.20
0.27 >=0.20	0.15 >=0.20
0.43 >=0.20	0.79 >=0.20
0.83 >=0.20	0.84 >=0.20
0.34 >=0.20	0.9 >=0.20
0.41 >=0.20	0.35 >=0.20

0.62 >=0.20	0.62 >=0.20
0.91 >=0.20	0.99 >=0.20
0.47 >=0.20	0.47 >=0.20
0.1 >=0.20	0.1 >=0.20
0.91 >=0.20	0.93 >=0.20
0.69 >=0.20	0.82 >=0.20
0.64 >=0.20	0.64 >=0.20
0.84 >=0.20	0.98 >=0.20
0.92 >=0.20	0.87 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	0.61 >=0.20
0.55 >=0.20	0.74 >=0.20
0.92 >=0.20	0.95 >=0.20
0.87 >=0.20	0.69 >=0.20
0.59 >=0.20	0.2 >=0.20
0.82 >=0.20	0.58 >=0.20
0.41 >=0.20	0.34 >=0.20
1 >=0.20	0.92 >=0.20
0.14 >=0.20	0.15 >=0.20
0.97 >=0.20	0.85 >=0.20
0.22 >=0.20	0.88 >=0.20
0.5 >=0.20	0.64 >=0.20
0.84 >=0.20	0.69 >=0.20
0.9 >=0.20	1 >=0.20
0.55 >=0.20	0.31 >=0.20
1 >=0.20	0.82 >=0.20
1 >=0.20	0.84 >=0.20
0.68 >=0.20	0.03 >=0.20
0.29 >=0.20	0.39 >=0.20
0.35 >=0.20	0.67 >=0.20
0.88 >=0.20	0.41 >=0.20
0.38 >=0.20	0.07 >=0.20
0.37 >=0.20	0.13 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.99 >=0.20
0.94 >=0.20	0.77 >=0.20
0.16 >=0.20	0.59 >=0.20
0.99 >=0.20	0.98 >=0.20
0.15 >=0.20	0.03 >=0.20
0.95 >=0.20	0.78 >=0.20
0.21 >=0.20	0.2 >=0.20
0.28 >=0.20	0.23 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.62 >=0.20
0.99 >=0.20	0.99 >=0.20
0.87 >=0.20	0.98 >=0.20
1 >=0.20	0.76 >=0.20

1 >=0.20	0.25 >=0.20
0.99 >=0.20	0.93 >=0.20
0.67 >=0.20	0.58 >=0.20
0.62 >=0.20	0.11 >=0.20
0.94 >=0.20	1 >=0.20
0.69 >=0.20	0.9 >=0.20
0.83 >=0.20	0.89 >=0.20
0.99 >=0.20	0.29 >=0.20
0.75 >=0.20	0.08 >=0.20
0.25 >=0.20	0.14 >=0.20
0.85 >=0.20	0.73 >=0.20
0.77 >=0.20	0.56 >=0.20
0.94 >=0.20	0.87 >=0.20
1 >=0.20	0.91 >=0.20
0.63 >=0.20	0.89 >=0.20
0.71 >=0.20	0.8 >=0.20
0.6 >=0.20	0.52 >=0.20
0.14 >=0.20	0.18 >=0.20
0.99 >=0.20	0.34 >=0.20
0.16 >=0.20	0.05 >=0.20
0.74 >=0.20	0.5 >=0.20
0.85 >=0.20	0.73 >=0.20
0.8 >=0.20	0.96 >=0.20
0.93 >=0.20	0.49 >=0.20
0.83 >=0.20	0.84 >=0.20
0.46 >=0.20	0.26 >=0.20
0.97 >=0.20	0.96 >=0.20
0.23 >=0.20	0.16 >=0.20
0.8 >=0.20	0.71 >=0.20
0.55 >=0.20	0.38 >=0.20
0.81 >=0.20	0.45 >=0.20
1 >=0.20	0.85 >=0.20
1 >=0.20	0.92 >=0.20
0.49 >=0.20	0.38 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.09 >=0.20
0.96 >=0.20	1 >=0.20
0.26 >=0.20	0.18 >=0.20
0.83 >=0.20	0.16 >=0.20
1 >=0.20	1 >=0.20
0.22 >=0.20	0.06 >=0.20
0.96 >=0.20	0.82 >=0.20
0.84 >=0.20	0.48 >=0.20
0.3 >=0.20	0.03 >=0.20
0.59 >=0.20	0.98 >=0.20
0.99 >=0.20	0.99 >=0.20
0.48 >=0.20	0.08 >=0.20

0.95 >=0.20	0.97 >=0.20
0.98 >=0.20	0.8 >=0.20
0.28 >=0.20	0.44 >=0.20
0.81 >=0.20	0.77 >=0.20
0.89 >=0.20	0.49 >=0.20
0.58 >=0.20	0.84 >=0.20
0.24 >=0.20	0.59 >=0.20
0.97 >=0.20	0.67 >=0.20
0.58 >=0.20	0.3 >=0.20
0.12 >=0.20	0.19 >=0.20
0.79 >=0.20	0.59 >=0.20
0.27 >=0.20	0.47 >=0.20
0.09 >=0.20	0.25 >=0.20
0.24 >=0.20	0.74 >=0.20
0.79 >=0.20	0.52 >=0.20
0.78 >=0.20	0.69 >=0.20
0.54 >=0.20	0.33 >=0.20
0.12 >=0.20	0.07 >=0.20
0.56 >=0.20	0.76 >=0.20
0.53 >=0.20	0.58 >=0.20
0.52 >=0.20	0.9 >=0.20
0.89 >=0.20	0.88 >=0.20
1 >=0.20	1 >=0.20
0.77 >=0.20	0.5 >=0.20
0.96 >=0.20	0.76 >=0.20
0.5 >=0.20	1 >=0.20
0.45 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
0.51 >=0.20	0.78 >=0.20
0.42 >=0.20	0.95 >=0.20
0.84 >=0.20	0.69 >=0.20
0.51 >=0.20	0.25 >=0.20
0.54 >=0.20	0.41 >=0.20
0.22 >=0.20	0.23 >=0.20
1 >=0.20	1 >=0.20
0.84 >=0.20	0.98 >=0.20
0.93 >=0.20	0.79 >=0.20
0.99 >=0.20	0.72 >=0.20
0.97 >=0.20	0.42 >=0.20
0.78 >=0.20	0.26 >=0.20
0.99 >=0.20	0.44 >=0.20
0.96 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.85 >=0.20
1 >=0.20	0.92 >=0.20
0.68 >=0.20	0.6 >=0.20

0.98 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
0.71 >=0.20	0.5 >=0.20
0.95 >=0.20	0.45 >=0.20
0.95 >=0.20	0.6 >=0.20
0.55 >=0.20	0.9 >=0.20
0.69 >=0.20	0.95 >=0.20
0.94 >=0.20	0.83 >=0.20
0.58 >=0.20	0.96 >=0.20
0.88 >=0.20	0.26 >=0.20
0.85 >=0.20	0.96 >=0.20
1 >=0.20	0.99 >=0.20
0.65 >=0.20	0.45 >=0.20
0.92 >=0.20	0.66 >=0.20
0.1 >=0.20	0.69 >=0.20
0.12 >=0.20	0.47 >=0.20
0.56 >=0.20	0.87 >=0.20
0.19 >=0.20	0.14 >=0.20
1 >=0.20	0.42 >=0.20
0.96 >=0.20	0.92 >=0.20
0.27 >=0.20	0.1 >=0.20
0.97 >=0.20	0.81 >=0.20
0.91 >=0.20	0.13 >=0.20
0.99 >=0.20	0.24 >=0.20
0.99 >=0.20	0.61 >=0.20
0.94 >=0.20	0.59 >=0.20
1 >=0.20	0.87 >=0.20
0.91 >=0.20	0.68 >=0.20
1 >=0.20	0.71 >=0.20
0.99 >=0.20	0.96 >=0.20
0.88 >=0.20	0.81 >=0.20
0.13 >=0.20	0.62 >=0.20
0.75 >=0.20	0.86 >=0.20
0.88 >=0.20	0.6 >=0.20
0.82 >=0.20	0.77 >=0.20
1 >=0.20	0.53 >=0.20
0.42 >=0.20	0.04 >=0.20
0.99 >=0.20	0.7 >=0.20
0.9 >=0.20	0.75 >=0.20
0.78 >=0.20	0.26 >=0.20
0.76 >=0.20	0.15 >=0.20
0.98 >=0.20	0.19 >=0.20
0.05 >=0.20	0.58 >=0.20
0.85 >=0.20	0.87 >=0.20
0.98 >=0.20	0.91 >=0.20
0.96 >=0.20	0.73 >=0.20
0.96 >=0.20	0.5 >=0.20

0.99 >=0.20	0.87 >=0.20
0.99 >=0.20	0.98 >=0.20
0.99 >=0.20	0.85 >=0.20
0.94 >=0.20	0.78 >=0.20
0.99 >=0.20	0.77 >=0.20
0.93 >=0.20	0.65 >=0.20
0.52 >=0.20	0.11 >=0.20
0.99 >=0.20	0.93 >=0.20
0.93 >=0.20	0.84 >=0.20
1 >=0.20	0.98 >=0.20
0.8 >=0.20	0.49 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.95 >=0.20
0.91 >=0.20	0.03 >=0.20
0.86 >=0.20	0.99 >=0.20
0.96 >=0.20	0.79 >=0.20
0.99 >=0.20	0.64 >=0.20
0.6 >=0.20	0.86 >=0.20
0.99 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.53 >=0.20	0.37 >=0.20
0.21 >=0.20	0.41 >=0.20
0.06 >=0.20	0.38 >=0.20
0.74 >=0.20	0.31 >=0.20
0.25 >=0.20	0.08 >=0.20
0.77 >=0.20	0.43 >=0.20
0.26 >=0.20	1 >=0.20
0.5 >=0.20	0.69 >=0.20
0.9 >=0.20	0.65 >=0.20
0.45 >=0.20	0.43 >=0.20
0.44 >=0.20	0.86 >=0.20
0.29 >=0.20	0.86 >=0.20
0.44 >=0.20	0.99 >=0.20
0.24 >=0.20	0.08 >=0.20
0.69 >=0.20	0.74 >=0.20
0.35 >=0.20	0.08 >=0.20
1 >=0.20	0.93 >=0.20
0.58 >=0.20	0.48 >=0.20
0.36 >=0.20	0.36 >=0.20
0.1 >=0.20	0.4 >=0.20
0.96 >=0.20	0.84 >=0.20
0.8 >=0.20	0.34 >=0.20
0.77 >=0.20	0.15 >=0.20
0.62 >=0.20	0.66 >=0.20
0.77 >=0.20	0.16 >=0.20

0.4 >=0.20	0.87 >=0.20
0.14 >=0.20	0.05 >=0.20
0.07 >=0.20	0.1 >=0.20
0.49 >=0.20	0.48 >=0.20
0.94 >=0.20	0.99 >=0.20
0.98 >=0.20	0.92 >=0.20
0.33 >=0.20	0.84 >=0.20
0.12 >=0.20	0.26 >=0.20
0.31 >=0.20	0.33 >=0.20
0.05 >=0.20	0.31 >=0.20
0.99 >=0.20	0.84 >=0.20
1 >=0.20	1 >=0.20
0.87 >=0.20	0.97 >=0.20
0.86 >=0.20	0.87 >=0.20
0.83 >=0.20	0.9 >=0.20
0.86 >=0.20	0.87 >=0.20
0.83 >=0.20	1 >=0.20
0.7 >=0.20	0.5 >=0.20
1 >=0.20	0.75 >=0.20
0.98 >=0.20	0.94 >=0.20
0.8 >=0.20	0.79 >=0.20
0.05 >=0.20	0.15 >=0.20
0.2 >=0.20	0.66 >=0.20
0.06 >=0.20	0.89 >=0.20
0.45 >=0.20	0.74 >=0.20
0.11 >=0.20	0.39 >=0.20
0.29 >=0.20	0.77 >=0.20
0.68 >=0.20	0.48 >=0.20
0.04 >=0.20	0.71 >=0.20
0.49 >=0.20	0.2 >=0.20
0.26 >=0.20	0.33 >=0.20
0.94 >=0.20	0.99 >=0.20
0.12 >=0.20	0.81 >=0.20
0.61 >=0.20	0.63 >=0.20
0.59 >=0.20	0.94 >=0.20
0.39 >=0.20	0.9 >=0.20
0.72 >=0.20	0.85 >=0.20
0.59 >=0.20	0.94 >=0.20
0.38 >=0.20	0.8 >=0.20
0.81 >=0.20	0.79 >=0.20
0.9 >=0.20	0.98 >=0.20
0.45 >=0.20	0.38 >=0.20
0.3 >=0.20	0.94 >=0.20
0.29 >=0.20	0.83 >=0.20
0.78 >=0.20	0.23 >=0.20
0.87 >=0.20	0.49 >=0.20
0.99 >=0.20	0.99 >=0.20

0.87 >=0.20	0.06 >=0.20
0.98 >=0.20	0.63 >=0.20
0.84 >=0.20	1 >=0.20
0.53 >=0.20	0.44 >=0.20
0.95 >=0.20	1 >=0.20
0.73 >=0.20	0.9 >=0.20
0.84 >=0.20	0.97 >=0.20
0.93 >=0.20	0.97 >=0.20
0.17 >=0.20	0.83 >=0.20
0.92 >=0.20	0.91 >=0.20
0.22 >=0.20	0.07 >=0.20
0.45 >=0.20	0.22 >=0.20
0.83 >=0.20	0.92 >=0.20
0.88 >=0.20	0.61 >=0.20
0.99 >=0.20	0.85 >=0.20
0.08 >=0.20	0.26 >=0.20
0.98 >=0.20	0.5 >=0.20
1 >=0.20	0.75 >=0.20
0.84 >=0.20	0.09 >=0.20
0.1 >=0.20	0.81 >=0.20
0.86 >=0.20	1 >=0.20
0.8 >=0.20	1 >=0.20
0.08 >=0.20	0.79 >=0.20
0.06 >=0.20	0.82 >=0.20
0.92 >=0.20	1 >=0.20
0.96 >=0.20	1 >=0.20
0.96 >=0.20	0.96 >=0.20
0.99 >=0.20	0.93 >=0.20
0.85 >=0.20	0.58 >=0.20
0.13 >=0.20	0.34 >=0.20
0.05 >=0.20	0.74 >=0.20
0.25 >=0.20	0.41 >=0.20
0.15 >=0.20	0.39 >=0.20
0.25 >=0.20	0.6 >=0.20
0.66 >=0.20	0.45 >=0.20
0.58 >=0.20	0.32 >=0.20
0.86 >=0.20	0.67 >=0.20
0.37 >=0.20	0.21 >=0.20
0.71 >=0.20	0.96 >=0.20
0.74 >=0.20	0.88 >=0.20
0.46 >=0.20	0.57 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.98 >=0.20
0.46 >=0.20	0.51 >=0.20
0.92 >=0.20	0.74 >=0.20
0.5 >=0.20	0.06 >=0.20
0.54 >=0.20	0.12 >=0.20

0.72 >=0.20	0.26 >=0.20
0.63 >=0.20	0.06 >=0.20
0.37 >=0.20	1 >=0.20
0.35 >=0.20	0.8 >=0.20
0.85 >=0.20	0.68 >=0.20
0.43 >=0.20	0.05 >=0.20
0.28 >=0.20	0.66 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.87 >=0.20	0.53 >=0.20
0.93 >=0.20	1 >=0.20
0.89 >=0.20	0.39 >=0.20
0.97 >=0.20	0.91 >=0.20
0.04 >=0.20	0.07 >=0.20
0.96 >=0.20	0.12 >=0.20
0.63 >=0.20	0.62 >=0.20
0.56 >=0.20	0.73 >=0.20
0.31 >=0.20	0.75 >=0.20
0.58 >=0.20	0.88 >=0.20
0.71 >=0.20	0.85 >=0.20
0.98 >=0.20	0.61 >=0.20
0.1 >=0.20	0.26 >=0.20
0.99 >=0.20	0.64 >=0.20
0.35 >=0.20	0.28 >=0.20
1 >=0.20	1 >=0.20
0.93 >=0.20	0.24 >=0.20
0.66 >=0.20	0.44 >=0.20
0.68 >=0.20	0.18 >=0.20
0.96 >=0.20	0.57 >=0.20
0.56 >=0.20	0.74 >=0.20
0.48 >=0.20	0.28 >=0.20
0.9 >=0.20	0.94 >=0.20
0.85 >=0.20	0.43 >=0.20
0.14 >=0.20	0.31 >=0.20
0.71 >=0.20	0.52 >=0.20
0.87 >=0.20	0.51 >=0.20
0.33 >=0.20	0.39 >=0.20
0.09 >=0.20	0.3 >=0.20
0.97 >=0.20	0.86 >=0.20
0.99 >=0.20	0.79 >=0.20
0.24 >=0.20	0.34 >=0.20
0.21 >=0.20	0.43 >=0.20
0.07 >=0.20	0.31 >=0.20
0.52 >=0.20	1 >=0.20
0.57 >=0.20	0.72 >=0.20
0.99 >=0.20	0.71 >=0.20
0.45 >=0.20	0.89 >=0.20

0.84 >=0.20	0.95 >=0.20
0.44 >=0.20	0.22 >=0.20
0.16 >=0.20	0.21 >=0.20
0.21 >=0.20	0.13 >=0.20
0.68 >=0.20	0.66 >=0.20
0.83 >=0.20	0.79 >=0.20
0.66 >=0.20	0.63 >=0.20
0.74 >=0.20	0.83 >=0.20
0.28 >=0.20	0.06 >=0.20
0.13 >=0.20	0.24 >=0.20
0.46 >=0.20	0.17 >=0.20
0.59 >=0.20	0.68 >=0.20
0.45 >=0.20	0.43 >=0.20
0.13 >=0.20	0.8 >=0.20
0.68 >=0.20	0.84 >=0.20
0.05 >=0.20	0.24 >=0.20
0.24 >=0.20	0.09 >=0.20
0.04 >=0.20	0.38 >=0.20
0.04 >=0.20	0.38 >=0.20
0.99 >=0.20	1 >=0.20
0.38 >=0.20	0.77 >=0.20
0.64 >=0.20	0.71 >=0.20
0.08 >=0.20	0.08 >=0.20
0.92 >=0.20	0.56 >=0.20
1 >=0.20	1 >=0.20
0.88 >=0.20	0.48 >=0.20
0.93 >=0.20	0.92 >=0.20
0.75 >=0.20	0.18 >=0.20
0.53 >=0.20	0.22 >=0.20
0.4 >=0.20	0.08 >=0.20
0.07 >=0.20	0.48 >=0.20
0.26 >=0.20	0.07 >=0.20
0.28 >=0.20	0.7 >=0.20
0.9 >=0.20	0.95 >=0.20
0.95 >=0.20	0.98 >=0.20
0.09 >=0.20	0.73 >=0.20
0.94 >=0.20	0.95 >=0.20
0.69 >=0.20	0.61 >=0.20
0.95 >=0.20	0.28 >=0.20
0.86 >=0.20	1 >=0.20
0.51 >=0.20	0.89 >=0.20
0.07 >=0.20	0.72 >=0.20
0.24 >=0.20	0.16 >=0.20
0.93 >=0.20	0.97 >=0.20
0.36 >=0.20	0.28 >=0.20
0.96 >=0.20	0.92 >=0.20
0.64 >=0.20	0.49 >=0.20

0.98 >=0.20	0.98 >=0.20
1 >=0.20	0.93 >=0.20
0.07 >=0.20	0.09 >=0.20
0.18 >=0.20	0.47 >=0.20
0.14 >=0.20	0.87 >=0.20
0.56 >=0.20	0.92 >=0.20
1 >=0.20	1 >=0.20
0.93 >=0.20	0.86 >=0.20
0.23 >=0.20	0.52 >=0.20
1 >=0.20	0.96 >=0.20
0.8 >=0.20	0.41 >=0.20
0.83 >=0.20	0.66 >=0.20
0.99 >=0.20	0.97 >=0.20
0.99 >=0.20	0.82 >=0.20
0.97 >=0.20	0.94 >=0.20
0.96 >=0.20	0.8 >=0.20
0.97 >=0.20	0.94 >=0.20
0.94 >=0.20	0.81 >=0.20
1 >=0.20	0.85 >=0.20
0.94 >=0.20	0.6 >=0.20
0.95 >=0.20	0.57 >=0.20
1 >=0.20	0.62 >=0.20
0.78 >=0.20	0.64 >=0.20
0.5 >=0.20	0.81 >=0.20
0.6 >=0.20	0.59 >=0.20
0.28 >=0.20	0.87 >=0.20
0.56 >=0.20	0.55 >=0.20
0.95 >=0.20	0.86 >=0.20
0.59 >=0.20	0.51 >=0.20
0.82 >=0.20	0.5 >=0.20
0.85 >=0.20	0.84 >=0.20
0.73 >=0.20	0.67 >=0.20
0.4 >=0.20	0.84 >=0.20
0.23 >=0.20	0.23 >=0.20
0.11 >=0.20	0.71 >=0.20
0.36 >=0.20	0.37 >=0.20
0.81 >=0.20	0.77 >=0.20
0.88 >=0.20	0.87 >=0.20
0.33 >=0.20	0.33 >=0.20
0.86 >=0.20	0.98 >=0.20
0.28 >=0.20	0.34 >=0.20
1 >=0.20	0.57 >=0.20
0.44 >=0.20	0.96 >=0.20
0.67 >=0.20	1 >=0.20
0.63 >=0.20	1 >=0.20
0.49 >=0.20	0.46 >=0.20
0.77 >=0.20	0.19 >=0.20

0.21 >=0.20	0.12 >=0.20
0.24 >=0.20	0.08 >=0.20
0.1 >=0.20	0.19 >=0.20
1 >=0.20	0.98 >=0.20
0.59 >=0.20	0.55 >=0.20
0.61 >=0.20	1 >=0.20
0.54 >=0.20	0.66 >=0.20
0.86 >=0.20	0.81 >=0.20
0.25 >=0.20	0.79 >=0.20
0.81 >=0.20	0.98 >=0.20
0.38 >=0.20	0.77 >=0.20
0.37 >=0.20	0.92 >=0.20
1 >=0.20	0.4 >=0.20
1 >=0.20	0.9 >=0.20
1 >=0.20	0.98 >=0.20
0.5 >=0.20	0.18 >=0.20
0.31 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
0.88 >=0.20	1 >=0.20
0.69 >=0.20	0.94 >=0.20
0.99 >=0.20	1 >=0.20
0.85 >=0.20	0.87 >=0.20
1 >=0.20	0.75 >=0.20
0.96 >=0.20	0.9 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.95 >=0.20	0.87 >=0.20
0.2 >=0.20	0.85 >=0.20
0.95 >=0.20	0.99 >=0.20
0.93 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
0.97 >=0.20	0.81 >=0.20
0.98 >=0.20	0.77 >=0.20
0.21 >=0.20	0.11 >=0.20
0.41 >=0.20	0.99 >=0.20
0.56 >=0.20	0.83 >=0.20
0.63 >=0.20	0.9 >=0.20
0.09 >=0.20	0.02 >=0.20
0.26 >=0.20	0.56 >=0.20
0.68 >=0.20	0.74 >=0.20
0.61 >=0.20	0.75 >=0.20
0.08 >=0.20	0.65 >=0.20
0.13 >=0.20	0.44 >=0.20
0.99 >=0.20	0.77 >=0.20
0.64 >=0.20	0.78 >=0.20
0.36 >=0.20	0.76 >=0.20

1	>=0.20	1	>=0.20
0.58	>=0.20	0.3	>=0.20
0.07	>=0.20	0.14	>=0.20
0.04	>=0.20	0.19	>=0.20
0.56	>=0.20	0.82	>=0.20
0.28	>=0.20	0.1	>=0.20
0.17	>=0.20	0.11	>=0.20
0.21	>=0.20	0.89	>=0.20
0.89	>=0.20	0.46	>=0.20
0.43	>=0.20	0.63	>=0.20
1	>=0.20	1	>=0.20
0.08	>=0.20	0.18	>=0.20
0.66	>=0.20	0.32	>=0.20
0.45	>=0.20	0.67	>=0.20
0.96	>=0.20	0.93	>=0.20
0.05	>=0.20	0.15	>=0.20
0.14	>=0.20	0.11	>=0.20
0.45	>=0.20	0.15	>=0.20
0.68	>=0.20	0.54	>=0.20
0.54	>=0.20	0.52	>=0.20
0.7	>=0.20	0.75	>=0.20
0.4	>=0.20	0.09	>=0.20
0.58	>=0.20	0.31	>=0.20
0.34	>=0.20	0.25	>=0.20
0.95	>=0.20	0.09	>=0.20
0.99	>=0.20	0.77	>=0.20
0.97	>=0.20	1	>=0.20
0.98	>=0.20	1	>=0.20
0.63	>=0.20	0.81	>=0.20
0.47	>=0.20	0.03	>=0.20
0.15	>=0.20	0.47	>=0.20
0.14	>=0.20	0.24	>=0.20
0.81	>=0.20	0.12	>=0.20
0.12	>=0.20	0.63	>=0.20
0.76	>=0.20	0.59	>=0.20
0.2	>=0.20	0.98	>=0.20
0.31	>=0.20	0.15	>=0.20
0.88	>=0.20	0.82	>=0.20
1	>=0.20	0.34	>=0.20
0.63	>=0.20	0.61	>=0.20
0.47	>=0.20	0.35	>=0.20
0.31	>=0.20	0.98	>=0.20
0.7	>=0.20	0.93	>=0.20
0.25	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
0.94	>=0.20	0.57	>=0.20
0.65	>=0.20	0.6	>=0.20

0.1 >=0.20	0.35 >=0.20
0.93 >=0.20	0.73 >=0.20
0.96 >=0.20	0.27 >=0.20
0.17 >=0.20	1 >=0.20
0.13 >=0.20	0.46 >=0.20
0.83 >=0.20	0.05 >=0.20
0.46 >=0.20	0.02 >=0.20
0.11 >=0.20	0.06 >=0.20
1 >=0.20	0.68 >=0.20
0.98 >=0.20	0.66 >=0.20
0.69 >=0.20	0.32 >=0.20
1 >=0.20	0.73 >=0.20
0.95 >=0.20	0.39 >=0.20
1 >=0.20	0.76 >=0.20
0.99 >=0.20	0.52 >=0.20
0.98 >=0.20	0.61 >=0.20
0.97 >=0.20	0.45 >=0.20
0.04 >=0.20	0.36 >=0.20
1 >=0.20	1 >=0.20
0.18 >=0.20	0.35 >=0.20
0.94 >=0.20	0.92 >=0.20
0.54 >=0.20	0.39 >=0.20
0.56 >=0.20	0.14 >=0.20
0.08 >=0.20	0.25 >=0.20
0.83 >=0.20	0.71 >=0.20
0.54 >=0.20	0.22 >=0.20
0.78 >=0.20	0.86 >=0.20
0.97 >=0.20	1 >=0.20
0.96 >=0.20	0.99 >=0.20
0.93 >=0.20	0.32 >=0.20
1 >=0.20	0.95 >=0.20
0.29 >=0.20	0.58 >=0.20
0.5 >=0.20	0.3 >=0.20
0.38 >=0.20	0.17 >=0.20
0.99 >=0.20	0.71 >=0.20
1 >=0.20	0.87 >=0.20
0.98 >=0.20	0.91 >=0.20
0.97 >=0.20	0.69 >=0.20
0.04 >=0.20	0.09 >=0.20
0.68 >=0.20	1 >=0.20
0.36 >=0.20	0.46 >=0.20
0.36 >=0.20	0.46 >=0.20
0.5 >=0.20	0.45 >=0.20
0.87 >=0.20	0.48 >=0.20
0.55 >=0.20	0.85 >=0.20
0.12 >=0.20	0.48 >=0.20
0.11 >=0.20	0.06 >=0.20

0.51 >=0.20	0.07 >=0.20
0.9 >=0.20	0.97 >=0.20
0.88 >=0.20	0.92 >=0.20
0.88 >=0.20	0.55 >=0.20
0.99 >=0.20	0.96 >=0.20
0.92 >=0.20	0.87 >=0.20
0.88 >=0.20	0.88 >=0.20
0.87 >=0.20	0.46 >=0.20
0.35 >=0.20	1 >=0.20
0.32 >=0.20	1 >=0.20
0.8 >=0.20	0.89 >=0.20
0.33 >=0.20	0.86 >=0.20
0.17 >=0.20	0.76 >=0.20
0.95 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
0.57 >=0.20	0.4 >=0.20
0.73 >=0.20	0.22 >=0.20
0.27 >=0.20	0.21 >=0.20
0.71 >=0.20	0.56 >=0.20
0.79 >=0.20	0.47 >=0.20
0.15 >=0.20	0.14 >=0.20
0.04 >=0.20	0.03 >=0.20
0.21 >=0.20	0.05 >=0.20
0.2 >=0.20	0.11 >=0.20
0.91 >=0.20	0.81 >=0.20
1 >=0.20	0.84 >=0.20
0.13 >=0.20	0.1 >=0.20
0.19 >=0.20	0.03 >=0.20
1 >=0.20	1 >=0.20
0.89 >=0.20	0.82 >=0.20
1 >=0.20	1 >=0.20
0.91 >=0.20	0.28 >=0.20
0.43 >=0.20	0.04 >=0.20
0.53 >=0.20	0.48 >=0.20
0.93 >=0.20	0.9 >=0.20
0.99 >=0.20	0.97 >=0.20
0.92 >=0.20	0.68 >=0.20
1 >=0.20	0.94 >=0.20
0.99 >=0.20	0.93 >=0.20
1 >=0.20	0.95 >=0.20
1 >=0.20	0.91 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.93 >=0.20
0.05 >=0.20	0.52 >=0.20
0.98 >=0.20	0.98 >=0.20
0.98 >=0.20	1 >=0.20

0.28 >=0.20	0.68 >=0.20
0.55 >=0.20	0.93 >=0.20
0.18 >=0.20	0.53 >=0.20
0.32 >=0.20	0.17 >=0.20
0.78 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	0.87 >=0.20
0.98 >=0.20	0.96 >=0.20
0.97 >=0.20	0.4 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.91 >=0.20	0.93 >=0.20
0.91 >=0.20	0.93 >=0.20
0.91 >=0.20	0.93 >=0.20
0.62 >=0.20	0.81 >=0.20
0.65 >=0.20	0.66 >=0.20
0.94 >=0.20	0.77 >=0.20
0.87 >=0.20	0.8 >=0.20
0.99 >=0.20	0.97 >=0.20
0.93 >=0.20	0.83 >=0.20
0.89 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.93 >=0.20
0.96 >=0.20	0.98 >=0.20
0.93 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.83 >=0.20	0.93 >=0.20
1 >=0.20	0.91 >=0.20
0.91 >=0.20	0.28 >=0.20
1 >=0.20	0.84 >=0.20
1 >=0.20	0.67 >=0.20
1 >=0.20	0.82 >=0.20
0.57 >=0.20	0.93 >=0.20
1 >=0.20	0.93 >=0.20
0.53 >=0.20	0.23 >=0.20
0.74 >=0.20	0.85 >=0.20
0.11 >=0.20	0.31 >=0.20
0.94 >=0.20	0.62 >=0.20
0.87 >=0.20	0.91 >=0.20
0.24 >=0.20	0.09 >=0.20
0.61 >=0.20	0.49 >=0.20
0.64 >=0.20	0.28 >=0.20
0.47 >=0.20	0.29 >=0.20

0.59 >=0.20	0.46 >=0.20
0.78 >=0.20	0.62 >=0.20
0.95 >=0.20	0.89 >=0.20
1 >=0.20	0.67 >=0.20
0.96 >=0.20	0.86 >=0.20
0.99 >=0.20	0.49 >=0.20
1 >=0.20	0.62 >=0.20
0.59 >=0.20	0.46 >=0.20
0.69 >=0.20	0.58 >=0.20
0.57 >=0.20	0.94 >=0.20
1 >=0.20	0.81 >=0.20
0.94 >=0.20	0.92 >=0.20
0.37 >=0.20	0.8 >=0.20
0.99 >=0.20	0.98 >=0.20
0.99 >=0.20	0.76 >=0.20
0.99 >=0.20	0.89 >=0.20
0.4 >=0.20	0.44 >=0.20
0.26 >=0.20	0.2 >=0.20
0.99 >=0.20	0.95 >=0.20
1 >=0.20	0.67 >=0.20
1 >=0.20	0.99 >=0.20
0.31 >=0.20	0.78 >=0.20
0.97 >=0.20	0.45 >=0.20
0.76 >=0.20	0.59 >=0.20
0.99 >=0.20	1 >=0.20
0.97 >=0.20	0.87 >=0.20
0.41 >=0.20	1 >=0.20
0.59 >=0.20	0.21 >=0.20
0.06 >=0.20	0.28 >=0.20
0.1 >=0.20	0.31 >=0.20
0.78 >=0.20	0.8 >=0.20
0.15 >=0.20	0.32 >=0.20
0.32 >=0.20	0.41 >=0.20
0.25 >=0.20	0.36 >=0.20
0.46 >=0.20	0.13 >=0.20
0.91 >=0.20	1 >=0.20
0.86 >=0.20	0.95 >=0.20
0.91 >=0.20	1 >=0.20
0.86 >=0.20	0.95 >=0.20
0.88 >=0.20	0.81 >=0.20
0.71 >=0.20	0.69 >=0.20
0.93 >=0.20	0.9 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.72 >=0.20	0.12 >=0.20
0.12 >=0.20	0.65 >=0.20
0.99 >=0.20	0.69 >=0.20

0.13 >=0.20	0.03 >=0.20
0.89 >=0.20	0.99 >=0.20
0.45 >=0.20	0.13 >=0.20
0.93 >=0.20	0.9 >=0.20
0.88 >=0.20	0.63 >=0.20
0.32 >=0.20	0.45 >=0.20
0.27 >=0.20	0.25 >=0.20
0.93 >=0.20	0.19 >=0.20
0.69 >=0.20	0.06 >=0.20
1 >=0.20	0.64 >=0.20
0.17 >=0.20	0.4 >=0.20
0.98 >=0.20	0.33 >=0.20
0.97 >=0.20	0.31 >=0.20
0.69 >=0.20	0.86 >=0.20
0.74 >=0.20	0.63 >=0.20
0.82 >=0.20	0.83 >=0.20
0.54 >=0.20	0.5 >=0.20
0.7 >=0.20	0.71 >=0.20
0.69 >=0.20	0.73 >=0.20
0.77 >=0.20	0.3 >=0.20
0.99 >=0.20	0.67 >=0.20
0.83 >=0.20	0.49 >=0.20
0.32 >=0.20	0.31 >=0.20
0.71 >=0.20	0.75 >=0.20
0.13 >=0.20	0.15 >=0.20
0.63 >=0.20	0.4 >=0.20
0.18 >=0.20	0.26 >=0.20
0.22 >=0.20	0.91 >=0.20
0.17 >=0.20	0.21 >=0.20
0.87 >=0.20	0.99 >=0.20
0.98 >=0.20	0.27 >=0.20
0.93 >=0.20	0.36 >=0.20
0.83 >=0.20	0.05 >=0.20
0.99 >=0.20	0.81 >=0.20
0.16 >=0.20	0.28 >=0.20
0.19 >=0.20	0.24 >=0.20
0.33 >=0.20	0.04 >=0.20
0.38 >=0.20	0.28 >=0.20
0.76 >=0.20	0.78 >=0.20
0.54 >=0.20	0.98 >=0.20
0.57 >=0.20	0.81 >=0.20
0.55 >=0.20	0.52 >=0.20
0.11 >=0.20	0.21 >=0.20
0.65 >=0.20	0.89 >=0.20
0.16 >=0.20	0.38 >=0.20
0.68 >=0.20	0.66 >=0.20
0.27 >=0.20	0.52 >=0.20

0.93 >=0.20	0.89 >=0.20
0.4 >=0.20	0.22 >=0.20
0.16 >=0.20	0.31 >=0.20
0.63 >=0.20	0.97 >=0.20
0.19 >=0.20	0.57 >=0.20
0.56 >=0.20	0.8 >=0.20
0.95 >=0.20	0.82 >=0.20
0.74 >=0.20	0.32 >=0.20
0.57 >=0.20	0.95 >=0.20
0.39 >=0.20	0.6 >=0.20
0.43 >=0.20	0.95 >=0.20
0.91 >=0.20	0.68 >=0.20
0.89 >=0.20	0.71 >=0.20
0.75 >=0.20	0.7 >=0.20
0.22 >=0.20	0.3 >=0.20
0.15 >=0.20	0.85 >=0.20
0.74 >=0.20	0.49 >=0.20
0.84 >=0.20	0.33 >=0.20
0.3 >=0.20	0.6 >=0.20
0.56 >=0.20	0.98 >=0.20
0.75 >=0.20	0.52 >=0.20
0.95 >=0.20	0.53 >=0.20
0.62 >=0.20	0.78 >=0.20
0.05 >=0.20	0.24 >=0.20
0.49 >=0.20	0.93 >=0.20
0.75 >=0.20	0.27 >=0.20
0.69 >=0.20	0.24 >=0.20
0.47 >=0.20	0.9 >=0.20
0.16 >=0.20	0.75 >=0.20
0.29 >=0.20	0.65 >=0.20
0.2 >=0.20	0.58 >=0.20
0.43 >=0.20	1 >=0.20
0.18 >=0.20	0.78 >=0.20
0.69 >=0.20	0.7 >=0.20
0.83 >=0.20	0.36 >=0.20
0.82 >=0.20	0.86 >=0.20
0.43 >=0.20	0.79 >=0.20
0.2 >=0.20	0.87 >=0.20
0.92 >=0.20	0.92 >=0.20
0.59 >=0.20	0.28 >=0.20
0.43 >=0.20	0.98 >=0.20
0.88 >=0.20	0.92 >=0.20
0.23 >=0.20	0.98 >=0.20
0.13 >=0.20	0.64 >=0.20
0.75 >=0.20	0.1 >=0.20
0.36 >=0.20	1 >=0.20
0.95 >=0.20	0.37 >=0.20

0.99 >=0.20	0.85 >=0.20
0.64 >=0.20	0.79 >=0.20
0.5 >=0.20	0.61 >=0.20
0.73 >=0.20	0.41 >=0.20
0.77 >=0.20	0.34 >=0.20
0.88 >=0.20	1 >=0.20
0.3 >=0.20	0.73 >=0.20
0.82 >=0.20	0.68 >=0.20
0.81 >=0.20	0.48 >=0.20
0.06 >=0.20	0.12 >=0.20
0.46 >=0.20	0.72 >=0.20
0.42 >=0.20	0.48 >=0.20
0.35 >=0.20	0.27 >=0.20
0.97 >=0.20	0.8 >=0.20
0.65 >=0.20	0.26 >=0.20
0.93 >=0.20	0.94 >=0.20
0.34 >=0.20	0.46 >=0.20
0.08 >=0.20	0.78 >=0.20
0.39 >=0.20	0.37 >=0.20
0.39 >=0.20	0.37 >=0.20
0.66 >=0.20	0.51 >=0.20
0.23 >=0.20	0.21 >=0.20
0.89 >=0.20	0.51 >=0.20
0.7 >=0.20	0.09 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
0.73 >=0.20	0.22 >=0.20
0.92 >=0.20	0.67 >=0.20
0.94 >=0.20	0.93 >=0.20
0.15 >=0.20	0.48 >=0.20
0.99 >=0.20	0.98 >=0.20
0.76 >=0.20	0.11 >=0.20
0.79 >=0.20	0.14 >=0.20
0.89 >=0.20	0.08 >=0.20
0.98 >=0.20	0.62 >=0.20
0.55 >=0.20	0.8 >=0.20
0.8 >=0.20	0.19 >=0.20
0.91 >=0.20	0.45 >=0.20
1 >=0.20	0.97 >=0.20
0.74 >=0.20	0.11 >=0.20
0.26 >=0.20	0.04 >=0.20
0.28 >=0.20	0.07 >=0.20
0.52 >=0.20	1 >=0.20
0.2 >=0.20	0.99 >=0.20
0.86 >=0.20	1 >=0.20
0.97 >=0.20	0.9 >=0.20
1 >=0.20	1 >=0.20

0.89 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.96 >=0.20
0.95 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.14 >=0.20
0.99 >=0.20	0.72 >=0.20
0.99 >=0.20	0.76 >=0.20
0.25 >=0.20	0.43 >=0.20
0.88 >=0.20	0.49 >=0.20
0.69 >=0.20	0.7 >=0.20
0.73 >=0.20	0.86 >=0.20
1 >=0.20	0.89 >=0.20
0.99 >=0.20	0.9 >=0.20
0.97 >=0.20	0.38 >=0.20
0.93 >=0.20	0.87 >=0.20
0.63 >=0.20	0.6 >=0.20
0.73 >=0.20	0.99 >=0.20
0.66 >=0.20	0.18 >=0.20
0.28 >=0.20	0.57 >=0.20
0.34 >=0.20	0.37 >=0.20
0.95 >=0.20	0.67 >=0.20
0.57 >=0.20	0.94 >=0.20
0.98 >=0.20	0.42 >=0.20
0.81 >=0.20	0.17 >=0.20
1 >=0.20	0.98 >=0.20
0.12 >=0.20	0.97 >=0.20
0.15 >=0.20	0.95 >=0.20
0.36 >=0.20	0.81 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
0.99 >=0.20	0.42 >=0.20
0.85 >=0.20	0.63 >=0.20
1 >=0.20	0.73 >=0.20
0.73 >=0.20	1 >=0.20
0.59 >=0.20	0.99 >=0.20
0.34 >=0.20	0.73 >=0.20
0.71 >=0.20	0.16 >=0.20
0.35 >=0.20	0.72 >=0.20
0.19 >=0.20	0.91 >=0.20
0.29 >=0.20	0.17 >=0.20
1 >=0.20	1 >=0.20
0.4 >=0.20	0.95 >=0.20
0.55 >=0.20	0.7 >=0.20
0.45 >=0.20	1 >=0.20

0.65 >=0.20	1 >=0.20
0.73 >=0.20	0.78 >=0.20
0.24 >=0.20	0.12 >=0.20
0.99 >=0.20	1 >=0.20
0.13 >=0.20	0.47 >=0.20
0.91 >=0.20	1 >=0.20
0.09 >=0.20	0.15 >=0.20
0.39 >=0.20	0.48 >=0.20
1 >=0.20	0.72 >=0.20
0.63 >=0.20	0.36 >=0.20
0.99 >=0.20	0.38 >=0.20
0.13 >=0.20	0.24 >=0.20
0.68 >=0.20	0.28 >=0.20
0.39 >=0.20	0.9 >=0.20
0.71 >=0.20	0.5 >=0.20
0.1 >=0.20	0.28 >=0.20
0.76 >=0.20	0.27 >=0.20
0.99 >=0.20	0.99 >=0.20
0.6 >=0.20	0.65 >=0.20
0.11 >=0.20	0.22 >=0.20
0.13 >=0.20	0.26 >=0.20
0.1 >=0.20	0.26 >=0.20
0.71 >=0.20	0.9 >=0.20
0.16 >=0.20	0.63 >=0.20
0.39 >=0.20	1 >=0.20
0.65 >=0.20	0.9 >=0.20
0.98 >=0.20	0.33 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
0.78 >=0.20	1 >=0.20
0.32 >=0.20	1 >=0.20
0.25 >=0.20	1 >=0.20
0.42 >=0.20	1 >=0.20
0.3 >=0.20	1 >=0.20
0.35 >=0.20	1 >=0.20
0.4 >=0.20	1 >=0.20
0.34 >=0.20	1 >=0.20
0.34 >=0.20	1 >=0.20
0.39 >=0.20	1 >=0.20
0.39 >=0.20	1 >=0.20
0.34 >=0.20	1 >=0.20
0.36 >=0.20	1 >=0.20
0.34 >=0.20	1 >=0.20
0.85 >=0.20	0.87 >=0.20
0.98 >=0.20	0.88 >=0.20
1 >=0.20	0.9 >=0.20
1 >=0.20	1 >=0.20

0.97 >=0.20	0.93 >=0.20
0.85 >=0.20	0.66 >=0.20
0.62 >=0.20	0.91 >=0.20
0.78 >=0.20	0.99 >=0.20
0.58 >=0.20	0.21 >=0.20
0.94 >=0.20	0.99 >=0.20
0.72 >=0.20	0.99 >=0.20
0.76 >=0.20	1 >=0.20
0.8 >=0.20	1 >=0.20
0.58 >=0.20	0.1 >=0.20
0.69 >=0.20	0.65 >=0.20
0.6 >=0.20	0.95 >=0.20
0.1 >=0.20	0.41 >=0.20
0.89 >=0.20	0.93 >=0.20
0.66 >=0.20	0.92 >=0.20
0.11 >=0.20	0.34 >=0.20
0.83 >=0.20	0.64 >=0.20
0.88 >=0.20	0.72 >=0.20
0.26 >=0.20	0.97 >=0.20
0.66 >=0.20	1 >=0.20
0.97 >=0.20	1 >=0.20
0.26 >=0.20	0.9 >=0.20
0.91 >=0.20	0.58 >=0.20
0.9 >=0.20	0.12 >=0.20
0.35 >=0.20	0.97 >=0.20
0.49 >=0.20	0.51 >=0.20
0.94 >=0.20	0.72 >=0.20
0.95 >=0.20	0.41 >=0.20
0.2 >=0.20	0.58 >=0.20
0.62 >=0.20	0.33 >=0.20
0.62 >=0.20	0.88 >=0.20
0.09 >=0.20	0.72 >=0.20
0.52 >=0.20	0.04 >=0.20
0.23 >=0.20	0.74 >=0.20
0.41 >=0.20	0.96 >=0.20
0.49 >=0.20	0.09 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.55 >=0.20	0.84 >=0.20
0.11 >=0.20	0.6 >=0.20
0.67 >=0.20	0.88 >=0.20
0.97 >=0.20	0.9 >=0.20
0.34 >=0.20	0.18 >=0.20
0.89 >=0.20	0.96 >=0.20
0.33 >=0.20	0.79 >=0.20
0.32 >=0.20	0.29 >=0.20
0.11 >=0.20	0.68 >=0.20

0.96 >=0.20	0.6 >=0.20
0.33 >=0.20	0.24 >=0.20
0.39 >=0.20	0.94 >=0.20
0.14 >=0.20	0.77 >=0.20
0.05 >=0.20	0.9 >=0.20
0.92 >=0.20	0.88 >=0.20
0.29 >=0.20	0.22 >=0.20
0.65 >=0.20	0.48 >=0.20
0.98 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.68 >=0.20	0.71 >=0.20
0.99 >=0.20	1 >=0.20
0.15 >=0.20	0.05 >=0.20
0.98 >=0.20	0.72 >=0.20
1 >=0.20	0.98 >=0.20
0.93 >=0.20	0.39 >=0.20
0.96 >=0.20	0.9 >=0.20
0.86 >=0.20	0.83 >=0.20
0.74 >=0.20	0.71 >=0.20
0.93 >=0.20	0.55 >=0.20
0.94 >=0.20	0.33 >=0.20
0.59 >=0.20	0.05 >=0.20
1 >=0.20	0.93 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	0.99 >=0.20
0.95 >=0.20	0.74 >=0.20
0.9 >=0.20	0.88 >=0.20
0.51 >=0.20	0.38 >=0.20
0.76 >=0.20	0.52 >=0.20
0.97 >=0.20	0.65 >=0.20
0.97 >=0.20	0.92 >=0.20
0.74 >=0.20	1 >=0.20
0.91 >=0.20	0.57 >=0.20
0.04 >=0.20	0.49 >=0.20
0.38 >=0.20	0.9 >=0.20
0.47 >=0.20	0.94 >=0.20
0.11 >=0.20	0.76 >=0.20
0.19 >=0.20	0.87 >=0.20
0.7 >=0.20	1 >=0.20
0.86 >=0.20	1 >=0.20
0.23 >=0.20	1 >=0.20
0.39 >=0.20	1 >=0.20
0.18 >=0.20	0.91 >=0.20
0.53 >=0.20	0.99 >=0.20
0.65 >=0.20	0.99 >=0.20
0.26 >=0.20	0.51 >=0.20

0.98 >=0.20	0.98 >=0.20
0.77 >=0.20	1 >=0.20
0.93 >=0.20	0.82 >=0.20
0.98 >=0.20	0.99 >=0.20
0.99 >=0.20	0.98 >=0.20
0.71 >=0.20	1 >=0.20
0.97 >=0.20	0.99 >=0.20
0.88 >=0.20	1 >=0.20
0.59 >=0.20	0.37 >=0.20
0.87 >=0.20	0.31 >=0.20
0.14 >=0.20	0.25 >=0.20
0.85 >=0.20	0.83 >=0.20
0.84 >=0.20	0.63 >=0.20
0.82 >=0.20	0.05 >=0.20
0.81 >=0.20	0.9 >=0.20
0.06 >=0.20	0.87 >=0.20
0.32 >=0.20	0.89 >=0.20
0.68 >=0.20	0.47 >=0.20
0.32 >=0.20	0.7 >=0.20
0.97 >=0.20	0.69 >=0.20
0.87 >=0.20	0.97 >=0.20
0.98 >=0.20	0.74 >=0.20
0.41 >=0.20	0.99 >=0.20
0.63 >=0.20	1 >=0.20
0.89 >=0.20	0.66 >=0.20
0.06 >=0.20	0.13 >=0.20
0.89 >=0.20	0.91 >=0.20
0.84 >=0.20	0.98 >=0.20
0.2 >=0.20	0.15 >=0.20
0.14 >=0.20	0.03 >=0.20
0.67 >=0.20	0.71 >=0.20
1 >=0.20	0.99 >=0.20
0.97 >=0.20	0.96 >=0.20
1 >=0.20	0.98 >=0.20
0.96 >=0.20	0.82 >=0.20
1 >=0.20	1 >=0.20
0.9 >=0.20	0.3 >=0.20
0.95 >=0.20	1 >=0.20
0.67 >=0.20	0.83 >=0.20
0.99 >=0.20	0.98 >=0.20
0.08 >=0.20	0.28 >=0.20
0.71 >=0.20	0.8 >=0.20
0.93 >=0.20	0.93 >=0.20
0.39 >=0.20	0.59 >=0.20
0.69 >=0.20	0.75 >=0.20
0.65 >=0.20	0.63 >=0.20
0.9 >=0.20	0.7 >=0.20

0.45 >=0.20	0.28 >=0.20
0.26 >=0.20	0.16 >=0.20
0.48 >=0.20	0.84 >=0.20
0.52 >=0.20	0.47 >=0.20
0.25 >=0.20	0.09 >=0.20
0.52 >=0.20	0.9 >=0.20
0.84 >=0.20	0.62 >=0.20
0.94 >=0.20	1 >=0.20
0.57 >=0.20	0.96 >=0.20
0.93 >=0.20	1 >=0.20
0.06 >=0.20	0.65 >=0.20
0.64 >=0.20	0.63 >=0.20
0.5 >=0.20	0.61 >=0.20
0.99 >=0.20	0.99 >=0.20
0.16 >=0.20	0.86 >=0.20
0.42 >=0.20	0.47 >=0.20
0.79 >=0.20	0.81 >=0.20
0.73 >=0.20	0.94 >=0.20
0.99 >=0.20	0.77 >=0.20
0.1 >=0.20	0.14 >=0.20
0.63 >=0.20	0.48 >=0.20
0.49 >=0.20	0.59 >=0.20
0.71 >=0.20	0.91 >=0.20
0.66 >=0.20	0.74 >=0.20
0.81 >=0.20	0.66 >=0.20
0.52 >=0.20	0.39 >=0.20
0.58 >=0.20	0.62 >=0.20
0.55 >=0.20	0.4 >=0.20
0.6 >=0.20	0.41 >=0.20
0.46 >=0.20	0.46 >=0.20
0.17 >=0.20	0.67 >=0.20
0.05 >=0.20	0.47 >=0.20
0.13 >=0.20	0.64 >=0.20
0.49 >=0.20	0.71 >=0.20
0.25 >=0.20	0.96 >=0.20
0.99 >=0.20	0.99 >=0.20
0.88 >=0.20	0.99 >=0.20
0.34 >=0.20	0.87 >=0.20
0.4 >=0.20	0.59 >=0.20
0.4 >=0.20	0.72 >=0.20
0.59 >=0.20	0.64 >=0.20
0.82 >=0.20	0.99 >=0.20
0.18 >=0.20	0.9 >=0.20
0.16 >=0.20	0.65 >=0.20
0.34 >=0.20	0.64 >=0.20
0.7 >=0.20	0.55 >=0.20
0.2 >=0.20	0.03 >=0.20

0.67 >=0.20	0.4 >=0.20
0.17 >=0.20	0.51 >=0.20
0.06 >=0.20	0.28 >=0.20
0.4 >=0.20	0.96 >=0.20
0.99 >=0.20	1 >=0.20
0.07 >=0.20	0.51 >=0.20
0.84 >=0.20	0.77 >=0.20
0.73 >=0.20	0.04 >=0.20
0.89 >=0.20	0.98 >=0.20
0.99 >=0.20	0.97 >=0.20
0.06 >=0.20	0.47 >=0.20
0.07 >=0.20	0.69 >=0.20
0.96 >=0.20	0.87 >=0.20
0.97 >=0.20	0.32 >=0.20
0.87 >=0.20	0.58 >=0.20
0.92 >=0.20	0.41 >=0.20
0.39 >=0.20	0.03 >=0.20
0.25 >=0.20	1 >=0.20
0.33 >=0.20	1 >=0.20
0.13 >=0.20	0.84 >=0.20
0.34 >=0.20	1 >=0.20
0.23 >=0.20	0.95 >=0.20
0.41 >=0.20	0.82 >=0.20
1 >=0.20	0.48 >=0.20
0.18 >=0.20	0.27 >=0.20
0.99 >=0.20	0.99 >=0.20
0.99 >=0.20	0.99 >=0.20
0.95 >=0.20	0.9 >=0.20
0.98 >=0.20	1 >=0.20
0.14 >=0.20	0.13 >=0.20
0.21 >=0.20	0.47 >=0.20
0.25 >=0.20	0.77 >=0.20
0.14 >=0.20	0.53 >=0.20
0.67 >=0.20	0.87 >=0.20
0.84 >=0.20	0.64 >=0.20
0.49 >=0.20	0.68 >=0.20
0.42 >=0.20	0.25 >=0.20
0.49 >=0.20	0.68 >=0.20
0.27 >=0.20	0.27 >=0.20
0.92 >=0.20	0.8 >=0.20
0.8 >=0.20	0.97 >=0.20
0.67 >=0.20	0.61 >=0.20
0.88 >=0.20	0.99 >=0.20
0.85 >=0.20	0.97 >=0.20
0.12 >=0.20	0.18 >=0.20
0.58 >=0.20	0.84 >=0.20
0.78 >=0.20	0.98 >=0.20

0.07 >=0.20	0.14 >=0.20
0.22 >=0.20	0.16 >=0.20
0.44 >=0.20	0.7 >=0.20
0.27 >=0.20	0.05 >=0.20
0.68 >=0.20	0.2 >=0.20
1 >=0.20	0.8 >=0.20
0.94 >=0.20	0.82 >=0.20
0.4 >=0.20	0.61 >=0.20
0.44 >=0.20	0.12 >=0.20
0.31 >=0.20	0.15 >=0.20
1 >=0.20	0.9 >=0.20
0.37 >=0.20	0.77 >=0.20
0.6 >=0.20	0.52 >=0.20
0.86 >=0.20	0.86 >=0.20
0.23 >=0.20	0.65 >=0.20
0.85 >=0.20	0.39 >=0.20
0.31 >=0.20	0.77 >=0.20
0.54 >=0.20	0.91 >=0.20
0.81 >=0.20	0.98 >=0.20
0.89 >=0.20	0.95 >=0.20
0.04 >=0.20	0.4 >=0.20
0.09 >=0.20	0.43 >=0.20
0.45 >=0.20	0.57 >=0.20
0.52 >=0.20	0.77 >=0.20
0.24 >=0.20	0.71 >=0.20
0.78 >=0.20	0.99 >=0.20
0.78 >=0.20	0.99 >=0.20
0.11 >=0.20	0.07 >=0.20
0.8 >=0.20	0.4 >=0.20
0.83 >=0.20	0.37 >=0.20
1 >=0.20	0.89 >=0.20
0.44 >=0.20	0.29 >=0.20
0.94 >=0.20	0.16 >=0.20
0.66 >=0.20	0.09 >=0.20
1 >=0.20	0.75 >=0.20
0.37 >=0.20	0.36 >=0.20
0.21 >=0.20	0.6 >=0.20
0.95 >=0.20	0.91 >=0.20
0.25 >=0.20	0.25 >=0.20
0.06 >=0.20	0.05 >=0.20
0.34 >=0.20	0.46 >=0.20
0.68 >=0.20	0.47 >=0.20
0.12 >=0.20	0.05 >=0.20
0.33 >=0.20	0.35 >=0.20
0.1 >=0.20	0.06 >=0.20
0.47 >=0.20	0.13 >=0.20
0.47 >=0.20	0.18 >=0.20

0.39 >=0.20	0.74 >=0.20
0.04 >=0.20	0.05 >=0.20
0.04 >=0.20	0.05 >=0.20
0.97 >=0.20	0.63 >=0.20
0.36 >=0.20	0.17 >=0.20
0.39 >=0.20	0.51 >=0.20
0.05 >=0.20	0.2 >=0.20
0.64 >=0.20	0.37 >=0.20
0.75 >=0.20	0.04 >=0.20
0.85 >=0.20	0.96 >=0.20
0.09 >=0.20	0.41 >=0.20
0.11 >=0.20	0.05 >=0.20
0.83 >=0.20	0.69 >=0.20
0.09 >=0.20	0.85 >=0.20
0.56 >=0.20	0.22 >=0.20
0.91 >=0.20	0.7 >=0.20
0.99 >=0.20	0.38 >=0.20
0.13 >=0.20	0.47 >=0.20
0.91 >=0.20	0.36 >=0.20
0.07 >=0.20	0.15 >=0.20
0.12 >=0.20	0.41 >=0.20
1 >=0.20	0.97 >=0.20
0.72 >=0.20	0.51 >=0.20
0.93 >=0.20	0.24 >=0.20
0.48 >=0.20	0.53 >=0.20
0.84 >=0.20	0.89 >=0.20
0.95 >=0.20	0.99 >=0.20
0.98 >=0.20	1 >=0.20
0.95 >=0.20	0.96 >=0.20
0.75 >=0.20	0.76 >=0.20
0.98 >=0.20	0.99 >=0.20
0.79 >=0.20	0.7 >=0.20
0.45 >=0.20	0.22 >=0.20
0.43 >=0.20	0.34 >=0.20
0.57 >=0.20	0.15 >=0.20
0.88 >=0.20	0.4 >=0.20
0.81 >=0.20	0.95 >=0.20
0.97 >=0.20	0.22 >=0.20
0.08 >=0.20	0.34 >=0.20
0.85 >=0.20	0.74 >=0.20
0.99 >=0.20	0.66 >=0.20
0.95 >=0.20	0.56 >=0.20
0.95 >=0.20	0.97 >=0.20
0.89 >=0.20	0.7 >=0.20
0.98 >=0.20	0.74 >=0.20
1 >=0.20	0.83 >=0.20
0.99 >=0.20	0.59 >=0.20

0.97 >=0.20	0.27 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.92 >=0.20
0.04 >=0.20	0.41 >=0.20
0.72 >=0.20	0.86 >=0.20
0.7 >=0.20	0.91 >=0.20
0.7 >=0.20	0.91 >=0.20
0.2 >=0.20	0.6 >=0.20
0.39 >=0.20	0.44 >=0.20
0.49 >=0.20	0.09 >=0.20
0.07 >=0.20	0.66 >=0.20
0.59 >=0.20	0.69 >=0.20
0.19 >=0.20	0.26 >=0.20
0.3 >=0.20	0.4 >=0.20
0.04 >=0.20	0.68 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
0.97 >=0.20	0.94 >=0.20
0.21 >=0.20	0.75 >=0.20
0.21 >=0.20	0.43 >=0.20
0.87 >=0.20	0.54 >=0.20
0.41 >=0.20	0.26 >=0.20
0.8 >=0.20	0.99 >=0.20
0.99 >=0.20	0.6 >=0.20
0.79 >=0.20	0.9 >=0.20
0.36 >=0.20	0.46 >=0.20
0.43 >=0.20	0.76 >=0.20
0.1 >=0.20	0.52 >=0.20
0.83 >=0.20	0.98 >=0.20
0.94 >=0.20	0.92 >=0.20
0.94 >=0.20	0.89 >=0.20
1 >=0.20	0.94 >=0.20
0.29 >=0.20	0.96 >=0.20
0.82 >=0.20	0.96 >=0.20
0.46 >=0.20	0.2 >=0.20
0.95 >=0.20	0.33 >=0.20
0.95 >=0.20	0.33 >=0.20
0.95 >=0.20	0.33 >=0.20
0.29 >=0.20	0.99 >=0.20
0.28 >=0.20	0.35 >=0.20
0.6 >=0.20	0.11 >=0.20
0.99 >=0.20	0.83 >=0.20
0.99 >=0.20	1 >=0.20
0.37 >=0.20	0.34 >=0.20
0.08 >=0.20	0.97 >=0.20
0.36 >=0.20	0.72 >=0.20
0.86 >=0.20	0.58 >=0.20

0.98 >=0.20	0.89 >=0.20
0.47 >=0.20	0.53 >=0.20
0.5 >=0.20	0.8 >=0.20
0.97 >=0.20	1 >=0.20
0.38 >=0.20	0.38 >=0.20
0.21 >=0.20	0.65 >=0.20
0.23 >=0.20	0.57 >=0.20
0.04 >=0.20	0.18 >=0.20
0.06 >=0.20	0.19 >=0.20
0.11 >=0.20	0.37 >=0.20
0.1 >=0.20	0.81 >=0.20
0.05 >=0.20	0.17 >=0.20
0.47 >=0.20	0.24 >=0.20
0.08 >=0.20	0.39 >=0.20
0.11 >=0.20	0.33 >=0.20
0.05 >=0.20	0.3 >=0.20
0.16 >=0.20	0.48 >=0.20
0.53 >=0.20	0.06 >=0.20
0.27 >=0.20	0.49 >=0.20
0.71 >=0.20	0.73 >=0.20
1 >=0.20	0.83 >=0.20
0.76 >=0.20	0.86 >=0.20
1 >=0.20	0.94 >=0.20
0.39 >=0.20	0.48 >=0.20
0.97 >=0.20	0.47 >=0.20
0.67 >=0.20	0.29 >=0.20
0.28 >=0.20	0.13 >=0.20
0.06 >=0.20	0.07 >=0.20
0.97 >=0.20	0.26 >=0.20
0.64 >=0.20	0.95 >=0.20
0.94 >=0.20	0.54 >=0.20
0.8 >=0.20	0.09 >=0.20
0.07 >=0.20	0.12 >=0.20
0.97 >=0.20	0.9 >=0.20
0.93 >=0.20	0.94 >=0.20
1 >=0.20	0.75 >=0.20
1 >=0.20	0.91 >=0.20
0.66 >=0.20	0.23 >=0.20
0.51 >=0.20	0.52 >=0.20
0.99 >=0.20	0.89 >=0.20
0.45 >=0.20	0.23 >=0.20
0.76 >=0.20	0.54 >=0.20
0.16 >=0.20	0.38 >=0.20
0.08 >=0.20	0.3 >=0.20
0.38 >=0.20	0.7 >=0.20
0.57 >=0.20	0.67 >=0.20
0.93 >=0.20	0.99 >=0.20

0.66 >=0.20	0.4 >=0.20
1 >=0.20	0.98 >=0.20
0.14 >=0.20	0.28 >=0.20
0.16 >=0.20	0.3 >=0.20
0.89 >=0.20	0.88 >=0.20
0.8 >=0.20	0.17 >=0.20
0.59 >=0.20	0.1 >=0.20
0.4 >=0.20	0.03 >=0.20
0.29 >=0.20	0.45 >=0.20
0.87 >=0.20	0.99 >=0.20
0.07 >=0.20	0.05 >=0.20
0.78 >=0.20	0.95 >=0.20
0.96 >=0.20	0.75 >=0.20
0.99 >=0.20	0.9 >=0.20
1 >=0.20	0.85 >=0.20
0.94 >=0.20	0.34 >=0.20
1 >=0.20	0.3 >=0.20
0.66 >=0.20	0.64 >=0.20
0.43 >=0.20	0.64 >=0.20
0.05 >=0.20	0.17 >=0.20
0.43 >=0.20	0.36 >=0.20
0.16 >=0.20	0.42 >=0.20
0.46 >=0.20	0.44 >=0.20
0.5 >=0.20	0.46 >=0.20
0.72 >=0.20	0.51 >=0.20
0.55 >=0.20	0.08 >=0.20
0.63 >=0.20	0.19 >=0.20
0.9 >=0.20	0.78 >=0.20
0.47 >=0.20	0.3 >=0.20
0.82 >=0.20	0.66 >=0.20
0.32 >=0.20	0.61 >=0.20
0.39 >=0.20	0.83 >=0.20
0.2 >=0.20	0.1 >=0.20
0.09 >=0.20	0.14 >=0.20
0.32 >=0.20	0.13 >=0.20
0.48 >=0.20	0.78 >=0.20
0.33 >=0.20	0.7 >=0.20
0.41 >=0.20	0.29 >=0.20
0.63 >=0.20	0.93 >=0.20
0.85 >=0.20	0.31 >=0.20
0.49 >=0.20	0.06 >=0.20
0.14 >=0.20	0.07 >=0.20
0.95 >=0.20	0.37 >=0.20
0.9 >=0.20	0.48 >=0.20
0.98 >=0.20	0.94 >=0.20
0.47 >=0.20	0.05 >=0.20
0.63 >=0.20	0.55 >=0.20

0.35 >=0.20	0.13 >=0.20
0.4 >=0.20	0.36 >=0.20
1 >=0.20	0.92 >=0.20
0.99 >=0.20	1 >=0.20
0.58 >=0.20	0.62 >=0.20
0.86 >=0.20	0.97 >=0.20
0.71 >=0.20	0.19 >=0.20
0.49 >=0.20	0.33 >=0.20
1 >=0.20	0.58 >=0.20
0.95 >=0.20	0.95 >=0.20
1 >=0.20	0.7 >=0.20
0.9 >=0.20	0.14 >=0.20
0.7 >=0.20	0.52 >=0.20
0.8 >=0.20	0.92 >=0.20
1 >=0.20	0.64 >=0.20
0.29 >=0.20	0.18 >=0.20
0.62 >=0.20	0.09 >=0.20
0.98 >=0.20	1 >=0.20
0.37 >=0.20	0.63 >=0.20
0.67 >=0.20	0.76 >=0.20
0.98 >=0.20	0.76 >=0.20
0.82 >=0.20	0.98 >=0.20
0.9 >=0.20	0.45 >=0.20
0.69 >=0.20	0.57 >=0.20
0.85 >=0.20	0.9 >=0.20
0.39 >=0.20	0.45 >=0.20
0.79 >=0.20	0.07 >=0.20
0.65 >=0.20	0.04 >=0.20
0.45 >=0.20	0.92 >=0.20
1 >=0.20	0.81 >=0.20
0.41 >=0.20	0.34 >=0.20
0.81 >=0.20	0.42 >=0.20
0.92 >=0.20	0.98 >=0.20
0.89 >=0.20	0.31 >=0.20
0.98 >=0.20	0.94 >=0.20
0.24 >=0.20	0.06 >=0.20
0.32 >=0.20	0.46 >=0.20
0.46 >=0.20	0.06 >=0.20
1 >=0.20	0.96 >=0.20
0.58 >=0.20	0.07 >=0.20
0.21 >=0.20	0.25 >=0.20
0.61 >=0.20	0.55 >=0.20
0.16 >=0.20	0.1 >=0.20
0.93 >=0.20	0.54 >=0.20
0.04 >=0.20	0.15 >=0.20
1 >=0.20	0.95 >=0.20
0.1 >=0.20	0.59 >=0.20

0.36 >=0.20	0.86 >=0.20
0.59 >=0.20	0.17 >=0.20
0.33 >=0.20	0.24 >=0.20
0.4 >=0.20	0.07 >=0.20
0.84 >=0.20	0.88 >=0.20
0.77 >=0.20	0.27 >=0.20
0.99 >=0.20	0.95 >=0.20
0.13 >=0.20	0.08 >=0.20
0.71 >=0.20	0.29 >=0.20
0.95 >=0.20	0.98 >=0.20
0.99 >=0.20	0.44 >=0.20
0.98 >=0.20	0.53 >=0.20
1 >=0.20	0.6 >=0.20
1 >=0.20	0.83 >=0.20
0.62 >=0.20	0.99 >=0.20
0.15 >=0.20	0.26 >=0.20
0.79 >=0.20	0.35 >=0.20
0.29 >=0.20	0.39 >=0.20
1 >=0.20	0.98 >=0.20
0.96 >=0.20	0.69 >=0.20
0.42 >=0.20	0.37 >=0.20
0.59 >=0.20	0.22 >=0.20
0.94 >=0.20	0.44 >=0.20
0.41 >=0.20	0.16 >=0.20
0.99 >=0.20	0.91 >=0.20
0.56 >=0.20	0.06 >=0.20
0.78 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.93 >=0.20	0.95 >=0.20
0.67 >=0.20	0.91 >=0.20
0.84 >=0.20	0.5 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.41 >=0.20	0.81 >=0.20
0.41 >=0.20	0.81 >=0.20
0.81 >=0.20	0.14 >=0.20
0.36 >=0.20	0.82 >=0.20
0.36 >=0.20	0.97 >=0.20
0.77 >=0.20	1 >=0.20
0.64 >=0.20	0.68 >=0.20
0.86 >=0.20	0.29 >=0.20
0.42 >=0.20	0.15 >=0.20
0.23 >=0.20	0.66 >=0.20
0.95 >=0.20	1 >=0.20
0.05 >=0.20	0.18 >=0.20
0.33 >=0.20	0.83 >=0.20

0.57 >=0.20	0.78 >=0.20
0.91 >=0.20	0.85 >=0.20
0.28 >=0.20	0.84 >=0.20
0.79 >=0.20	0.97 >=0.20
0.68 >=0.20	0.98 >=0.20
0.54 >=0.20	0.85 >=0.20
0.54 >=0.20	0.85 >=0.20
0.47 >=0.20	0.93 >=0.20
0.81 >=0.20	0.98 >=0.20
0.62 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.96 >=0.20
0.9 >=0.20	0.78 >=0.20
1 >=0.20	0.93 >=0.20
0.95 >=0.20	0.57 >=0.20
0.7 >=0.20	0.67 >=0.20
0.86 >=0.20	0.73 >=0.20
0.97 >=0.20	0.6 >=0.20
0.88 >=0.20	0.42 >=0.20
1 >=0.20	0.73 >=0.20
1 >=0.20	0.97 >=0.20
0.98 >=0.20	0.61 >=0.20
0.79 >=0.20	0.98 >=0.20
0.89 >=0.20	0.69 >=0.20
1 >=0.20	0.8 >=0.20
0.25 >=0.20	0.8 >=0.20
0.76 >=0.20	0.66 >=0.20
0.99 >=0.20	0.97 >=0.20
0.73 >=0.20	0.7 >=0.20
0.78 >=0.20	0.92 >=0.20
0.12 >=0.20	0.3 >=0.20
0.05 >=0.20	0.12 >=0.20
0.98 >=0.20	0.95 >=0.20
0.81 >=0.20	0.91 >=0.20
0.62 >=0.20	0.25 >=0.20
0.86 >=0.20	0.51 >=0.20
1 >=0.20	1 >=0.20
0.08 >=0.20	0.23 >=0.20
0.93 >=0.20	0.38 >=0.20
0.94 >=0.20	0.5 >=0.20
0.89 >=0.20	0.54 >=0.20
1 >=0.20	0.85 >=0.20
0.99 >=0.20	0.86 >=0.20
0.84 >=0.20	0.3 >=0.20
0.9 >=0.20	0.73 >=0.20
0.99 >=0.20	0.41 >=0.20
0.62 >=0.20	0.08 >=0.20

1 >=0.20	0.48 >=0.20
0.04 >=0.20	0.23 >=0.20
0.91 >=0.20	1 >=0.20
0.86 >=0.20	0.95 >=0.20
0.22 >=0.20	0.5 >=0.20
0.53 >=0.20	0.81 >=0.20
1 >=0.20	1 >=0.20
0.86 >=0.20	0.98 >=0.20
0.99 >=0.20	0.56 >=0.20
0.19 >=0.20	0.71 >=0.20
0.18 >=0.20	0.27 >=0.20
0.48 >=0.20	0.69 >=0.20
0.31 >=0.20	0.29 >=0.20
0.66 >=0.20	0.97 >=0.20
0.15 >=0.20	0.29 >=0.20
0.99 >=0.20	0.4 >=0.20
0.8 >=0.20	0.92 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
0.58 >=0.20	0.94 >=0.20
0.66 >=0.20	0.88 >=0.20
0.54 >=0.20	0.56 >=0.20
0.5 >=0.20	0.23 >=0.20
0.66 >=0.20	0.95 >=0.20
0.99 >=0.20	0.98 >=0.20
0.97 >=0.20	0.53 >=0.20
1 >=0.20	1 >=0.20
0.49 >=0.20	0.98 >=0.20
0.18 >=0.20	0.97 >=0.20
0.22 >=0.20	0.89 >=0.20
0.07 >=0.20	0.98 >=0.20
0.23 >=0.20	0.86 >=0.20
0.17 >=0.20	0.54 >=0.20
0.32 >=0.20	0.32 >=0.20
0.13 >=0.20	0.22 >=0.20
0.05 >=0.20	0.34 >=0.20
0.95 >=0.20	0.34 >=0.20
0.78 >=0.20	0.37 >=0.20
0.11 >=0.20	0.84 >=0.20
0.97 >=0.20	0.97 >=0.20
0.28 >=0.20	0.85 >=0.20
0.25 >=0.20	0.55 >=0.20
0.22 >=0.20	0.76 >=0.20

0.91 >=0.20	0.33 >=0.20
0.37 >=0.20	0.27 >=0.20
0.24 >=0.20	0.89 >=0.20
0.23 >=0.20	0.85 >=0.20
0.24 >=0.20	0.89 >=0.20
0.21 >=0.20	0.83 >=0.20
0.26 >=0.20	0.68 >=0.20
0.43 >=0.20	0.9 >=0.20
0.24 >=0.20	0.91 >=0.20
0.48 >=0.20	0.96 >=0.20
0.05 >=0.20	0.34 >=0.20
0.3 >=0.20	0.94 >=0.20
0.99 >=0.20	0.99 >=0.20
0.04 >=0.20	0.98 >=0.20
0.31 >=0.20	0.78 >=0.20
0.29 >=0.20	0.99 >=0.20
0.06 >=0.20	0.97 >=0.20
0.23 >=0.20	0.97 >=0.20
0.78 >=0.20	1 >=0.20
0.78 >=0.20	1 >=0.20
0.41 >=0.20	0.99 >=0.20
0.88 >=0.20	0.85 >=0.20
0.36 >=0.20	1 >=0.20
0.44 >=0.20	1 >=0.20
0.14 >=0.20	0.85 >=0.20
0.94 >=0.20	0.95 >=0.20
0.5 >=0.20	0.21 >=0.20
0.74 >=0.20	0.67 >=0.20
0.41 >=0.20	0.86 >=0.20
0.19 >=0.20	0.26 >=0.20
0.72 >=0.20	0.2 >=0.20
0.16 >=0.20	0.89 >=0.20
0.93 >=0.20	0.61 >=0.20
0.52 >=0.20	0.67 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	0.96 >=0.20
0.9 >=0.20	0.89 >=0.20
0.12 >=0.20	0.26 >=0.20
0.09 >=0.20	0.58 >=0.20
0.48 >=0.20	0.31 >=0.20
0.8 >=0.20	0.37 >=0.20
0.99 >=0.20	0.88 >=0.20
0.95 >=0.20	0.72 >=0.20
0.91 >=0.20	0.64 >=0.20
0.07 >=0.20	0.53 >=0.20
0.62 >=0.20	0.92 >=0.20
1 >=0.20	0.99 >=0.20

0.62	>=0.20	0.73	>=0.20
1	>=0.20	1	>=0.20
0.38	>=0.20	0.91	>=0.20
0.92	>=0.20	1	>=0.20
0.91	>=0.20	0.98	>=0.20
0.13	>=0.20	0.98	>=0.20
0.12	>=0.20	0.98	>=0.20
0.48	>=0.20	0.92	>=0.20
0.64	>=0.20	0.31	>=0.20
0.68	>=0.20	0.94	>=0.20
0.92	>=0.20	0.52	>=0.20
1	>=0.20	1	>=0.20
0.35	>=0.20	0.99	>=0.20
1	>=0.20	0.99	>=0.20
0.26	>=0.20	0.04	>=0.20
0.29	>=0.20	0.26	>=0.20
0.13	>=0.20	0.21	>=0.20
0.28	>=0.20	0.37	>=0.20
0.55	>=0.20	0.83	>=0.20
0.65	>=0.20	0.98	>=0.20
0.4	>=0.20	1	>=0.20
0.15	>=0.20	0.15	>=0.20
0.84	>=0.20	0.43	>=0.20
0.19	>=0.20	0.16	>=0.20
0.31	>=0.20	0.34	>=0.20
0.92	>=0.20	1	>=0.20
0.67	>=0.20	1	>=0.20
0.84	>=0.20	0.29	>=0.20
0.99	>=0.20	0.48	>=0.20
0.27	>=0.20	0.45	>=0.20
0.97	>=0.20	0.78	>=0.20
0.99	>=0.20	0.43	>=0.20
0.86	>=0.20	0.15	>=0.20
0.91	>=0.20	0.65	>=0.20
0.99	>=0.20	0.59	>=0.20
0.81	>=0.20	0.27	>=0.20
0.58	>=0.20	0.98	>=0.20
0.98	>=0.20	1	>=0.20
0.95	>=0.20	0.42	>=0.20
0.92	>=0.20	0.99	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	0.99	>=0.20
0.97	>=0.20	0.18	>=0.20
0.86	>=0.20	0.58	>=0.20
0.85	>=0.20	0.48	>=0.20
0.85	>=0.20	0.19	>=0.20
0.61	>=0.20	0.32	>=0.20

0.98 >=0.20	0.39 >=0.20
0.94 >=0.20	0.65 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.98 >=0.20
0.09 >=0.20	0.31 >=0.20
0.3 >=0.20	0.16 >=0.20
0.63 >=0.20	0.35 >=0.20
0.51 >=0.20	0.26 >=0.20
0.82 >=0.20	0.89 >=0.20
0.57 >=0.20	0.24 >=0.20
0.13 >=0.20	0.42 >=0.20
0.6 >=0.20	0.38 >=0.20
0.9 >=0.20	0.87 >=0.20
0.59 >=0.20	0.2 >=0.20
0.95 >=0.20	0.56 >=0.20
0.88 >=0.20	0.48 >=0.20
0.88 >=0.20	0.7 >=0.20
0.56 >=0.20	0.97 >=0.20
0.04 >=0.20	0.1 >=0.20
0.32 >=0.20	0.57 >=0.20
0.47 >=0.20	0.95 >=0.20
0.8 >=0.20	0.73 >=0.20
0.85 >=0.20	0.55 >=0.20
0.33 >=0.20	0.15 >=0.20
0.06 >=0.20	0.08 >=0.20
0.85 >=0.20	0.14 >=0.20
0.77 >=0.20	0.97 >=0.20
0.97 >=0.20	1 >=0.20
0.5 >=0.20	0.98 >=0.20
0.07 >=0.20	0.39 >=0.20
0.95 >=0.20	0.69 >=0.20
0.47 >=0.20	0.59 >=0.20
0.14 >=0.20	0.07 >=0.20
0.06 >=0.20	0.04 >=0.20
0.28 >=0.20	0.83 >=0.20
0.24 >=0.20	0.7 >=0.20
0.38 >=0.20	0.67 >=0.20
0.22 >=0.20	0.72 >=0.20
0.17 >=0.20	0.23 >=0.20
0.09 >=0.20	0.23 >=0.20
0.43 >=0.20	0.58 >=0.20
0.42 >=0.20	0.33 >=0.20
0.47 >=0.20	0.87 >=0.20
0.74 >=0.20	0.95 >=0.20
0.55 >=0.20	0.92 >=0.20
0.55 >=0.20	0.65 >=0.20
0.77 >=0.20	0.9 >=0.20

0.67 >=0.20	0.85 >=0.20
0.19 >=0.20	0.47 >=0.20
0.39 >=0.20	0.57 >=0.20
0.36 >=0.20	0.69 >=0.20
0.35 >=0.20	0.73 >=0.20
0.16 >=0.20	0.42 >=0.20
0.22 >=0.20	0.17 >=0.20
0.44 >=0.20	0.83 >=0.20
0.09 >=0.20	0.16 >=0.20
0.86 >=0.20	0.75 >=0.20
0.84 >=0.20	0.83 >=0.20
0.06 >=0.20	0.32 >=0.20
0.17 >=0.20	0.37 >=0.20
0.94 >=0.20	0.98 >=0.20
1 >=0.20	0.62 >=0.20
0.44 >=0.20	0.22 >=0.20
0.38 >=0.20	0.8 >=0.20
0.45 >=0.20	0.74 >=0.20
0.15 >=0.20	0.97 >=0.20
0.55 >=0.20	0.83 >=0.20
0.95 >=0.20	0.66 >=0.20
0.19 >=0.20	0.8 >=0.20
0.41 >=0.20	0.66 >=0.20
0.27 >=0.20	0.89 >=0.20
0.46 >=0.20	0.04 >=0.20
0.97 >=0.20	0.84 >=0.20
0.99 >=0.20	1 >=0.20
0.94 >=0.20	0.79 >=0.20
0.52 >=0.20	0.5 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.79 >=0.20
0.68 >=0.20	0.07 >=0.20
0.9 >=0.20	0.99 >=0.20
0.99 >=0.20	0.95 >=0.20
0.74 >=0.20	0.71 >=0.20
0.89 >=0.20	0.99 >=0.20
0.78 >=0.20	0.77 >=0.20
0.92 >=0.20	0.74 >=0.20
0.63 >=0.20	0.91 >=0.20
0.86 >=0.20	0.99 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	0.81 >=0.20
0.93 >=0.20	0.36 >=0.20
1 >=0.20	0.84 >=0.20
0.97 >=0.20	0.36 >=0.20
0.94 >=0.20	0.98 >=0.20
1 >=0.20	0.98 >=0.20

1 >=0.20	0.99 >=0.20
1 >=0.20	0.85 >=0.20
0.85 >=0.20	0.86 >=0.20
0.95 >=0.20	0.99 >=0.20
0.79 >=0.20	0.58 >=0.20
0.82 >=0.20	0.87 >=0.20
0.1 >=0.20	0.4 >=0.20
0.86 >=0.20	0.36 >=0.20
0.31 >=0.20	0.03 >=0.20
0.17 >=0.20	0.63 >=0.20
0.71 >=0.20	0.25 >=0.20
0.6 >=0.20	0.22 >=0.20
0.68 >=0.20	0.17 >=0.20
0.08 >=0.20	0.06 >=0.20
0.78 >=0.20	0.92 >=0.20
0.65 >=0.20	0.9 >=0.20
0.08 >=0.20	0.75 >=0.20
0.05 >=0.20	0.05 >=0.20
0.35 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.9 >=0.20	0.27 >=0.20
0.83 >=0.20	0.21 >=0.20
0.27 >=0.20	0.05 >=0.20
0.74 >=0.20	0.16 >=0.20
0.96 >=0.20	0.92 >=0.20
1 >=0.20	0.93 >=0.20
0.36 >=0.20	0.13 >=0.20
0.12 >=0.20	0.04 >=0.20
0.96 >=0.20	0.69 >=0.20
0.47 >=0.20	0.26 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.92 >=0.20
0.47 >=0.20	0.16 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.73 >=0.20
0.98 >=0.20	0.61 >=0.20
0.88 >=0.20	0.82 >=0.20
0.2 >=0.20	0.11 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.29 >=0.20
0.06 >=0.20	0.22 >=0.20
0.42 >=0.20	0.2 >=0.20
0.82 >=0.20	0.87 >=0.20
0.17 >=0.20	0.52 >=0.20
0.82 >=0.20	0.33 >=0.20

0.97 >=0.20	0.48 >=0.20
0.7 >=0.20	0.89 >=0.20
0.99 >=0.20	1 >=0.20
0.8 >=0.20	0.85 >=0.20
0.51 >=0.20	0.75 >=0.20
0.96 >=0.20	0.98 >=0.20
0.96 >=0.20	0.98 >=0.20
0.89 >=0.20	0.5 >=0.20
0.57 >=0.20	0.45 >=0.20
0.54 >=0.20	0.97 >=0.20
0.95 >=0.20	0.7 >=0.20
0.99 >=0.20	1 >=0.20
0.99 >=0.20	0.39 >=0.20
0.36 >=0.20	0.46 >=0.20
0.96 >=0.20	0.93 >=0.20
0.08 >=0.20	0.19 >=0.20
0.29 >=0.20	0.73 >=0.20
0.97 >=0.20	0.97 >=0.20
0.12 >=0.20	0.87 >=0.20
0.05 >=0.20	0.03 >=0.20
0.5 >=0.20	0.41 >=0.20
1 >=0.20	0.96 >=0.20
0.6 >=0.20	0.34 >=0.20
0.07 >=0.20	0.47 >=0.20
0.85 >=0.20	0.97 >=0.20
0.07 >=0.20	0.54 >=0.20
0.34 >=0.20	1 >=0.20
0.97 >=0.20	0.83 >=0.20
0.95 >=0.20	0.97 >=0.20
0.88 >=0.20	0.43 >=0.20
0.06 >=0.20	0.62 >=0.20
0.42 >=0.20	0.47 >=0.20
0.42 >=0.20	0.96 >=0.20
0.2 >=0.20	0.19 >=0.20
0.23 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.03 >=0.20
0.17 >=0.20	0.44 >=0.20
0.99 >=0.20	0.99 >=0.20
0.21 >=0.20	0.63 >=0.20
0.36 >=0.20	0.54 >=0.20
1 >=0.20	0.97 >=0.20
0.48 >=0.20	0.51 >=0.20
0.12 >=0.20	0.2 >=0.20
0.45 >=0.20	0.98 >=0.20
0.41 >=0.20	0.43 >=0.20
0.99 >=0.20	0.81 >=0.20

0.26 >=0.20	0.82 >=0.20
0.88 >=0.20	1 >=0.20
0.45 >=0.20	0.79 >=0.20
0.82 >=0.20	0.96 >=0.20
0.45 >=0.20	0.79 >=0.20
0.1 >=0.20	0.15 >=0.20
0.19 >=0.20	0.29 >=0.20
0.81 >=0.20	0.98 >=0.20
0.15 >=0.20	0.35 >=0.20
0.09 >=0.20	0.64 >=0.20
0.47 >=0.20	0.82 >=0.20
0.96 >=0.20	0.93 >=0.20
0.83 >=0.20	0.86 >=0.20
0.9 >=0.20	0.54 >=0.20
0.08 >=0.20	0.07 >=0.20
0.82 >=0.20	0.96 >=0.20
0.18 >=0.20	0.65 >=0.20
0.3 >=0.20	0.5 >=0.20
0.97 >=0.20	0.97 >=0.20
0.05 >=0.20	0.03 >=0.20
0.7 >=0.20	0.32 >=0.20
0.27 >=0.20	0.62 >=0.20
0.52 >=0.20	0.89 >=0.20
0.63 >=0.20	0.69 >=0.20
0.69 >=0.20	0.7 >=0.20
0.51 >=0.20	0.18 >=0.20
0.6 >=0.20	0.82 >=0.20
0.25 >=0.20	0.19 >=0.20
0.24 >=0.20	0.31 >=0.20
0.82 >=0.20	0.62 >=0.20
1 >=0.20	0.9 >=0.20
0.38 >=0.20	0.85 >=0.20
0.47 >=0.20	0.82 >=0.20
0.06 >=0.20	0.24 >=0.20
0.19 >=0.20	0.43 >=0.20
0.85 >=0.20	0.97 >=0.20
1 >=0.20	0.91 >=0.20
0.98 >=0.20	0.61 >=0.20
0.47 >=0.20	0.82 >=0.20
0.13 >=0.20	0.16 >=0.20
0.98 >=0.20	0.72 >=0.20
0.37 >=0.20	0.38 >=0.20
0.98 >=0.20	0.84 >=0.20
0.32 >=0.20	0.31 >=0.20
0.36 >=0.20	1 >=0.20
0.75 >=0.20	0.9 >=0.20
0.18 >=0.20	0.78 >=0.20

0.26 >=0.20	0.82 >=0.20
0.15 >=0.20	0.42 >=0.20
0.68 >=0.20	0.46 >=0.20
0.76 >=0.20	0.18 >=0.20
0.95 >=0.20	0.92 >=0.20
0.91 >=0.20	0.98 >=0.20
0.08 >=0.20	0.07 >=0.20
0.93 >=0.20	0.07 >=0.20
0.51 >=0.20	0.94 >=0.20
0.18 >=0.20	0.78 >=0.20
0.14 >=0.20	0.72 >=0.20
0.11 >=0.20	0.75 >=0.20
0.51 >=0.20	0.94 >=0.20
0.24 >=0.20	0.87 >=0.20
0.18 >=0.20	0.78 >=0.20
0.04 >=0.20	0.05 >=0.20
0.6 >=0.20	0.89 >=0.20
0.23 >=0.20	0.88 >=0.20
0.29 >=0.20	0.9 >=0.20
0.87 >=0.20	0.62 >=0.20
0.46 >=0.20	0.59 >=0.20
0.31 >=0.20	0.93 >=0.20
0.95 >=0.20	0.99 >=0.20
0.04 >=0.20	0.65 >=0.20
0.07 >=0.20	0.03 >=0.20
0.7 >=0.20	0.64 >=0.20
0.38 >=0.20	0.94 >=0.20
0.38 >=0.20	0.94 >=0.20
0.51 >=0.20	0.95 >=0.20
0.44 >=0.20	0.94 >=0.20
0.38 >=0.20	0.94 >=0.20
0.38 >=0.20	0.94 >=0.20
0.49 >=0.20	0.96 >=0.20
0.8 >=0.20	0.73 >=0.20
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0.84 >=0.20	0.78 >=0.20
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0.98 >=0.20	0.82 >=0.20
0.98 >=0.20	0.84 >=0.20
0.98 >=0.20	0.84 >=0.20
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0.77 >=0.20	0.79 >=0.20
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0.99 >=0.20	1 >=0.20
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0.67 >=0.20	1 >=0.20
0.95 >=0.20	0.98 >=0.20
0.96 >=0.20	0.58 >=0.20
0.77 >=0.20	0.94 >=0.20
0.7 >=0.20	0.3 >=0.20
0.61 >=0.20	0.54 >=0.20
0.31 >=0.20	0.15 >=0.20
0.57 >=0.20	0.81 >=0.20
0.13 >=0.20	0.5 >=0.20
0.99 >=0.20	1 >=0.20
0.96 >=0.20	0.96 >=0.20
0.19 >=0.20	0.62 >=0.20
0.68 >=0.20	0.19 >=0.20
0.79 >=0.20	0.64 >=0.20
0.5 >=0.20	0.68 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	0.83 >=0.20
0.94 >=0.20	0.83 >=0.20
0.76 >=0.20	0.5 >=0.20
0.09 >=0.20	0.63 >=0.20
0.56 >=0.20	0.32 >=0.20
0.97 >=0.20	0.3 >=0.20
0.64 >=0.20	0.08 >=0.20
0.07 >=0.20	0.14 >=0.20
0.34 >=0.20	0.65 >=0.20
0.76 >=0.20	0.31 >=0.20
0.96 >=0.20	0.93 >=0.20
0.48 >=0.20	0.64 >=0.20
0.94 >=0.20	0.72 >=0.20
0.29 >=0.20	0.05 >=0.20
0.73 >=0.20	0.2 >=0.20
0.53 >=0.20	0.38 >=0.20
0.99 >=0.20	0.88 >=0.20
0.67 >=0.20	0.51 >=0.20
0.85 >=0.20	0.04 >=0.20
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0.99 >=0.20	0.95 >=0.20
1 >=0.20	0.88 >=0.20
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0.89 >=0.20	0.98 >=0.20
0.07 >=0.20	0.54 >=0.20
0.12 >=0.20	0.04 >=0.20
0.33 >=0.20	0.31 >=0.20
0.61 >=0.20	0.33 >=0.20
0.61 >=0.20	0.32 >=0.20
0.41 >=0.20	0.59 >=0.20
0.6 >=0.20	0.68 >=0.20
0.17 >=0.20	0.74 >=0.20
0.87 >=0.20	0.98 >=0.20
0.97 >=0.20	0.33 >=0.20
0.58 >=0.20	0.27 >=0.20
0.98 >=0.20	0.87 >=0.20
0.17 >=0.20	0.72 >=0.20
0.72 >=0.20	0.93 >=0.20
0.24 >=0.20	0.57 >=0.20
0.43 >=0.20	1 >=0.20
0.07 >=0.20	0.13 >=0.20
0.48 >=0.20	0.32 >=0.20
0.96 >=0.20	0.78 >=0.20
0.2 >=0.20	0.1 >=0.20
0.96 >=0.20	0.88 >=0.20
0.36 >=0.20	0.62 >=0.20
0.83 >=0.20	0.63 >=0.20
0.88 >=0.20	0.66 >=0.20
0.49 >=0.20	1 >=0.20
1 >=0.20	0.91 >=0.20
0.7 >=0.20	1 >=0.20
0.82 >=0.20	0.99 >=0.20
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0.93 >=0.20	0.96 >=0.20
0.61 >=0.20	0.97 >=0.20
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1 >=0.20	0.89 >=0.20
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0.58 >=0.20	0.24 >=0.20
0.92 >=0.20	0.86 >=0.20
0.14 >=0.20	0.19 >=0.20
0.85 >=0.20	0.55 >=0.20
0.84 >=0.20	0.98 >=0.20
0.5 >=0.20	0.64 >=0.20
0.38 >=0.20	0.45 >=0.20
0.84 >=0.20	0.54 >=0.20
1 >=0.20	1 >=0.20
0.54 >=0.20	0.47 >=0.20
0.81 >=0.20	0.69 >=0.20
0.18 >=0.20	0.23 >=0.20
0.16 >=0.20	0.31 >=0.20
0.99 >=0.20	0.86 >=0.20
0.82 >=0.20	0.99 >=0.20
0.79 >=0.20	0.97 >=0.20
0.96 >=0.20	0.98 >=0.20
0.15 >=0.20	0.54 >=0.20
0.73 >=0.20	0.95 >=0.20
0.66 >=0.20	0.98 >=0.20
0.53 >=0.20	0.71 >=0.20
0.98 >=0.20	0.68 >=0.20
0.91 >=0.20	0.29 >=0.20
0.23 >=0.20	0.91 >=0.20
0.13 >=0.20	0.96 >=0.20
0.43 >=0.20	0.99 >=0.20
0.16 >=0.20	0.98 >=0.20
0.15 >=0.20	0.97 >=0.20
0.19 >=0.20	0.95 >=0.20
0.05 >=0.20	0.89 >=0.20
0.34 >=0.20	0.99 >=0.20
0.04 >=0.20	0.53 >=0.20
0.11 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.82 >=0.20	0.68 >=0.20
0.89 >=0.20	0.54 >=0.20
0.7 >=0.20	0.97 >=0.20
0.88 >=0.20	0.63 >=0.20
0.8 >=0.20	0.81 >=0.20
0.7 >=0.20	0.97 >=0.20
0.99 >=0.20	0.55 >=0.20
0.96 >=0.20	0.17 >=0.20

0.87 >=0.20	0.05 >=0.20
0.95 >=0.20	0.73 >=0.20
1 >=0.20	0.99 >=0.20
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0.99 >=0.20	1 >=0.20
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0.88 >=0.20	0.96 >=0.20
0.58 >=0.20	0.25 >=0.20
0.46 >=0.20	0.17 >=0.20
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0.11 >=0.20	0.05 >=0.20
0.09 >=0.20	0.24 >=0.20
0.04 >=0.20	0.27 >=0.20
0.18 >=0.20	0.21 >=0.20
0.87 >=0.20	0.98 >=0.20
0.99 >=0.20	0.99 >=0.20
0.99 >=0.20	1 >=0.20
0.58 >=0.20	0.53 >=0.20
0.43 >=0.20	0.86 >=0.20
0.58 >=0.20	0.91 >=0.20
0.22 >=0.20	0.03 >=0.20
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0.53 >=0.20	0.07 >=0.20
0.18 >=0.20	0.11 >=0.20
0.78 >=0.20	0.69 >=0.20
0.52 >=0.20	0.91 >=0.20
0.93 >=0.20	0.94 >=0.20
0.06 >=0.20	0.41 >=0.20
1 >=0.20	0.71 >=0.20
0.56 >=0.20	0.34 >=0.20
0.93 >=0.20	0.18 >=0.20
0.87 >=0.20	0.77 >=0.20
0.88 >=0.20	0.49 >=0.20
0.07 >=0.20	0.07 >=0.20
0.28 >=0.20	0.08 >=0.20
0.04 >=0.20	0.31 >=0.20
0.94 >=0.20	1 >=0.20
0.12 >=0.20	0.93 >=0.20
0.29 >=0.20	0.94 >=0.20
0.13 >=0.20	0.68 >=0.20
0.82 >=0.20	0.91 >=0.20
0.91 >=0.20	0.46 >=0.20
0.73 >=0.20	0.97 >=0.20
0.08 >=0.20	0.36 >=0.20
0.87 >=0.20	0.33 >=0.20

1	>=0.20	1	>=0.20
0.05	>=0.20	0.46	>=0.20
0.05	>=0.20	0.46	>=0.20
0.55	>=0.20	0.95	>=0.20
0.06	>=0.20	0.17	>=0.20
0.17	>=0.20	0.21	>=0.20
0.11	>=0.20	0.12	>=0.20
0.61	>=0.20	0.99	>=0.20
0.53	>=0.20	0.79	>=0.20
0.61	>=0.20	0.96	>=0.20
0.84	>=0.20	0.88	>=0.20
0.04	>=0.20	0.28	>=0.20
0.71	>=0.20	0.98	>=0.20
0.06	>=0.20	0.39	>=0.20
0.91	>=0.20	0.95	>=0.20
0.97	>=0.20	0.96	>=0.20
0.7	>=0.20	0.29	>=0.20
0.92	>=0.20	0.63	>=0.20
0.96	>=0.20	0.48	>=0.20
0.33	>=0.20	0.95	>=0.20
0.9	>=0.20	0.51	>=0.20
0.24	>=0.20	0.4	>=0.20
0.28	>=0.20	0.89	>=0.20
0.85	>=0.20	1	>=0.20
0.46	>=0.20	0.85	>=0.20
1	>=0.20	0.94	>=0.20
0.21	>=0.20	0.08	>=0.20
0.6	>=0.20	0.35	>=0.20
0.11	>=0.20	0.05	>=0.20
0.11	>=0.20	0.05	>=0.20
0.11	>=0.20	0.05	>=0.20
0.36	>=0.20	0.24	>=0.20
0.11	>=0.20	0.05	>=0.20
0.2	>=0.20	0.1	>=0.20
0.1	>=0.20	0.05	>=0.20
0.4	>=0.20	0.06	>=0.20
0.14	>=0.20	0.11	>=0.20
0.11	>=0.20	0.05	>=0.20
0.15	>=0.20	0.11	>=0.20
0.11	>=0.20	0.05	>=0.20
0.24	>=0.20	0.15	>=0.20
1	>=0.20	0.84	>=0.20
0.68	>=0.20	0.91	>=0.20
1	>=0.20	0.96	>=0.20
0.06	>=0.20	0.03	>=0.20
0.84	>=0.20	0.98	>=0.20
1	>=0.20	0.98	>=0.20

1 >=0.20	0.94 >=0.20
0.95 >=0.20	0.05 >=0.20
0.8 >=0.20	0.34 >=0.20
1 >=0.20	0.94 >=0.20
0.98 >=0.20	0.92 >=0.20
0.48 >=0.20	0.51 >=0.20
0.99 >=0.20	0.99 >=0.20
0.6 >=0.20	0.52 >=0.20
1 >=0.20	0.98 >=0.20
0.99 >=0.20	0.57 >=0.20
0.18 >=0.20	0.32 >=0.20
0.93 >=0.20	0.75 >=0.20
0.94 >=0.20	0.91 >=0.20
0.86 >=0.20	0.27 >=0.20
0.27 >=0.20	0.65 >=0.20
0.92 >=0.20	0.16 >=0.20
0.86 >=0.20	0.92 >=0.20
0.97 >=0.20	0.8 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.85 >=0.20
0.07 >=0.20	0.03 >=0.20
1 >=0.20	0.78 >=0.20
0.1 >=0.20	0.83 >=0.20
0.71 >=0.20	0.93 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.99 >=0.20
0.88 >=0.20	1 >=0.20
0.57 >=0.20	0.42 >=0.20
0.31 >=0.20	0.22 >=0.20
0.34 >=0.20	0.18 >=0.20
0.08 >=0.20	0.12 >=0.20
0.16 >=0.20	0.72 >=0.20
0.85 >=0.20	0.25 >=0.20
0.79 >=0.20	0.87 >=0.20
0.05 >=0.20	0.23 >=0.20
0.98 >=0.20	0.59 >=0.20
0.98 >=0.20	0.86 >=0.20
1 >=0.20	0.79 >=0.20
1 >=0.20	0.8 >=0.20
0.18 >=0.20	0.27 >=0.20
0.4 >=0.20	0.14 >=0.20
0.97 >=0.20	0.68 >=0.20
0.95 >=0.20	0.47 >=0.20
0.04 >=0.20	0.26 >=0.20
1 >=0.20	0.99 >=0.20

0.12 >=0.20	0.75 >=0.20
0.15 >=0.20	0.16 >=0.20
0.88 >=0.20	0.79 >=0.20
0.18 >=0.20	0.13 >=0.20
0.38 >=0.20	0.12 >=0.20
0.3 >=0.20	0.07 >=0.20
0.98 >=0.20	0.95 >=0.20
0.95 >=0.20	0.92 >=0.20
0.97 >=0.20	0.89 >=0.20
0.96 >=0.20	0.94 >=0.20
0.84 >=0.20	0.82 >=0.20
0.89 >=0.20	0.84 >=0.20
0.75 >=0.20	0.71 >=0.20
0.86 >=0.20	0.92 >=0.20
0.78 >=0.20	0.7 >=0.20
0.84 >=0.20	0.82 >=0.20
0.83 >=0.20	0.89 >=0.20
0.78 >=0.20	0.64 >=0.20
0.8 >=0.20	0.8 >=0.20
0.77 >=0.20	0.97 >=0.20
0.99 >=0.20	0.84 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.97 >=0.20
0.92 >=0.20	0.88 >=0.20
0.75 >=0.20	0.76 >=0.20
1 >=0.20	0.6 >=0.20
0.75 >=0.20	0.76 >=0.20
0.99 >=0.20	0.82 >=0.20
0.93 >=0.20	0.56 >=0.20
1 >=0.20	0.86 >=0.20
0.68 >=0.20	0.56 >=0.20
0.44 >=0.20	0.4 >=0.20
0.34 >=0.20	0.84 >=0.20
0.46 >=0.20	1 >=0.20
0.29 >=0.20	0.85 >=0.20
0.63 >=0.20	0.96 >=0.20
0.24 >=0.20	0.36 >=0.20
0.42 >=0.20	0.07 >=0.20
0.37 >=0.20	0.33 >=0.20
0.96 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
0.32 >=0.20	0.83 >=0.20
0.3 >=0.20	0.5 >=0.20
0.08 >=0.20	0.4 >=0.20
0.19 >=0.20	0.75 >=0.20
0.19 >=0.20	0.75 >=0.20
0.19 >=0.20	0.75 >=0.20

1 >=0.20	0.51 >=0.20
0.95 >=0.20	0.45 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.87 >=0.20	0.95 >=0.20
1 >=0.20	1 >=0.20
0.75 >=0.20	0.99 >=0.20
0.99 >=0.20	1 >=0.20
0.45 >=0.20	0.07 >=0.20
0.87 >=0.20	0.93 >=0.20
0.74 >=0.20	0.84 >=0.20
0.99 >=0.20	1 >=0.20
0.96 >=0.20	1 >=0.20
0.65 >=0.20	0.95 >=0.20
0.52 >=0.20	0.94 >=0.20
0.53 >=0.20	0.19 >=0.20
0.33 >=0.20	0.05 >=0.20
0.66 >=0.20	0.83 >=0.20
0.27 >=0.20	0.35 >=0.20
0.15 >=0.20	0.39 >=0.20
0.95 >=0.20	1 >=0.20
0.92 >=0.20	0.83 >=0.20
0.98 >=0.20	0.73 >=0.20
0.1 >=0.20	0.3 >=0.20
0.61 >=0.20	0.91 >=0.20
0.94 >=0.20	0.98 >=0.20
0.73 >=0.20	0.32 >=0.20
0.6 >=0.20	0.34 >=0.20
0.82 >=0.20	0.24 >=0.20
0.97 >=0.20	0.49 >=0.20
0.46 >=0.20	0.39 >=0.20
0.95 >=0.20	0.39 >=0.20
0.87 >=0.20	0.18 >=0.20
0.75 >=0.20	0.39 >=0.20
1 >=0.20	1 >=0.20
0.67 >=0.20	0.52 >=0.20
0.47 >=0.20	0.35 >=0.20
0.74 >=0.20	0.58 >=0.20
0.82 >=0.20	0.79 >=0.20
0.66 >=0.20	0.31 >=0.20
0.81 >=0.20	0.56 >=0.20
0.96 >=0.20	0.66 >=0.20
0.13 >=0.20	0.63 >=0.20
0.05 >=0.20	0.93 >=0.20
0.2 >=0.20	0.85 >=0.20
0.26 >=0.20	0.95 >=0.20
0.53 >=0.20	0.64 >=0.20

0.97 >=0.20	0.98 >=0.20
0.92 >=0.20	0.99 >=0.20
0.78 >=0.20	0.3 >=0.20
0.32 >=0.20	0.2 >=0.20
0.88 >=0.20	0.79 >=0.20
0.7 >=0.20	0.86 >=0.20
0.9 >=0.20	1 >=0.20
0.48 >=0.20	0.86 >=0.20
0.51 >=0.20	0.32 >=0.20
0.65 >=0.20	0.66 >=0.20
0.95 >=0.20	0.6 >=0.20
0.34 >=0.20	0.31 >=0.20
0.64 >=0.20	0.94 >=0.20
0.21 >=0.20	0.96 >=0.20
0.21 >=0.20	0.98 >=0.20
0.42 >=0.20	0.84 >=0.20
0.85 >=0.20	0.55 >=0.20
0.99 >=0.20	0.99 >=0.20
0.53 >=0.20	0.75 >=0.20
0.87 >=0.20	0.13 >=0.20
0.95 >=0.20	0.41 >=0.20
0.95 >=0.20	0.77 >=0.20
0.04 >=0.20	0.72 >=0.20
0.18 >=0.20	0.36 >=0.20
0.99 >=0.20	0.55 >=0.20
1 >=0.20	0.55 >=0.20
0.99 >=0.20	0.96 >=0.20
0.86 >=0.20	0.5 >=0.20
0.89 >=0.20	0.32 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.48 >=0.20
0.83 >=0.20	0.1 >=0.20
0.99 >=0.20	0.89 >=0.20
0.98 >=0.20	0.91 >=0.20
1 >=0.20	1 >=0.20
0.29 >=0.20	0.17 >=0.20
0.2 >=0.20	0.13 >=0.20
0.24 >=0.20	0.67 >=0.20
0.04 >=0.20	0.35 >=0.20
0.04 >=0.20	0.5 >=0.20
0.05 >=0.20	0.2 >=0.20
0.42 >=0.20	0.1 >=0.20
0.87 >=0.20	0.68 >=0.20
1 >=0.20	1 >=0.20
0.4 >=0.20	0.92 >=0.20
1 >=0.20	1 >=0.20
0.8 >=0.20	0.99 >=0.20

0.08 >=0.20	0.2 >=0.20
0.74 >=0.20	0.67 >=0.20
0.69 >=0.20	0.27 >=0.20
0.36 >=0.20	0.42 >=0.20
0.06 >=0.20	0.07 >=0.20
0.53 >=0.20	0.4 >=0.20
0.28 >=0.20	0.19 >=0.20
0.98 >=0.20	0.88 >=0.20
0.17 >=0.20	0.31 >=0.20
0.82 >=0.20	0.44 >=0.20
0.17 >=0.20	0.13 >=0.20
0.35 >=0.20	0.87 >=0.20
0.13 >=0.20	0.21 >=0.20
0.41 >=0.20	0.14 >=0.20
0.98 >=0.20	0.91 >=0.20
0.16 >=0.20	0.46 >=0.20
0.25 >=0.20	0.53 >=0.20
0.66 >=0.20	0.66 >=0.20
0.58 >=0.20	0.34 >=0.20
0.21 >=0.20	0.29 >=0.20
0.69 >=0.20	0.89 >=0.20
0.7 >=0.20	0.52 >=0.20
0.87 >=0.20	0.43 >=0.20
0.9 >=0.20	0.53 >=0.20
0.98 >=0.20	0.8 >=0.20
0.99 >=0.20	0.71 >=0.20
0.67 >=0.20	0.58 >=0.20
0.76 >=0.20	0.99 >=0.20
0.81 >=0.20	0.72 >=0.20
0.9 >=0.20	0.48 >=0.20
0.31 >=0.20	0.53 >=0.20
0.99 >=0.20	0.87 >=0.20
0.99 >=0.20	0.85 >=0.20
0.65 >=0.20	0.38 >=0.20
0.85 >=0.20	0.49 >=0.20
0.82 >=0.20	0.97 >=0.20
0.66 >=0.20	0.31 >=0.20
0.83 >=0.20	0.23 >=0.20
0.6 >=0.20	0.24 >=0.20
0.6 >=0.20	0.49 >=0.20
0.79 >=0.20	0.37 >=0.20
0.63 >=0.20	0.19 >=0.20
0.6 >=0.20	0.46 >=0.20
0.98 >=0.20	0.95 >=0.20
0.06 >=0.20	0.15 >=0.20
0.06 >=0.20	0.15 >=0.20
0.06 >=0.20	0.15 >=0.20

0.06 >=0.20	0.33 >=0.20
0.7 >=0.20	0.4 >=0.20
0.67 >=0.20	0.11 >=0.20
0.89 >=0.20	0.37 >=0.20
0.83 >=0.20	0.42 >=0.20
0.36 >=0.20	0.15 >=0.20
0.33 >=0.20	0.21 >=0.20
0.47 >=0.20	0.25 >=0.20
0.34 >=0.20	1 >=0.20
0.36 >=0.20	0.28 >=0.20
0.95 >=0.20	0.99 >=0.20
0.22 >=0.20	0.9 >=0.20
0.49 >=0.20	0.68 >=0.20
0.57 >=0.20	0.75 >=0.20
0.21 >=0.20	0.33 >=0.20
0.7 >=0.20	0.55 >=0.20
0.32 >=0.20	0.58 >=0.20
0.04 >=0.20	0.15 >=0.20
0.73 >=0.20	0.86 >=0.20
1 >=0.20	1 >=0.20
0.24 >=0.20	0.57 >=0.20
0.12 >=0.20	0.45 >=0.20
0.99 >=0.20	0.91 >=0.20
0.63 >=0.20	0.35 >=0.20
0.78 >=0.20	0.71 >=0.20
0.87 >=0.20	0.92 >=0.20
0.2 >=0.20	0.27 >=0.20
0.99 >=0.20	0.69 >=0.20
0.82 >=0.20	0.66 >=0.20
1 >=0.20	0.89 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.91 >=0.20
0.99 >=0.20	0.91 >=0.20
0.97 >=0.20	0.95 >=0.20
0.94 >=0.20	0.88 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.7 >=0.20
0.99 >=0.20	0.97 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.87 >=0.20
1 >=0.20	0.77 >=0.20
0.95 >=0.20	0.96 >=0.20
0.77 >=0.20	0.28 >=0.20
0.99 >=0.20	0.69 >=0.20
0.26 >=0.20	0.95 >=0.20
0.26 >=0.20	0.95 >=0.20
0.26 >=0.20	0.95 >=0.20

0.34 >=0.20	0.81 >=0.20
0.28 >=0.20	0.38 >=0.20
0.09 >=0.20	0.42 >=0.20
0.58 >=0.20	0.21 >=0.20
0.99 >=0.20	0.93 >=0.20
0.52 >=0.20	0.87 >=0.20
0.09 >=0.20	0.37 >=0.20
0.97 >=0.20	0.88 >=0.20
0.68 >=0.20	0.38 >=0.20
0.8 >=0.20	0.58 >=0.20
0.5 >=0.20	0.82 >=0.20
0.31 >=0.20	0.71 >=0.20
0.55 >=0.20	0.81 >=0.20
0.88 >=0.20	0.96 >=0.20
0.81 >=0.20	0.91 >=0.20
0.04 >=0.20	0.16 >=0.20
0.09 >=0.20	0.36 >=0.20
0.05 >=0.20	0.4 >=0.20
0.38 >=0.20	0.85 >=0.20
0.11 >=0.20	0.66 >=0.20
0.04 >=0.20	0.65 >=0.20
0.88 >=0.20	0.93 >=0.20
0.08 >=0.20	0.36 >=0.20
0.22 >=0.20	0.64 >=0.20
0.14 >=0.20	0.56 >=0.20
0.13 >=0.20	0.69 >=0.20
0.54 >=0.20	0.87 >=0.20
0.94 >=0.20	0.91 >=0.20
0.99 >=0.20	0.93 >=0.20
0.99 >=0.20	0.94 >=0.20
0.99 >=0.20	0.64 >=0.20
0.99 >=0.20	0.99 >=0.20
0.99 >=0.20	0.89 >=0.20
0.99 >=0.20	0.76 >=0.20
0.08 >=0.20	0.19 >=0.20
0.79 >=0.20	0.6 >=0.20
0.93 >=0.20	0.92 >=0.20
0.93 >=0.20	0.92 >=0.20
0.94 >=0.20	1 >=0.20
0.82 >=0.20	0.83 >=0.20
0.79 >=0.20	0.98 >=0.20
0.55 >=0.20	0.13 >=0.20
0.97 >=0.20	0.53 >=0.20
0.89 >=0.20	0.57 >=0.20
0.98 >=0.20	0.53 >=0.20
0.82 >=0.20	0.62 >=0.20
0.82 >=0.20	0.62 >=0.20

0.57 >=0.20	0.39 >=0.20
0.99 >=0.20	0.95 >=0.20
0.72 >=0.20	0.32 >=0.20
0.12 >=0.20	0.08 >=0.20
0.88 >=0.20	0.63 >=0.20
0.93 >=0.20	0.68 >=0.20
0.93 >=0.20	0.68 >=0.20
1 >=0.20	0.89 >=0.20
0.52 >=0.20	0.98 >=0.20
0.91 >=0.20	0.78 >=0.20
0.94 >=0.20	0.48 >=0.20
0.84 >=0.20	0.98 >=0.20
0.8 >=0.20	0.54 >=0.20
0.86 >=0.20	0.95 >=0.20
0.9 >=0.20	0.3 >=0.20
0.97 >=0.20	0.68 >=0.20
0.93 >=0.20	0.27 >=0.20
0.94 >=0.20	0.2 >=0.20
0.84 >=0.20	0.57 >=0.20
0.94 >=0.20	0.66 >=0.20
0.99 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
0.53 >=0.20	0.11 >=0.20
0.97 >=0.20	0.93 >=0.20
1 >=0.20	0.88 >=0.20
1 >=0.20	0.8 >=0.20
1 >=0.20	0.86 >=0.20
0.37 >=0.20	0.77 >=0.20
0.82 >=0.20	0.76 >=0.20
1 >=0.20	0.76 >=0.20
0.9 >=0.20	0.78 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	0.77 >=0.20
0.52 >=0.20	0.53 >=0.20
0.67 >=0.20	0.44 >=0.20
0.55 >=0.20	0.48 >=0.20
0.66 >=0.20	1 >=0.20
0.42 >=0.20	0.67 >=0.20
1 >=0.20	1 >=0.20
0.78 >=0.20	0.22 >=0.20
0.45 >=0.20	0.15 >=0.20
0.7 >=0.20	0.91 >=0.20
0.16 >=0.20	0.94 >=0.20
0.06 >=0.20	0.85 >=0.20
0.72 >=0.20	0.66 >=0.20
0.32 >=0.20	0.92 >=0.20
0.88 >=0.20	0.3 >=0.20

0.43	>=0.20	0.2	>=0.20
0.3	>=0.20	0.74	>=0.20
0.99	>=0.20	0.72	>=0.20
0.29	>=0.20	0.36	>=0.20
0.32	>=0.20	0.19	>=0.20
0.43	>=0.20	0.49	>=0.20
0.73	>=0.20	0.34	>=0.20
1	>=0.20	0.79	>=0.20
0.12	>=0.20	0.05	>=0.20
0.04	>=0.20	0.5	>=0.20
0.97	>=0.20	0.83	>=0.20
0.89	>=0.20	0.28	>=0.20
0.49	>=0.20	0.81	>=0.20
0.08	>=0.20	0.19	>=0.20
0.04	>=0.20	0.27	>=0.20
0.75	>=0.20	0.54	>=0.20
0.93	>=0.20	1	>=0.20
0.76	>=0.20	0.95	>=0.20
0.82	>=0.20	0.69	>=0.20
0.9	>=0.20	0.63	>=0.20
1	>=0.20	0.52	>=0.20
0.94	>=0.20	0.94	>=0.20
0.91	>=0.20	0.9	>=0.20
0.67	>=0.20	0.98	>=0.20
0.82	>=0.20	0.54	>=0.20
0.92	>=0.20	0.5	>=0.20
0.55	>=0.20	0.28	>=0.20
0.6	>=0.20	0.37	>=0.20
0.68	>=0.20	0.29	>=0.20
0.55	>=0.20	0.28	>=0.20
0.68	>=0.20	0.29	>=0.20
0.6	>=0.20	0.34	>=0.20
0.68	>=0.20	0.29	>=0.20
0.68	>=0.20	0.29	>=0.20
0.68	>=0.20	0.29	>=0.20
0.33	>=0.20	0.43	>=0.20
1	>=0.20	0.83	>=0.20
1	>=0.20	0.93	>=0.20
1	>=0.20	0.9	>=0.20
1	>=0.20	0.94	>=0.20
1	>=0.20	0.93	>=0.20
1	>=0.20	0.93	>=0.20
0.96	>=0.20	0.64	>=0.20
1	>=0.20	0.93	>=0.20
1	>=0.20	0.93	>=0.20
0.99	>=0.20	0.89	>=0.20
0.98	>=0.20	0.84	>=0.20

0.99 >=0.20	0.76 >=0.20
0.93 >=0.20	0.71 >=0.20
0.96 >=0.20	0.93 >=0.20
0.96 >=0.20	0.93 >=0.20
0.96 >=0.20	0.93 >=0.20
0.96 >=0.20	0.93 >=0.20
0.96 >=0.20	0.93 >=0.20
0.94 >=0.20	0.93 >=0.20
0.96 >=0.20	0.93 >=0.20
0.96 >=0.20	0.93 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.86 >=0.20	0.35 >=0.20
0.86 >=0.20	0.35 >=0.20
0.65 >=0.20	0.12 >=0.20
0.98 >=0.20	0.67 >=0.20
1 >=0.20	0.92 >=0.20
0.93 >=0.20	0.94 >=0.20
0.95 >=0.20	0.74 >=0.20
0.95 >=0.20	0.74 >=0.20
0.12 >=0.20	0.15 >=0.20
0.12 >=0.20	0.15 >=0.20
0.74 >=0.20	0.51 >=0.20
1 >=0.20	0.93 >=0.20
0.3 >=0.20	0.69 >=0.20
0.12 >=0.20	0.15 >=0.20
0.07 >=0.20	0.21 >=0.20
0.99 >=0.20	0.99 >=0.20
0.57 >=0.20	0.59 >=0.20
0.65 >=0.20	0.64 >=0.20
0.09 >=0.20	0.3 >=0.20
0.78 >=0.20	0.84 >=0.20
0.82 >=0.20	0.73 >=0.20
0.78 >=0.20	0.84 >=0.20
0.65 >=0.20	0.63 >=0.20
0.97 >=0.20	0.71 >=0.20
0.79 >=0.20	1 >=0.20
0.78 >=0.20	0.9 >=0.20

0.99 >=0.20	1 >=0.20
0.66 >=0.20	0.46 >=0.20
0.09 >=0.20	0.52 >=0.20
0.78 >=0.20	0.99 >=0.20
0.84 >=0.20	0.58 >=0.20
0.4 >=0.20	0.48 >=0.20
0.3 >=0.20	0.3 >=0.20
0.67 >=0.20	0.5 >=0.20
0.96 >=0.20	0.87 >=0.20
0.68 >=0.20	0.95 >=0.20
0.09 >=0.20	0.82 >=0.20
0.31 >=0.20	0.82 >=0.20
0.42 >=0.20	0.9 >=0.20
0.23 >=0.20	0.72 >=0.20
0.51 >=0.20	0.94 >=0.20
0.43 >=0.20	0.76 >=0.20
0.34 >=0.20	0.73 >=0.20
0.11 >=0.20	0.46 >=0.20
0.21 >=0.20	0.83 >=0.20
0.21 >=0.20	0.83 >=0.20
0.47 >=0.20	0.93 >=0.20
0.29 >=0.20	0.9 >=0.20
0.53 >=0.20	0.97 >=0.20
0.31 >=0.20	0.95 >=0.20
0.5 >=0.20	0.97 >=0.20
0.31 >=0.20	0.93 >=0.20
0.31 >=0.20	0.93 >=0.20
0.27 >=0.20	0.99 >=0.20
0.08 >=0.20	0.05 >=0.20
0.51 >=0.20	0.45 >=0.20
1 >=0.20	0.99 >=0.20
0.56 >=0.20	0.22 >=0.20
0.1 >=0.20	0.29 >=0.20
0.1 >=0.20	0.18 >=0.20
0.46 >=0.20	0.2 >=0.20
0.17 >=0.20	0.29 >=0.20
0.04 >=0.20	0.08 >=0.20
0.12 >=0.20	0.04 >=0.20
0.05 >=0.20	0.05 >=0.20
0.04 >=0.20	0.15 >=0.20
0.63 >=0.20	0.38 >=0.20
1 >=0.20	0.99 >=0.20
0.82 >=0.20	0.69 >=0.20
0.98 >=0.20	1 >=0.20
0.93 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20

0.04 >=0.20	0.21 >=0.20
0.24 >=0.20	0.02 >=0.20
0.06 >=0.20	0.03 >=0.20
0.91 >=0.20	0.25 >=0.20
0.86 >=0.20	0.13 >=0.20
0.75 >=0.20	0.15 >=0.20
0.55 >=0.20	0.42 >=0.20
0.75 >=0.20	0.75 >=0.20
0.99 >=0.20	0.52 >=0.20
0.36 >=0.20	0.8 >=0.20
0.06 >=0.20	0.73 >=0.20
0.62 >=0.20	0.77 >=0.20
0.06 >=0.20	0.06 >=0.20
1 >=0.20	1 >=0.20
0.27 >=0.20	0.61 >=0.20
0.47 >=0.20	0.75 >=0.20
0.49 >=0.20	0.33 >=0.20
0.86 >=0.20	0.67 >=0.20
0.99 >=0.20	0.56 >=0.20
0.93 >=0.20	0.96 >=0.20
0.13 >=0.20	0.14 >=0.20
0.09 >=0.20	0.35 >=0.20
0.08 >=0.20	0.35 >=0.20
0.84 >=0.20	0.67 >=0.20
0.88 >=0.20	0.5 >=0.20
0.89 >=0.20	0.13 >=0.20
0.33 >=0.20	0.27 >=0.20
0.61 >=0.20	0.55 >=0.20
0.94 >=0.20	0.78 >=0.20
0.95 >=0.20	0.5 >=0.20
0.54 >=0.20	0.48 >=0.20
0.07 >=0.20	0.29 >=0.20
0.99 >=0.20	0.97 >=0.20
0.37 >=0.20	0.41 >=0.20
0.04 >=0.20	0.63 >=0.20
0.98 >=0.20	0.92 >=0.20
1 >=0.20	0.99 >=0.20
0.3 >=0.20	0.44 >=0.20
0.96 >=0.20	0.06 >=0.20
0.92 >=0.20	0.5 >=0.20
1 >=0.20	0.79 >=0.20
1 >=0.20	0.99 >=0.20
0.65 >=0.20	0.25 >=0.20
0.99 >=0.20	0.76 >=0.20
0.59 >=0.20	0.05 >=0.20
0.06 >=0.20	0.58 >=0.20
0.77 >=0.20	0.58 >=0.20

1 >=0.20	0.99 >=0.20
0.14 >=0.20	0.62 >=0.20
0.28 >=0.20	0.2 >=0.20
0.45 >=0.20	0.23 >=0.20
0.47 >=0.20	0.69 >=0.20
0.99 >=0.20	0.89 >=0.20
0.97 >=0.20	0.79 >=0.20
0.83 >=0.20	0.4 >=0.20
0.67 >=0.20	0.68 >=0.20
0.49 >=0.20	0.39 >=0.20
0.18 >=0.20	0.25 >=0.20
0.5 >=0.20	0.38 >=0.20
0.04 >=0.20	0.19 >=0.20
0.25 >=0.20	0.62 >=0.20
0.54 >=0.20	0.23 >=0.20
0.63 >=0.20	0.9 >=0.20
0.73 >=0.20	0.98 >=0.20
0.05 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.05 >=0.20	0.03 >=0.20
0.28 >=0.20	0.5 >=0.20
0.28 >=0.20	0.55 >=0.20
0.1 >=0.20	0.05 >=0.20
0.09 >=0.20	0.04 >=0.20
0.05 >=0.20	0.04 >=0.20
0.43 >=0.20	0.57 >=0.20
0.36 >=0.20	0.5 >=0.20
0.09 >=0.20	0.04 >=0.20
0.09 >=0.20	0.04 >=0.20
0.57 >=0.20	0.35 >=0.20
0.33 >=0.20	0.16 >=0.20
0.19 >=0.20	0.09 >=0.20
0.51 >=0.20	0.21 >=0.20
0.2 >=0.20	0.12 >=0.20
0.08 >=0.20	0.25 >=0.20
0.34 >=0.20	0.46 >=0.20
0.99 >=0.20	0.98 >=0.20
0.38 >=0.20	0.5 >=0.20
0.08 >=0.20	0.05 >=0.20
0.39 >=0.20	0.48 >=0.20
0.6 >=0.20	0.65 >=0.20
0.43 >=0.20	0.52 >=0.20
0.43 >=0.20	0.53 >=0.20

0.41 >=0.20	0.54 >=0.20
0.09 >=0.20	0.04 >=0.20
0.39 >=0.20	0.6 >=0.20
0.09 >=0.20	0.04 >=0.20
0.11 >=0.20	0.06 >=0.20
0.09 >=0.20	0.06 >=0.20
0.41 >=0.20	0.59 >=0.20
0.09 >=0.20	0.04 >=0.20
0.41 >=0.20	0.54 >=0.20
0.09 >=0.20	0.04 >=0.20
0.44 >=0.20	0.59 >=0.20
0.41 >=0.20	0.54 >=0.20
0.08 >=0.20	0.04 >=0.20
0.38 >=0.20	0.51 >=0.20
0.09 >=0.20	0.04 >=0.20
0.09 >=0.20	0.04 >=0.20
0.09 >=0.20	0.04 >=0.20
0.09 >=0.20	0.04 >=0.20
0.43 >=0.20	0.54 >=0.20
0.09 >=0.20	0.04 >=0.20
0.36 >=0.20	0.47 >=0.20
0.2 >=0.20	0.4 >=0.20
0.28 >=0.20	0.42 >=0.20
0.14 >=0.20	0.05 >=0.20
0.58 >=0.20	0.45 >=0.20
0.11 >=0.20	0.05 >=0.20
0.35 >=0.20	0.35 >=0.20
0.07 >=0.20	0.03 >=0.20
0.31 >=0.20	0.49 >=0.20
0.2 >=0.20	0.03 >=0.20
0.32 >=0.20	0.34 >=0.20
0.24 >=0.20	0.16 >=0.20
0.09 >=0.20	0.04 >=0.20
0.35 >=0.20	0.44 >=0.20
0.09 >=0.20	0.04 >=0.20
0.49 >=0.20	0.58 >=0.20
0.23 >=0.20	0.19 >=0.20
0.69 >=0.20	0.5 >=0.20
0.12 >=0.20	0.52 >=0.20
0.58 >=0.20	0.79 >=0.20
0.98 >=0.20	0.96 >=0.20
0.74 >=0.20	0.72 >=0.20
0.98 >=0.20	0.97 >=0.20
0.74 >=0.20	0.75 >=0.20
0.04 >=0.20	0.62 >=0.20
0.73 >=0.20	1 >=0.20
0.41 >=0.20	0.62 >=0.20

0.13 >=0.20	0.64 >=0.20
1 >=0.20	1 >=0.20
0.59 >=0.20	0.92 >=0.20
0.91 >=0.20	0.28 >=0.20
0.9 >=0.20	0.95 >=0.20
0.13 >=0.20	0.05 >=0.20
0.55 >=0.20	0.44 >=0.20
0.99 >=0.20	0.99 >=0.20
0.92 >=0.20	0.99 >=0.20
0.9 >=0.20	0.32 >=0.20
0.94 >=0.20	0.93 >=0.20
0.98 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
0.87 >=0.20	0.76 >=0.20
0.68 >=0.20	0.98 >=0.20
0.89 >=0.20	0.62 >=0.20
0.7 >=0.20	0.42 >=0.20
0.98 >=0.20	0.99 >=0.20
0.98 >=0.20	0.52 >=0.20
0.75 >=0.20	0.34 >=0.20
0.83 >=0.20	0.51 >=0.20
0.09 >=0.20	0.81 >=0.20
0.54 >=0.20	0.12 >=0.20
0.99 >=0.20	0.84 >=0.20
0.89 >=0.20	0.9 >=0.20
0.45 >=0.20	0.24 >=0.20
0.99 >=0.20	0.92 >=0.20
0.99 >=0.20	0.72 >=0.20
1 >=0.20	0.61 >=0.20
0.16 >=0.20	0.03 >=0.20
0.9 >=0.20	0.6 >=0.20
0.71 >=0.20	0.3 >=0.20
0.71 >=0.20	0.87 >=0.20
0.08 >=0.20	0.99 >=0.20
0.39 >=0.20	0.1 >=0.20
0.56 >=0.20	0.11 >=0.20
0.64 >=0.20	0.74 >=0.20
0.5 >=0.20	0.63 >=0.20
0.18 >=0.20	0.07 >=0.20
0.27 >=0.20	0.05 >=0.20
1 >=0.20	0.96 >=0.20
0.32 >=0.20	0.15 >=0.20
0.27 >=0.20	0.11 >=0.20
0.88 >=0.20	0.22 >=0.20
0.94 >=0.20	0.2 >=0.20
0.7 >=0.20	0.2 >=0.20

0.12 >=0.20	0.19 >=0.20
0.12 >=0.20	0.19 >=0.20
0.91 >=0.20	0.3 >=0.20
0.89 >=0.20	0.41 >=0.20
0.49 >=0.20	0.42 >=0.20
0.23 >=0.20	0.27 >=0.20
0.39 >=0.20	0.36 >=0.20
0.93 >=0.20	0.27 >=0.20
0.55 >=0.20	0.59 >=0.20
0.25 >=0.20	0.4 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	0.94 >=0.20
0.04 >=0.20	0.08 >=0.20
0.89 >=0.20	0.2 >=0.20
0.91 >=0.20	0.45 >=0.20
0.43 >=0.20	0.09 >=0.20
0.04 >=0.20	0.03 >=0.20
0.64 >=0.20	0.14 >=0.20
0.35 >=0.20	0.03 >=0.20
0.37 >=0.20	0.23 >=0.20
0.9 >=0.20	0.75 >=0.20
0.99 >=0.20	0.68 >=0.20
0.33 >=0.20	0.05 >=0.20
0.77 >=0.20	0.3 >=0.20
1 >=0.20	0.69 >=0.20
0.99 >=0.20	0.53 >=0.20
0.31 >=0.20	0.6 >=0.20
1 >=0.20	1 >=0.20
0.24 >=0.20	0.61 >=0.20
0.46 >=0.20	0.32 >=0.20
0.96 >=0.20	0.87 >=0.20
0.46 >=0.20	0.22 >=0.20
0.6 >=0.20	0.4 >=0.20
0.04 >=0.20	0.03 >=0.20
0.79 >=0.20	0.91 >=0.20
0.99 >=0.20	0.83 >=0.20
0.59 >=0.20	0.66 >=0.20
1 >=0.20	0.69 >=0.20
0.85 >=0.20	0.48 >=0.20
0.99 >=0.20	0.94 >=0.20
0.08 >=0.20	0.41 >=0.20
0.07 >=0.20	0.12 >=0.20
0.23 >=0.20	0.37 >=0.20
0.24 >=0.20	0.27 >=0.20
0.14 >=0.20	0.19 >=0.20
0.15 >=0.20	0.1 >=0.20
0.36 >=0.20	0.11 >=0.20

0.9 >=0.20	0.28 >=0.20
0.24 >=0.20	0.66 >=0.20
0.1 >=0.20	0.19 >=0.20
0.84 >=0.20	0.73 >=0.20
0.67 >=0.20	0.41 >=0.20
0.68 >=0.20	0.4 >=0.20
0.53 >=0.20	0.45 >=0.20
0.34 >=0.20	0.72 >=0.20
1 >=0.20	0.86 >=0.20
0.92 >=0.20	0.65 >=0.20
0.31 >=0.20	0.18 >=0.20
0.24 >=0.20	0.94 >=0.20
0.3 >=0.20	0.04 >=0.20
0.17 >=0.20	0.13 >=0.20
0.96 >=0.20	0.19 >=0.20
0.63 >=0.20	0.57 >=0.20
0.13 >=0.20	0.05 >=0.20
1 >=0.20	0.96 >=0.20
0.6 >=0.20	0.17 >=0.20
0.47 >=0.20	0.18 >=0.20
0.83 >=0.20	0.77 >=0.20
0.69 >=0.20	0.26 >=0.20
0.15 >=0.20	0.22 >=0.20
0.71 >=0.20	0.32 >=0.20
0.67 >=0.20	0.29 >=0.20
0.67 >=0.20	0.24 >=0.20
0.48 >=0.20	0.8 >=0.20
0.52 >=0.20	0.2 >=0.20
0.99 >=0.20	0.97 >=0.20
0.99 >=0.20	0.62 >=0.20
0.27 >=0.20	0.08 >=0.20
0.23 >=0.20	0.52 >=0.20
0.65 >=0.20	0.42 >=0.20
0.85 >=0.20	0.72 >=0.20
0.43 >=0.20	0.28 >=0.20
0.97 >=0.20	0.99 >=0.20
0.93 >=0.20	0.48 >=0.20
0.14 >=0.20	0.32 >=0.20
0.48 >=0.20	0.34 >=0.20
0.07 >=0.20	0.1 >=0.20
0.27 >=0.20	0.27 >=0.20
0.7 >=0.20	0.68 >=0.20
1 >=0.20	1 >=0.20
0.71 >=0.20	0.88 >=0.20
1 >=0.20	0.99 >=0.20
0.47 >=0.20	0.05 >=0.20
0.7 >=0.20	0.05 >=0.20

0.06 >=0.20	0.03 >=0.20
0.43 >=0.20	0.28 >=0.20
0.99 >=0.20	0.88 >=0.20
0.9 >=0.20	0.82 >=0.20
0.19 >=0.20	0.32 >=0.20
0.33 >=0.20	0.03 >=0.20
0.58 >=0.20	0.34 >=0.20
0.06 >=0.20	0.58 >=0.20
0.1 >=0.20	0.43 >=0.20
0.71 >=0.20	0.14 >=0.20
0.72 >=0.20	0.35 >=0.20
0.79 >=0.20	0.49 >=0.20
0.13 >=0.20	0.33 >=0.20
0.14 >=0.20	0.07 >=0.20
0.55 >=0.20	0.19 >=0.20
0.94 >=0.20	0.67 >=0.20
0.88 >=0.20	0.53 >=0.20
0.15 >=0.20	0.06 >=0.20
0.21 >=0.20	0.59 >=0.20
0.19 >=0.20	0.07 >=0.20
0.95 >=0.20	0.35 >=0.20
0.97 >=0.20	1 >=0.20
0.81 >=0.20	0.46 >=0.20
0.79 >=0.20	0.43 >=0.20
0.5 >=0.20	0.34 >=0.20
0.42 >=0.20	0.1 >=0.20
0.83 >=0.20	0.07 >=0.20
0.83 >=0.20	0.08 >=0.20
1 >=0.20	0.39 >=0.20
0.85 >=0.20	0.54 >=0.20
0.09 >=0.20	0.22 >=0.20
0.4 >=0.20	0.77 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
1 >=0.20	0.99 >=0.20
0.26 >=0.20	0.68 >=0.20
0.99 >=0.20	0.54 >=0.20
0.78 >=0.20	0.29 >=0.20
0.68 >=0.20	0.59 >=0.20
0.47 >=0.20	0.51 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
0.79 >=0.20	0.56 >=0.20
0.54 >=0.20	0.57 >=0.20
0.97 >=0.20	0.47 >=0.20
0.68 >=0.20	0.27 >=0.20
0.35 >=0.20	0.12 >=0.20

0.99 >=0.20	0.74 >=0.20
0.63 >=0.20	0.31 >=0.20
0.97 >=0.20	0.57 >=0.20
0.32 >=0.20	0.18 >=0.20
0.06 >=0.20	0.28 >=0.20
0.93 >=0.20	0.08 >=0.20
0.04 >=0.20	0.04 >=0.20
0.13 >=0.20	0.55 >=0.20
0.13 >=0.20	0.08 >=0.20
0.97 >=0.20	0.95 >=0.20
0.62 >=0.20	0.44 >=0.20
0.53 >=0.20	0.46 >=0.20
0.96 >=0.20	0.97 >=0.20
0.25 >=0.20	0.99 >=0.20
0.12 >=0.20	0.9 >=0.20
0.24 >=0.20	0.82 >=0.20
0.22 >=0.20	0.88 >=0.20
0.99 >=0.20	0.96 >=0.20
0.94 >=0.20	0.99 >=0.20
0.94 >=0.20	1 >=0.20
0.23 >=0.20	0.89 >=0.20
0.43 >=0.20	0.81 >=0.20
0.79 >=0.20	0.77 >=0.20
0.34 >=0.20	0.96 >=0.20
0.81 >=0.20	0.82 >=0.20
1 >=0.20	0.97 >=0.20
0.81 >=0.20	0.87 >=0.20
0.99 >=0.20	0.97 >=0.20
0.11 >=0.20	0.09 >=0.20
0.97 >=0.20	0.95 >=0.20
0.9 >=0.20	0.83 >=0.20
1 >=0.20	0.53 >=0.20
0.32 >=0.20	0.97 >=0.20
0.28 >=0.20	0.99 >=0.20
0.85 >=0.20	0.75 >=0.20
0.36 >=0.20	0.49 >=0.20
0.76 >=0.20	0.86 >=0.20
0.61 >=0.20	0.47 >=0.20
0.89 >=0.20	0.54 >=0.20
0.94 >=0.20	0.94 >=0.20
0.04 >=0.20	0.23 >=0.20
0.86 >=0.20	0.2 >=0.20
1 >=0.20	0.74 >=0.20
0.2 >=0.20	0.16 >=0.20
0.85 >=0.20	0.06 >=0.20
0.13 >=0.20	0.55 >=0.20
0.09 >=0.20	0.63 >=0.20

1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.54 >=0.20	0.96 >=0.20
0.27 >=0.20	0.25 >=0.20
0.13 >=0.20	0.82 >=0.20
0.44 >=0.20	0.77 >=0.20
0.8 >=0.20	0.48 >=0.20
0.48 >=0.20	0.78 >=0.20
0.31 >=0.20	0.23 >=0.20
0.2 >=0.20	0.63 >=0.20
0.29 >=0.20	0.93 >=0.20
0.08 >=0.20	0.24 >=0.20
0.07 >=0.20	0.23 >=0.20
0.99 >=0.20	0.15 >=0.20
0.64 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
0.7 >=0.20	0.15 >=0.20
0.06 >=0.20	0.08 >=0.20
0.34 >=0.20	0.03 >=0.20
0.77 >=0.20	0.53 >=0.20
0.37 >=0.20	0.26 >=0.20
0.39 >=0.20	0.36 >=0.20
0.43 >=0.20	0.47 >=0.20
0.37 >=0.20	1 >=0.20
1 >=0.20	0.65 >=0.20
0.99 >=0.20	0.42 >=0.20
0.99 >=0.20	0.57 >=0.20
0.88 >=0.20	0.31 >=0.20
0.08 >=0.20	0.4 >=0.20
0.23 >=0.20	0.75 >=0.20
0.98 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
0.33 >=0.20	0.33 >=0.20
0.44 >=0.20	0.85 >=0.20
0.2 >=0.20	0.04 >=0.20
0.34 >=0.20	0.24 >=0.20
0.04 >=0.20	0.72 >=0.20
0.48 >=0.20	0.6 >=0.20
0.94 >=0.20	0.51 >=0.20
0.18 >=0.20	0.1 >=0.20
0.08 >=0.20	0.3 >=0.20
0.04 >=0.20	0.4 >=0.20

0.36	>=0.20	0.8	>=0.20
0.5	>=0.20	0.94	>=0.20
0.12	>=0.20	0.35	>=0.20
0.99	>=0.20	0.65	>=0.20
0.61	>=0.20	0.45	>=0.20
0.55	>=0.20	0.48	>=0.20
0.7	>=0.20	0.21	>=0.20
0.95	>=0.20	0.94	>=0.20
0.93	>=0.20	1	>=0.20
0.99	>=0.20	1	>=0.20
0.99	>=0.20	1	>=0.20
0.83	>=0.20	0.98	>=0.20
0.68	>=0.20	0.99	>=0.20
1	>=0.20	0.98	>=0.20
0.21	>=0.20	0.98	>=0.20
0.94	>=0.20	0.92	>=0.20
0.87	>=0.20	0.94	>=0.20
0.97	>=0.20	0.25	>=0.20
0.53	>=0.20	0.28	>=0.20
0.98	>=0.20	0.58	>=0.20
0.99	>=0.20	0.9	>=0.20
0.69	>=0.20	0.99	>=0.20
0.92	>=0.20	0.83	>=0.20
0.05	>=0.20	0.33	>=0.20
0.05	>=0.20	0.71	>=0.20
0.45	>=0.20	0.69	>=0.20
0.48	>=0.20	0.99	>=0.20
0.25	>=0.20	0.26	>=0.20
0.97	>=0.20	0.98	>=0.20
0.08	>=0.20	0.04	>=0.20
0.97	>=0.20	1	>=0.20
0.63	>=0.20	0.98	>=0.20
0.96	>=0.20	0.58	>=0.20
0.6	>=0.20	0.14	>=0.20
0.74	>=0.20	0.81	>=0.20
0.41	>=0.20	0.87	>=0.20
1	>=0.20	0.88	>=0.20
1	>=0.20	1	>=0.20
0.82	>=0.20	0.74	>=0.20
0.67	>=0.20	0.64	>=0.20
0.86	>=0.20	0.3	>=0.20
0.98	>=0.20	0.06	>=0.20
0.16	>=0.20	0.49	>=0.20
0.13	>=0.20	0.05	>=0.20
0.96	>=0.20	0.61	>=0.20
0.18	>=0.20	0.17	>=0.20
0.13	>=0.20	0.84	>=0.20

1	>=0.20	1	>=0.20
0.15	>=0.20	0.94	>=0.20
0.63	>=0.20	0.12	>=0.20
0.79	>=0.20	0.3	>=0.20
0.93	>=0.20	0.23	>=0.20
0.72	>=0.20	0.43	>=0.20
0.56	>=0.20	0.09	>=0.20
0.81	>=0.20	0.19	>=0.20
0.16	>=0.20	0.23	>=0.20
0.52	>=0.20	0.28	>=0.20
0.86	>=0.20	0.6	>=0.20
1	>=0.20	0.41	>=0.20
0.99	>=0.20	1	>=0.20
0.9	>=0.20	0.24	>=0.20
0.27	>=0.20	0.04	>=0.20
0.57	>=0.20	0.1	>=0.20
0.08	>=0.20	0.12	>=0.20
0.23	>=0.20	0.54	>=0.20
0.06	>=0.20	0.41	>=0.20
0.44	>=0.20	0.43	>=0.20
0.05	>=0.20	0.5	>=0.20
0.47	>=0.20	0.44	>=0.20
0.72	>=0.20	0.99	>=0.20
0.99	>=0.20	0.93	>=0.20
0.19	>=0.20	0.18	>=0.20
0.43	>=0.20	0.98	>=0.20
0.98	>=0.20	0.62	>=0.20
1	>=0.20	1	>=0.20
0.85	>=0.20	0.47	>=0.20
0.5	>=0.20	0.88	>=0.20
0.41	>=0.20	0.15	>=0.20
0.4	>=0.20	0.58	>=0.20
1	>=0.20	0.41	>=0.20
0.78	>=0.20	0.75	>=0.20
1	>=0.20	0.98	>=0.20
0.98	>=0.20	0.57	>=0.20
0.91	>=0.20	0.68	>=0.20
1	>=0.20	0.81	>=0.20
0.35	>=0.20	0.97	>=0.20
0.33	>=0.20	0.86	>=0.20
0.99	>=0.20	0.74	>=0.20
0.98	>=0.20	0.2	>=0.20
0.11	>=0.20	0.2	>=0.20
0.56	>=0.20	0.57	>=0.20
0.37	>=0.20	0.48	>=0.20
0.14	>=0.20	0.98	>=0.20
1	>=0.20	0.98	>=0.20

0.99 >=0.20	1 >=0.20
0.99 >=0.20	0.93 >=0.20
0.99 >=0.20	0.79 >=0.20
0.18 >=0.20	0.04 >=0.20
0.99 >=0.20	0.56 >=0.20
1 >=0.20	0.92 >=0.20
0.6 >=0.20	0.71 >=0.20
0.89 >=0.20	0.11 >=0.20
0.12 >=0.20	0.14 >=0.20
0.97 >=0.20	1 >=0.20
0.33 >=0.20	0.64 >=0.20
0.94 >=0.20	0.58 >=0.20
0.07 >=0.20	0.66 >=0.20
0.23 >=0.20	0.12 >=0.20
0.62 >=0.20	0.41 >=0.20
0.37 >=0.20	0.94 >=0.20
0.09 >=0.20	0.69 >=0.20
1 >=0.20	0.95 >=0.20
0.66 >=0.20	1 >=0.20
0.56 >=0.20	0.09 >=0.20
0.52 >=0.20	0.22 >=0.20
0.62 >=0.20	0.91 >=0.20
0.07 >=0.20	0.39 >=0.20
0.19 >=0.20	0.96 >=0.20
0.17 >=0.20	0.73 >=0.20
0.04 >=0.20	0.6 >=0.20
0.79 >=0.20	0.14 >=0.20
0.88 >=0.20	0.93 >=0.20
0.08 >=0.20	0.36 >=0.20
0.19 >=0.20	0.06 >=0.20
0.63 >=0.20	0.59 >=0.20
0.98 >=0.20	0.95 >=0.20
0.94 >=0.20	0.11 >=0.20
0.58 >=0.20	0.25 >=0.20
0.97 >=0.20	0.28 >=0.20
0.1 >=0.20	0.4 >=0.20
0.98 >=0.20	1 >=0.20
0.79 >=0.20	0.48 >=0.20
0.83 >=0.20	0.49 >=0.20
0.19 >=0.20	0.54 >=0.20
0.93 >=0.20	0.72 >=0.20
0.95 >=0.20	0.92 >=0.20
0.75 >=0.20	0.38 >=0.20
0.92 >=0.20	1 >=0.20
0.99 >=0.20	0.54 >=0.20
0.91 >=0.20	0.79 >=0.20
0.55 >=0.20	0.61 >=0.20

0.71 >=0.20	0.68 >=0.20
0.99 >=0.20	0.97 >=0.20
0.41 >=0.20	0.62 >=0.20
0.11 >=0.20	0.08 >=0.20
0.94 >=0.20	0.34 >=0.20
0.93 >=0.20	0.7 >=0.20
0.99 >=0.20	0.81 >=0.20
0.7 >=0.20	0.15 >=0.20
1 >=0.20	1 >=0.20
0.64 >=0.20	0.29 >=0.20
1 >=0.20	1 >=0.20
0.7 >=0.20	0.77 >=0.20
0.99 >=0.20	0.72 >=0.20
0.99 >=0.20	0.84 >=0.20
1 >=0.20	0.96 >=0.20
0.99 >=0.20	0.99 >=0.20
0.49 >=0.20	0.03 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.98 >=0.20
0.5 >=0.20	0.21 >=0.20
0.32 >=0.20	1 >=0.20
0.96 >=0.20	0.4 >=0.20
0.75 >=0.20	0.43 >=0.20
0.65 >=0.20	0.08 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.63 >=0.20	0.4 >=0.20
0.32 >=0.20	1 >=0.20
0.39 >=0.20	1 >=0.20
0.52 >=0.20	1 >=0.20
0.26 >=0.20	0.33 >=0.20
0.8 >=0.20	0.63 >=0.20
0.73 >=0.20	0.18 >=0.20
0.67 >=0.20	0.95 >=0.20
0.82 >=0.20	0.87 >=0.20
0.05 >=0.20	0.11 >=0.20
0.93 >=0.20	0.58 >=0.20
0.2 >=0.20	0.72 >=0.20
0.71 >=0.20	0.71 >=0.20
0.39 >=0.20	1 >=0.20
0.66 >=0.20	0.04 >=0.20
0.29 >=0.20	0.31 >=0.20
0.86 >=0.20	0.36 >=0.20
0.98 >=0.20	0.36 >=0.20
0.74 >=0.20	0.2 >=0.20
0.9 >=0.20	0.25 >=0.20
0.96 >=0.20	0.13 >=0.20

0.84 >=0.20	0.96 >=0.20
0.26 >=0.20	0.17 >=0.20
0.82 >=0.20	0.84 >=0.20
0.96 >=0.20	0.89 >=0.20
0.98 >=0.20	0.99 >=0.20
0.37 >=0.20	1 >=0.20
0.92 >=0.20	0.73 >=0.20
0.31 >=0.20	0.15 >=0.20
0.49 >=0.20	0.61 >=0.20
1 >=0.20	0.82 >=0.20
0.04 >=0.20	0.1 >=0.20
0.58 >=0.20	0.73 >=0.20
0.09 >=0.20	0.11 >=0.20
0.67 >=0.20	0.38 >=0.20
0.11 >=0.20	0.08 >=0.20
0.54 >=0.20	0.56 >=0.20
0.35 >=0.20	0.36 >=0.20
0.99 >=0.20	0.94 >=0.20
0.05 >=0.20	0.56 >=0.20
0.49 >=0.20	0.78 >=0.20
0.53 >=0.20	0.71 >=0.20
0.44 >=0.20	1 >=0.20
0.56 >=0.20	1 >=0.20
1 >=0.20	0.91 >=0.20
0.61 >=0.20	0.2 >=0.20
0.99 >=0.20	0.2 >=0.20
0.21 >=0.20	0.43 >=0.20
0.85 >=0.20	0.63 >=0.20
0.7 >=0.20	0.33 >=0.20
0.4 >=0.20	0.03 >=0.20
0.86 >=0.20	0.17 >=0.20
0.35 >=0.20	0.24 >=0.20
0.93 >=0.20	0.74 >=0.20
0.51 >=0.20	0.6 >=0.20
0.84 >=0.20	0.24 >=0.20
0.56 >=0.20	0.24 >=0.20
1 >=0.20	1 >=0.20
0.25 >=0.20	0.22 >=0.20
0.56 >=0.20	0.84 >=0.20
0.92 >=0.20	0.25 >=0.20
0.35 >=0.20	0.7 >=0.20
0.04 >=0.20	0.67 >=0.20
0.67 >=0.20	0.42 >=0.20
0.24 >=0.20	0.32 >=0.20
0.27 >=0.20	0.42 >=0.20
0.98 >=0.20	0.74 >=0.20
0.17 >=0.20	0.52 >=0.20

1 >=0.20	0.82 >=0.20
0.69 >=0.20	0.71 >=0.20
0.06 >=0.20	0.12 >=0.20
0.99 >=0.20	1 >=0.20
0.33 >=0.20	0.3 >=0.20
0.68 >=0.20	0.44 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
0.99 >=0.20	1 >=0.20
0.5 >=0.20	0.56 >=0.20
0.83 >=0.20	0.87 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.72 >=0.20	0.83 >=0.20
0.99 >=0.20	0.88 >=0.20
0.98 >=0.20	0.93 >=0.20
0.7 >=0.20	0.63 >=0.20
0.69 >=0.20	0.74 >=0.20
0.74 >=0.20	0.26 >=0.20
0.4 >=0.20	0.26 >=0.20
0.27 >=0.20	0.27 >=0.20
0.79 >=0.20	0.99 >=0.20
0.91 >=0.20	0.46 >=0.20
0.2 >=0.20	0.2 >=0.20
0.42 >=0.20	0.21 >=0.20
0.18 >=0.20	0.13 >=0.20
0.55 >=0.20	0.8 >=0.20
0.75 >=0.20	0.46 >=0.20
0.92 >=0.20	0.61 >=0.20
0.52 >=0.20	0.17 >=0.20
0.93 >=0.20	0.64 >=0.20
0.24 >=0.20	0.04 >=0.20
0.26 >=0.20	0.71 >=0.20
0.69 >=0.20	0.96 >=0.20
0.25 >=0.20	0.1 >=0.20
0.65 >=0.20	0.65 >=0.20
0.99 >=0.20	0.84 >=0.20
0.95 >=0.20	0.67 >=0.20
0.75 >=0.20	0.88 >=0.20
0.52 >=0.20	0.84 >=0.20
0.55 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
0.09 >=0.20	0.04 >=0.20
0.39 >=0.20	0.41 >=0.20
0.38 >=0.20	0.9 >=0.20
0.13 >=0.20	0.23 >=0.20
0.26 >=0.20	0.6 >=0.20

0.78 >=0.20	0.23 >=0.20
0.99 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.22 >=0.20	0.53 >=0.20
0.04 >=0.20	0.71 >=0.20
0.85 >=0.20	0.63 >=0.20
0.04 >=0.20	0.71 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.89 >=0.20
0.83 >=0.20	0.86 >=0.20
0.96 >=0.20	0.7 >=0.20
0.99 >=0.20	0.84 >=0.20
0.92 >=0.20	0.53 >=0.20
0.96 >=0.20	0.73 >=0.20
0.75 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.99 >=0.20
0.94 >=0.20	0.65 >=0.20
0.52 >=0.20	0.64 >=0.20
0.96 >=0.20	0.97 >=0.20
0.96 >=0.20	0.36 >=0.20
0.16 >=0.20	0.3 >=0.20
0.16 >=0.20	0.34 >=0.20
0.95 >=0.20	0.93 >=0.20
0.6 >=0.20	0.37 >=0.20
0.77 >=0.20	1 >=0.20
0.98 >=0.20	0.45 >=0.20
1 >=0.20	1 >=0.20
0.91 >=0.20	0.6 >=0.20
0.98 >=0.20	1 >=0.20
0.07 >=0.20	0.5 >=0.20
0.07 >=0.20	0.5 >=0.20
0.26 >=0.20	0.56 >=0.20
1 >=0.20	0.99 >=0.20
0.16 >=0.20	0.66 >=0.20
0.97 >=0.20	0.69 >=0.20
0.99 >=0.20	0.98 >=0.20
0.2 >=0.20	0.19 >=0.20
0.39 >=0.20	0.17 >=0.20
0.6 >=0.20	0.85 >=0.20
0.58 >=0.20	0.87 >=0.20
0.14 >=0.20	0.39 >=0.20

0.27 >=0.20	0.53 >=0.20
0.31 >=0.20	0.54 >=0.20
0.25 >=0.20	0.03 >=0.20
0.8 >=0.20	1 >=0.20
0.92 >=0.20	0.7 >=0.20
0.13 >=0.20	0.65 >=0.20
0.31 >=0.20	0.89 >=0.20
0.09 >=0.20	0.82 >=0.20
0.94 >=0.20	0.15 >=0.20
0.58 >=0.20	0.11 >=0.20
0.27 >=0.20	0.12 >=0.20
0.75 >=0.20	0.11 >=0.20
0.79 >=0.20	0.99 >=0.20
0.95 >=0.20	0.12 >=0.20
0.83 >=0.20	0.66 >=0.20
0.85 >=0.20	0.17 >=0.20
0.84 >=0.20	0.16 >=0.20
0.71 >=0.20	0.03 >=0.20
0.85 >=0.20	0.17 >=0.20
0.77 >=0.20	0.22 >=0.20
0.82 >=0.20	0.16 >=0.20
0.97 >=0.20	0.64 >=0.20
0.9 >=0.20	0.82 >=0.20
0.42 >=0.20	0.29 >=0.20
0.43 >=0.20	0.16 >=0.20
0.6 >=0.20	0.66 >=0.20
0.28 >=0.20	0.27 >=0.20
0.73 >=0.20	0.96 >=0.20
0.91 >=0.20	0.83 >=0.20
0.68 >=0.20	0.98 >=0.20
0.43 >=0.20	0.15 >=0.20
0.31 >=0.20	0.75 >=0.20
0.62 >=0.20	0.75 >=0.20
0.5 >=0.20	0.56 >=0.20
0.05 >=0.20	0.28 >=0.20
0.5 >=0.20	0.12 >=0.20
0.06 >=0.20	0.26 >=0.20
0.99 >=0.20	0.77 >=0.20
0.14 >=0.20	0.73 >=0.20
0.49 >=0.20	1 >=0.20
0.69 >=0.20	1 >=0.20
0.38 >=0.20	1 >=0.20
0.12 >=0.20	0.99 >=0.20
0.68 >=0.20	0.98 >=0.20
0.12 >=0.20	0.93 >=0.20
0.54 >=0.20	1 >=0.20
0.23 >=0.20	0.48 >=0.20

0.11 >=0.20	0.25 >=0.20
0.68 >=0.20	0.15 >=0.20
0.07 >=0.20	0.03 >=0.20
0.36 >=0.20	1 >=0.20
0.18 >=0.20	0.97 >=0.20
0.51 >=0.20	0.76 >=0.20
0.73 >=0.20	0.75 >=0.20
0.15 >=0.20	0.19 >=0.20
1 >=0.20	0.99 >=0.20
0.04 >=0.20	0.04 >=0.20
0.93 >=0.20	0.44 >=0.20
0.68 >=0.20	0.7 >=0.20
0.08 >=0.20	0.07 >=0.20
0.99 >=0.20	0.87 >=0.20
0.07 >=0.20	0.17 >=0.20
0.14 >=0.20	0.54 >=0.20
0.74 >=0.20	1 >=0.20
0.45 >=0.20	0.82 >=0.20
0.25 >=0.20	0.24 >=0.20
0.83 >=0.20	0.96 >=0.20
0.32 >=0.20	0.47 >=0.20
0.96 >=0.20	1 >=0.20
0.57 >=0.20	0.46 >=0.20
0.82 >=0.20	0.83 >=0.20
0.78 >=0.20	0.99 >=0.20
0.77 >=0.20	0.96 >=0.20
0.62 >=0.20	0.66 >=0.20
0.87 >=0.20	0.47 >=0.20
0.55 >=0.20	0.53 >=0.20
0.5 >=0.20	0.29 >=0.20
0.21 >=0.20	0.21 >=0.20
1 >=0.20	0.81 >=0.20
0.97 >=0.20	0.67 >=0.20
0.89 >=0.20	0.65 >=0.20
0.97 >=0.20	0.79 >=0.20
0.46 >=0.20	0.72 >=0.20
0.45 >=0.20	0.51 >=0.20
0.19 >=0.20	0.06 >=0.20
0.28 >=0.20	0.08 >=0.20
0.71 >=0.20	0.96 >=0.20
0.96 >=0.20	0.99 >=0.20
0.56 >=0.20	0.13 >=0.20
0.95 >=0.20	0.97 >=0.20
0.91 >=0.20	0.48 >=0.20
0.95 >=0.20	0.08 >=0.20
0.33 >=0.20	0.04 >=0.20
0.16 >=0.20	0.15 >=0.20

0.84 >=0.20	0.98 >=0.20
0.88 >=0.20	0.74 >=0.20
0.04 >=0.20	0.03 >=0.20
0.47 >=0.20	0.53 >=0.20
0.99 >=0.20	0.9 >=0.20
0.3 >=0.20	0.09 >=0.20
0.04 >=0.20	0.06 >=0.20
0.67 >=0.20	0.46 >=0.20
0.89 >=0.20	0.63 >=0.20
1 >=0.20	0.99 >=0.20
0.98 >=0.20	0.32 >=0.20
0.16 >=0.20	0.03 >=0.20
0.25 >=0.20	0.23 >=0.20
0.28 >=0.20	0.26 >=0.20
0.72 >=0.20	0.52 >=0.20
0.43 >=0.20	0.31 >=0.20
0.94 >=0.20	0.72 >=0.20
0.15 >=0.20	0.27 >=0.20
0.99 >=0.20	0.84 >=0.20
0.33 >=0.20	0.03 >=0.20
0.98 >=0.20	0.65 >=0.20
0.33 >=0.20	1 >=0.20
1 >=0.20	0.95 >=0.20
0.58 >=0.20	0.47 >=0.20
1 >=0.20	0.97 >=0.20
0.12 >=0.20	0.49 >=0.20
0.9 >=0.20	0.94 >=0.20
0.94 >=0.20	0.91 >=0.20
0.92 >=0.20	0.91 >=0.20
0.93 >=0.20	0.95 >=0.20
0.73 >=0.20	0.06 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.21 >=0.20
0.93 >=0.20	0.6 >=0.20
0.84 >=0.20	0.77 >=0.20
0.42 >=0.20	0.79 >=0.20
0.18 >=0.20	0.85 >=0.20
0.73 >=0.20	0.23 >=0.20
0.59 >=0.20	0.18 >=0.20
0.51 >=0.20	0.95 >=0.20
0.52 >=0.20	0.13 >=0.20
0.66 >=0.20	0.59 >=0.20
0.95 >=0.20	0.92 >=0.20
0.91 >=0.20	0.6 >=0.20
0.75 >=0.20	0.89 >=0.20
0.33 >=0.20	0.06 >=0.20
0.55 >=0.20	0.77 >=0.20

0.25 >=0.20	0.97 >=0.20
0.23 >=0.20	0.98 >=0.20
0.64 >=0.20	1 >=0.20
0.44 >=0.20	1 >=0.20
0.12 >=0.20	0.92 >=0.20
0.24 >=0.20	0.95 >=0.20
0.19 >=0.20	0.91 >=0.20
0.29 >=0.20	0.99 >=0.20
0.52 >=0.20	0.82 >=0.20
0.94 >=0.20	0.85 >=0.20
0.23 >=0.20	0.88 >=0.20
0.37 >=0.20	0.39 >=0.20
0.65 >=0.20	0.1 >=0.20
0.79 >=0.20	0.45 >=0.20
0.92 >=0.20	0.38 >=0.20
1 >=0.20	0.89 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.68 >=0.20
0.81 >=0.20	0.86 >=0.20
0.8 >=0.20	0.93 >=0.20
0.43 >=0.20	0.93 >=0.20
0.4 >=0.20	0.83 >=0.20
0.61 >=0.20	0.93 >=0.20
0.77 >=0.20	0.98 >=0.20
0.28 >=0.20	0.52 >=0.20
0.19 >=0.20	0.86 >=0.20
0.69 >=0.20	0.88 >=0.20
0.32 >=0.20	0.63 >=0.20
0.78 >=0.20	0.99 >=0.20
0.74 >=0.20	0.92 >=0.20
0.8 >=0.20	0.97 >=0.20
0.64 >=0.20	0.95 >=0.20
0.93 >=0.20	1 >=0.20
0.77 >=0.20	0.58 >=0.20
0.35 >=0.20	0.59 >=0.20
0.56 >=0.20	0.82 >=0.20
0.51 >=0.20	0.77 >=0.20
0.6 >=0.20	0.95 >=0.20
0.57 >=0.20	0.94 >=0.20
0.59 >=0.20	0.81 >=0.20
0.65 >=0.20	0.93 >=0.20
0.32 >=0.20	0.85 >=0.20
0.4 >=0.20	0.89 >=0.20
0.55 >=0.20	0.9 >=0.20
0.52 >=0.20	0.87 >=0.20
0.72 >=0.20	0.96 >=0.20
0.64 >=0.20	0.91 >=0.20

0.9 >=0.20	0.97 >=0.20
0.85 >=0.20	0.1 >=0.20
0.69 >=0.20	0.15 >=0.20
0.39 >=0.20	0.32 >=0.20
0.99 >=0.20	0.71 >=0.20
0.43 >=0.20	0.62 >=0.20
0.69 >=0.20	1 >=0.20
0.77 >=0.20	1 >=0.20
0.65 >=0.20	1 >=0.20
0.84 >=0.20	1 >=0.20
0.9 >=0.20	0.99 >=0.20
0.58 >=0.20	0.67 >=0.20
0.53 >=0.20	0.88 >=0.20
0.99 >=0.20	0.97 >=0.20
0.7 >=0.20	0.96 >=0.20
0.27 >=0.20	0.46 >=0.20
0.1 >=0.20	0.14 >=0.20
1 >=0.20	1 >=0.20
0.8 >=0.20	0.76 >=0.20
0.28 >=0.20	0.74 >=0.20
0.64 >=0.20	0.82 >=0.20
0.04 >=0.20	0.41 >=0.20
0.14 >=0.20	0.3 >=0.20
0.06 >=0.20	0.54 >=0.20
0.72 >=0.20	0.77 >=0.20
0.21 >=0.20	0.65 >=0.20
0.99 >=0.20	0.87 >=0.20
0.94 >=0.20	1 >=0.20
0.64 >=0.20	0.62 >=0.20
0.07 >=0.20	0.04 >=0.20
1 >=0.20	0.95 >=0.20
1 >=0.20	0.96 >=0.20
0.94 >=0.20	0.91 >=0.20
1 >=0.20	0.94 >=0.20
0.99 >=0.20	0.98 >=0.20
0.87 >=0.20	0.29 >=0.20
0.75 >=0.20	0.84 >=0.20
0.63 >=0.20	0.71 >=0.20
0.95 >=0.20	0.98 >=0.20
0.95 >=0.20	0.99 >=0.20
1 >=0.20	0.97 >=0.20
0.99 >=0.20	0.86 >=0.20
0.99 >=0.20	0.86 >=0.20
0.97 >=0.20	0.95 >=0.20
0.57 >=0.20	0.09 >=0.20
1 >=0.20	1 >=0.20
0.29 >=0.20	0.93 >=0.20

0.35 >=0.20	0.16 >=0.20
0.31 >=0.20	0.57 >=0.20
0.98 >=0.20	0.65 >=0.20
0.98 >=0.20	0.65 >=0.20
0.97 >=0.20	0.68 >=0.20
0.41 >=0.20	0.09 >=0.20
0.21 >=0.20	0.16 >=0.20
0.81 >=0.20	0.84 >=0.20
1 >=0.20	0.97 >=0.20
0.99 >=0.20	0.82 >=0.20
0.68 >=0.20	0.9 >=0.20
0.84 >=0.20	0.75 >=0.20
0.68 >=0.20	0.9 >=0.20
0.77 >=0.20	0.61 >=0.20
0.67 >=0.20	0.91 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	0.88 >=0.20
0.48 >=0.20	0.99 >=0.20
0.72 >=0.20	0.43 >=0.20
0.05 >=0.20	0.36 >=0.20
0.04 >=0.20	0.08 >=0.20
0.3 >=0.20	0.18 >=0.20
0.63 >=0.20	0.07 >=0.20
0.46 >=0.20	0.88 >=0.20
0.05 >=0.20	0.39 >=0.20
0.46 >=0.20	0.82 >=0.20
0.89 >=0.20	0.96 >=0.20
0.6 >=0.20	0.88 >=0.20
0.47 >=0.20	0.81 >=0.20
0.83 >=0.20	0.94 >=0.20
0.18 >=0.20	0.94 >=0.20
0.68 >=0.20	0.68 >=0.20
0.56 >=0.20	0.96 >=0.20
0.99 >=0.20	0.99 >=0.20
0.54 >=0.20	0.18 >=0.20
0.95 >=0.20	1 >=0.20
0.99 >=0.20	0.97 >=0.20
0.99 >=0.20	0.57 >=0.20
0.87 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
0.78 >=0.20	0.99 >=0.20
0.73 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
0.99 >=0.20	0.97 >=0.20
0.93 >=0.20	0.99 >=0.20
0.97 >=0.20	0.98 >=0.20
0.96 >=0.20	1 >=0.20

0.82 >=0.20	1 >=0.20
0.79 >=0.20	1 >=0.20
0.94 >=0.20	0.98 >=0.20
0.85 >=0.20	1 >=0.20
0.44 >=0.20	0.89 >=0.20
0.97 >=0.20	1 >=0.20
0.44 >=0.20	0.13 >=0.20
0.98 >=0.20	1 >=0.20
0.42 >=0.20	0.86 >=0.20
0.76 >=0.20	0.38 >=0.20
0.67 >=0.20	0.96 >=0.20
0.41 >=0.20	0.3 >=0.20
0.3 >=0.20	0.95 >=0.20
0.4 >=0.20	1 >=0.20
0.92 >=0.20	1 >=0.20
0.57 >=0.20	0.84 >=0.20
0.98 >=0.20	0.98 >=0.20
0.99 >=0.20	0.96 >=0.20
0.98 >=0.20	0.99 >=0.20
0.06 >=0.20	0.04 >=0.20
0.06 >=0.20	0.08 >=0.20
0.13 >=0.20	0.2 >=0.20
0.05 >=0.20	0.03 >=0.20
0.46 >=0.20	0.82 >=0.20
0.83 >=0.20	0.62 >=0.20
1 >=0.20	0.89 >=0.20
0.96 >=0.20	0.78 >=0.20
0.56 >=0.20	0.97 >=0.20
0.98 >=0.20	0.83 >=0.20
0.58 >=0.20	0.86 >=0.20
0.58 >=0.20	0.86 >=0.20
0.41 >=0.20	0.71 >=0.20
0.22 >=0.20	0.45 >=0.20
0.39 >=0.20	0.92 >=0.20
0.05 >=0.20	0.73 >=0.20
0.62 >=0.20	0.78 >=0.20
0.04 >=0.20	0.51 >=0.20
0.29 >=0.20	0.04 >=0.20
0.38 >=0.20	1 >=0.20
0.4 >=0.20	0.95 >=0.20
0.41 >=0.20	0.89 >=0.20
0.3 >=0.20	0.84 >=0.20
0.71 >=0.20	0.91 >=0.20
0.66 >=0.20	0.92 >=0.20
0.24 >=0.20	0.89 >=0.20
0.84 >=0.20	0.96 >=0.20
0.46 >=0.20	1 >=0.20

0.19 >=0.20	0.99 >=0.20
0.37 >=0.20	0.99 >=0.20
0.29 >=0.20	0.99 >=0.20
0.32 >=0.20	0.27 >=0.20
0.07 >=0.20	0.47 >=0.20
0.43 >=0.20	1 >=0.20
0.19 >=0.20	0.51 >=0.20
0.14 >=0.20	0.88 >=0.20
0.66 >=0.20	0.33 >=0.20
0.51 >=0.20	0.27 >=0.20
0.8 >=0.20	0.21 >=0.20
0.97 >=0.20	0.63 >=0.20
0.65 >=0.20	0.81 >=0.20
0.4 >=0.20	0.25 >=0.20
0.99 >=0.20	0.64 >=0.20
0.85 >=0.20	0.85 >=0.20
0.28 >=0.20	0.17 >=0.20
0.14 >=0.20	0.51 >=0.20
0.05 >=0.20	0.48 >=0.20
0.15 >=0.20	0.72 >=0.20
0.95 >=0.20	1 >=0.20
0.55 >=0.20	0.89 >=0.20
0.8 >=0.20	0.88 >=0.20
0.81 >=0.20	0.86 >=0.20
0.26 >=0.20	0.95 >=0.20
0.95 >=0.20	0.99 >=0.20
0.95 >=0.20	0.99 >=0.20
0.88 >=0.20	0.63 >=0.20
0.93 >=0.20	0.68 >=0.20
0.52 >=0.20	0.74 >=0.20
0.66 >=0.20	0.73 >=0.20
0.12 >=0.20	0.06 >=0.20
0.04 >=0.20	0.5 >=0.20
0.98 >=0.20	0.87 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.59 >=0.20	0.23 >=0.20
0.76 >=0.20	0.87 >=0.20
0.97 >=0.20	0.69 >=0.20
0.98 >=0.20	0.88 >=0.20
1 >=0.20	0.76 >=0.20
1 >=0.20	0.84 >=0.20
0.99 >=0.20	0.89 >=0.20
0.64 >=0.20	0.42 >=0.20
1 >=0.20	0.88 >=0.20
1 >=0.20	0.92 >=0.20
0.99 >=0.20	0.9 >=0.20

0.97 >=0.20	0.97 >=0.20
0.89 >=0.20	1 >=0.20
1 >=0.20	0.88 >=0.20
0.38 >=0.20	0.07 >=0.20
0.61 >=0.20	0.36 >=0.20
0.29 >=0.20	0.34 >=0.20
0.99 >=0.20	1 >=0.20
0.54 >=0.20	0.78 >=0.20
0.88 >=0.20	0.35 >=0.20
0.1 >=0.20	0.84 >=0.20
0.99 >=0.20	0.87 >=0.20
1 >=0.20	0.9 >=0.20
0.38 >=0.20	0.89 >=0.20
0.38 >=0.20	0.18 >=0.20
0.18 >=0.20	0.22 >=0.20
0.35 >=0.20	0.46 >=0.20
0.46 >=0.20	0.36 >=0.20
0.49 >=0.20	0.75 >=0.20
0.12 >=0.20	0.97 >=0.20
0.13 >=0.20	0.36 >=0.20
0.24 >=0.20	0.4 >=0.20
0.09 >=0.20	0.54 >=0.20
0.92 >=0.20	0.58 >=0.20
0.35 >=0.20	0.37 >=0.20
0.3 >=0.20	0.27 >=0.20
0.09 >=0.20	0.32 >=0.20
0.15 >=0.20	0.26 >=0.20
0.68 >=0.20	0.61 >=0.20
0.11 >=0.20	0.08 >=0.20
0.17 >=0.20	0.46 >=0.20
0.5 >=0.20	0.68 >=0.20
0.09 >=0.20	0.19 >=0.20
0.28 >=0.20	0.63 >=0.20
0.05 >=0.20	0.32 >=0.20
0.05 >=0.20	0.22 >=0.20
0.35 >=0.20	0.62 >=0.20
0.07 >=0.20	0.16 >=0.20
0.07 >=0.20	0.65 >=0.20
0.15 >=0.20	0.84 >=0.20
0.84 >=0.20	0.91 >=0.20
0.05 >=0.20	0.71 >=0.20
0.1 >=0.20	0.7 >=0.20
0.2 >=0.20	0.47 >=0.20
0.83 >=0.20	0.92 >=0.20
0.94 >=0.20	1 >=0.20
0.87 >=0.20	0.66 >=0.20
0.77 >=0.20	0.79 >=0.20

0.4 >=0.20	0.57 >=0.20
0.6 >=0.20	0.94 >=0.20
0.84 >=0.20	0.78 >=0.20
0.92 >=0.20	0.61 >=0.20
0.99 >=0.20	0.85 >=0.20
0.98 >=0.20	0.84 >=0.20
0.98 >=0.20	0.82 >=0.20
0.98 >=0.20	0.82 >=0.20
0.98 >=0.20	0.84 >=0.20
0.86 >=0.20	0.97 >=0.20
0.61 >=0.20	0.74 >=0.20
0.93 >=0.20	0.71 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.48 >=0.20	0.22 >=0.20
0.48 >=0.20	0.71 >=0.20
0.34 >=0.20	0.41 >=0.20
0.42 >=0.20	0.75 >=0.20
0.16 >=0.20	0.09 >=0.20
0.16 >=0.20	0.13 >=0.20
0.99 >=0.20	0.9 >=0.20
0.5 >=0.20	0.88 >=0.20
0.87 >=0.20	0.77 >=0.20
0.07 >=0.20	0.37 >=0.20
0.11 >=0.20	0.25 >=0.20
0.8 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.91 >=0.20	0.38 >=0.20
0.17 >=0.20	0.37 >=0.20
0.55 >=0.20	0.48 >=0.20
0.87 >=0.20	0.57 >=0.20
0.99 >=0.20	0.46 >=0.20
0.99 >=0.20	0.93 >=0.20
0.92 >=0.20	0.43 >=0.20
0.17 >=0.20	0.13 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.93 >=0.20	0.62 >=0.20
0.98 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
1 >=0.20	0.96 >=0.20
0.99 >=0.20	0.97 >=0.20
0.85 >=0.20	0.99 >=0.20
1 >=0.20	0.92 >=0.20
1 >=0.20	0.98 >=0.20
0.99 >=0.20	0.91 >=0.20
0.99 >=0.20	0.98 >=0.20

0.86 >=0.20	0.86 >=0.20
0.8 >=0.20	1 >=0.20
0.85 >=0.20	0.95 >=0.20
0.99 >=0.20	1 >=0.20
0.6 >=0.20	0.23 >=0.20
0.47 >=0.20	0.1 >=0.20
0.19 >=0.20	0.38 >=0.20
0.08 >=0.20	0.39 >=0.20
0.24 >=0.20	0.73 >=0.20
0.78 >=0.20	0.98 >=0.20
0.12 >=0.20	0.13 >=0.20
0.93 >=0.20	0.95 >=0.20
0.99 >=0.20	1 >=0.20
0.39 >=0.20	0.46 >=0.20
0.69 >=0.20	0.04 >=0.20
0.49 >=0.20	0.24 >=0.20
0.6 >=0.20	0.16 >=0.20
0.81 >=0.20	0.44 >=0.20
0.86 >=0.20	0.48 >=0.20
0.99 >=0.20	0.88 >=0.20
0.67 >=0.20	0.51 >=0.20
0.97 >=0.20	0.99 >=0.20
0.95 >=0.20	0.8 >=0.20
0.9 >=0.20	0.57 >=0.20
0.93 >=0.20	0.92 >=0.20
0.94 >=0.20	0.87 >=0.20
0.73 >=0.20	0.23 >=0.20
1 >=0.20	0.7 >=0.20
0.46 >=0.20	0.86 >=0.20
0.32 >=0.20	0.86 >=0.20
0.91 >=0.20	0.56 >=0.20
0.98 >=0.20	0.73 >=0.20
0.59 >=0.20	0.49 >=0.20
0.98 >=0.20	0.21 >=0.20
1 >=0.20	0.85 >=0.20
0.61 >=0.20	0.4 >=0.20
0.58 >=0.20	0.6 >=0.20
0.99 >=0.20	0.96 >=0.20
1 >=0.20	0.96 >=0.20
0.36 >=0.20	0.55 >=0.20
0.08 >=0.20	0.4 >=0.20
0.62 >=0.20	0.39 >=0.20
0.28 >=0.20	0.44 >=0.20
0.67 >=0.20	0.41 >=0.20
0.55 >=0.20	0.89 >=0.20
1 >=0.20	0.99 >=0.20
0.96 >=0.20	0.08 >=0.20

0.98	>=0.20	0.97	>=0.20
0.99	>=0.20	0.89	>=0.20
0.77	>=0.20	0.05	>=0.20
0.91	>=0.20	0.65	>=0.20
1	>=0.20	0.96	>=0.20
0.9	>=0.20	0.99	>=0.20
0.93	>=0.20	0.99	>=0.20
0.99	>=0.20	0.99	>=0.20
1	>=0.20	0.5	>=0.20
0.82	>=0.20	0.39	>=0.20
0.96	>=0.20	0.58	>=0.20
0.24	>=0.20	0.67	>=0.20
0.13	>=0.20	0.24	>=0.20
0.12	>=0.20	0.59	>=0.20
0.68	>=0.20	0.99	>=0.20
0.81	>=0.20	0.69	>=0.20
0.78	>=0.20	0.7	>=0.20
0.78	>=0.20	0.84	>=0.20
0.82	>=0.20	0.73	>=0.20
0.78	>=0.20	0.84	>=0.20
0.78	>=0.20	0.7	>=0.20
0.09	>=0.20	0.14	>=0.20
0.15	>=0.20	0.63	>=0.20
0.98	>=0.20	0.87	>=0.20
0.98	>=0.20	0.87	>=0.20
0.98	>=0.20	0.87	>=0.20
0.98	>=0.20	0.83	>=0.20
0.58	>=0.20	0.86	>=0.20
0.47	>=0.20	0.64	>=0.20
0.28	>=0.20	0.79	>=0.20
0.05	>=0.20	0.07	>=0.20
0.23	>=0.20	0.04	>=0.20
0.88	>=0.20	0.09	>=0.20
0.49	>=0.20	0.64	>=0.20
1	>=0.20	1	>=0.20
0.76	>=0.20	0.89	>=0.20
0.62	>=0.20	0.96	>=0.20
0.62	>=0.20	0.96	>=0.20
0.87	>=0.20	0.54	>=0.20
0.18	>=0.20	0.92	>=0.20
1	>=0.20	0.99	>=0.20
0.95	>=0.20	0.98	>=0.20
0.41	>=0.20	0.94	>=0.20
0.97	>=0.20	0.85	>=0.20
0.9	>=0.20	0.26	>=0.20
0.9	>=0.20	0.79	>=0.20
1	>=0.20	1	>=0.20

0.73 >=0.20	0.78 >=0.20
0.88 >=0.20	0.54 >=0.20
0.45 >=0.20	0.45 >=0.20
0.76 >=0.20	0.32 >=0.20
0.81 >=0.20	0.47 >=0.20
0.34 >=0.20	0.07 >=0.20
0.35 >=0.20	0.71 >=0.20
0.36 >=0.20	1 >=0.20
0.42 >=0.20	1 >=0.20
0.43 >=0.20	1 >=0.20
0.09 >=0.20	0.17 >=0.20
0.99 >=0.20	0.84 >=0.20
0.66 >=0.20	0.36 >=0.20
0.99 >=0.20	0.83 >=0.20
0.98 >=0.20	0.83 >=0.20
0.98 >=0.20	0.85 >=0.20
0.99 >=0.20	0.89 >=0.20
0.45 >=0.20	0.44 >=0.20
0.98 >=0.20	0.74 >=0.20
0.95 >=0.20	0.87 >=0.20
0.48 >=0.20	0.4 >=0.20
0.66 >=0.20	0.47 >=0.20
1 >=0.20	0.96 >=0.20
0.97 >=0.20	0.8 >=0.20
0.98 >=0.20	0.95 >=0.20
0.98 >=0.20	0.85 >=0.20
0.98 >=0.20	0.84 >=0.20
0.98 >=0.20	0.86 >=0.20
0.7 >=0.20	0.3 >=0.20
0.97 >=0.20	0.84 >=0.20
0.97 >=0.20	0.83 >=0.20
0.99 >=0.20	0.87 >=0.20
0.96 >=0.20	0.86 >=0.20
0.96 >=0.20	0.78 >=0.20
0.98 >=0.20	0.83 >=0.20
0.99 >=0.20	0.91 >=0.20
0.93 >=0.20	0.8 >=0.20
0.63 >=0.20	0.58 >=0.20
0.8 >=0.20	0.73 >=0.20
0.94 >=0.20	0.81 >=0.20
0.97 >=0.20	0.82 >=0.20
0.92 >=0.20	0.67 >=0.20
0.99 >=0.20	0.81 >=0.20
0.99 >=0.20	0.86 >=0.20
0.98 >=0.20	0.84 >=0.20
0.99 >=0.20	0.95 >=0.20
0.99 >=0.20	0.87 >=0.20

0.39 >=0.20	0.78 >=0.20
0.46 >=0.20	0.49 >=0.20
1 >=0.20	0.62 >=0.20
0.8 >=0.20	0.92 >=0.20
0.26 >=0.20	0.32 >=0.20
0.88 >=0.20	0.41 >=0.20
0.68 >=0.20	0.86 >=0.20
1 >=0.20	1 >=0.20
0.63 >=0.20	0.93 >=0.20
0.5 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
0.4 >=0.20	0.95 >=0.20
0.96 >=0.20	0.97 >=0.20
0.99 >=0.20	0.87 >=0.20
0.94 >=0.20	0.78 >=0.20
0.98 >=0.20	0.67 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
0.56 >=0.20	0.54 >=0.20
0.54 >=0.20	0.36 >=0.20
0.46 >=0.20	0.99 >=0.20
0.48 >=0.20	0.83 >=0.20
0.98 >=0.20	0.64 >=0.20
1 >=0.20	0.32 >=0.20
1 >=0.20	0.98 >=0.20
0.86 >=0.20	0.65 >=0.20
0.89 >=0.20	0.87 >=0.20
0.77 >=0.20	0.83 >=0.20
0.98 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.66 >=0.20	0.39 >=0.20
0.86 >=0.20	1 >=0.20
0.99 >=0.20	0.24 >=0.20
0.78 >=0.20	1 >=0.20
0.48 >=0.20	0.4 >=0.20
0.31 >=0.20	0.81 >=0.20
0.65 >=0.20	0.99 >=0.20
0.12 >=0.20	0.09 >=0.20
1 >=0.20	0.92 >=0.20
0.04 >=0.20	0.12 >=0.20
1 >=0.20	1 >=0.20
0.53 >=0.20	0.99 >=0.20
0.73 >=0.20	0.9 >=0.20
0.88 >=0.20	0.95 >=0.20

0.43 >=0.20	0.14 >=0.20
0.26 >=0.20	0.95 >=0.20
0.26 >=0.20	0.95 >=0.20
0.91 >=0.20	0.04 >=0.20
0.62 >=0.20	0.97 >=0.20
0.45 >=0.20	0.7 >=0.20
0.95 >=0.20	0.27 >=0.20
0.93 >=0.20	0.99 >=0.20
0.52 >=0.20	0.15 >=0.20
0.73 >=0.20	0.06 >=0.20
0.6 >=0.20	0.56 >=0.20
0.23 >=0.20	0.96 >=0.20
0.22 >=0.20	0.22 >=0.20
0.91 >=0.20	0.05 >=0.20
1 >=0.20	1 >=0.20
0.71 >=0.20	0.82 >=0.20
0.83 >=0.20	0.4 >=0.20
0.91 >=0.20	0.34 >=0.20
0.53 >=0.20	0.12 >=0.20
0.92 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
0.6 >=0.20	0.91 >=0.20
0.69 >=0.20	0.94 >=0.20
0.45 >=0.20	0.78 >=0.20
0.3 >=0.20	0.94 >=0.20
0.96 >=0.20	1 >=0.20
0.87 >=0.20	0.31 >=0.20
0.99 >=0.20	0.83 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
0.95 >=0.20	0.82 >=0.20
0.6 >=0.20	0.91 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
0.96 >=0.20	1 >=0.20
0.91 >=0.20	0.99 >=0.20
0.81 >=0.20	0.72 >=0.20
0.98 >=0.20	0.25 >=0.20
0.96 >=0.20	0.21 >=0.20
0.98 >=0.20	0.21 >=0.20
0.45 >=0.20	0.9 >=0.20
0.84 >=0.20	1 >=0.20
0.7 >=0.20	0.07 >=0.20
0.24 >=0.20	0.52 >=0.20
0.74 >=0.20	0.99 >=0.20
0.57 >=0.20	0.05 >=0.20
0.23 >=0.20	0.86 >=0.20

0.87 >=0.20	0.26 >=0.20
0.9 >=0.20	0.93 >=0.20
0.67 >=0.20	0.89 >=0.20
0.08 >=0.20	0.31 >=0.20
0.97 >=0.20	0.32 >=0.20
0.91 >=0.20	0.48 >=0.20
0.85 >=0.20	1 >=0.20
0.84 >=0.20	0.95 >=0.20
0.96 >=0.20	0.97 >=0.20
0.98 >=0.20	0.59 >=0.20
0.54 >=0.20	0.04 >=0.20
0.95 >=0.20	0.89 >=0.20
0.82 >=0.20	0.62 >=0.20
0.98 >=0.20	0.62 >=0.20
0.64 >=0.20	0.5 >=0.20
0.23 >=0.20	0.96 >=0.20
0.18 >=0.20	0.94 >=0.20
0.75 >=0.20	0.92 >=0.20
0.75 >=0.20	0.92 >=0.20
0.99 >=0.20	0.94 >=0.20
0.94 >=0.20	0.98 >=0.20
0.95 >=0.20	0.98 >=0.20
0.95 >=0.20	0.79 >=0.20
0.18 >=0.20	0.52 >=0.20
0.46 >=0.20	0.85 >=0.20
1 >=0.20	0.97 >=0.20
0.98 >=0.20	0.99 >=0.20
0.97 >=0.20	0.98 >=0.20
0.98 >=0.20	0.97 >=0.20
0.97 >=0.20	1 >=0.20
0.98 >=0.20	0.97 >=0.20
0.93 >=0.20	0.99 >=0.20
0.85 >=0.20	0.84 >=0.20
0.96 >=0.20	0.34 >=0.20
0.06 >=0.20	0.17 >=0.20
0.71 >=0.20	0.8 >=0.20
0.99 >=0.20	0.98 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
0.98 >=0.20	0.97 >=0.20
0.99 >=0.20	0.94 >=0.20
0.99 >=0.20	1 >=0.20
0.89 >=0.20	0.87 >=0.20
0.86 >=0.20	0.8 >=0.20
0.91 >=0.20	0.85 >=0.20
0.88 >=0.20	0.99 >=0.20
0.98 >=0.20	0.99 >=0.20

0.83	>=0.20	0.95	>=0.20
0.9	>=0.20	0.65	>=0.20
0.99	>=0.20	0.98	>=0.20
1	>=0.20	1	>=0.20
0.99	>=0.20	0.99	>=0.20
0.83	>=0.20	0.91	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
0.61	>=0.20	0.94	>=0.20
1	>=0.20	1	>=0.20
0.96	>=0.20	0.97	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	0.97	>=0.20
0.93	>=0.20	0.89	>=0.20
0.98	>=0.20	0.93	>=0.20
0.71	>=0.20	0.54	>=0.20
1	>=0.20	0.89	>=0.20
0.53	>=0.20	0.69	>=0.20
0.84	>=0.20	0.91	>=0.20
0.5	>=0.20	0.74	>=0.20
1	>=0.20	1	>=0.20
0.54	>=0.20	0.84	>=0.20
0.8	>=0.20	0.88	>=0.20
0.99	>=0.20	1	>=0.20
0.15	>=0.20	0.09	>=0.20
0.52	>=0.20	0.86	>=0.20
0.8	>=0.20	0.97	>=0.20
0.98	>=0.20	0.34	>=0.20
0.85	>=0.20	0.64	>=0.20
0.91	>=0.20	0.87	>=0.20
0.93	>=0.20	0.97	>=0.20
0.93	>=0.20	0.72	>=0.20
0.91	>=0.20	0.71	>=0.20
0.91	>=0.20	0.4	>=0.20
0.08	>=0.20	0.11	>=0.20
0.17	>=0.20	0.33	>=0.20
0.09	>=0.20	0.04	>=0.20
0.49	>=0.20	0.12	>=0.20
0.11	>=0.20	0.14	>=0.20
0.46	>=0.20	0.37	>=0.20
0.88	>=0.20	1	>=0.20
0.05	>=0.20	0.1	>=0.20

0.84 >=0.20	0.84 >=0.20
1 >=0.20	1 >=0.20
0.87 >=0.20	0.15 >=0.20
1 >=0.20	0.78 >=0.20
0.43 >=0.20	0.13 >=0.20
1 >=0.20	1 >=0.20
0.66 >=0.20	0.79 >=0.20
0.05 >=0.20	0.39 >=0.20
0.99 >=0.20	0.98 >=0.20
0.25 >=0.20	0.91 >=0.20
0.21 >=0.20	0.51 >=0.20
0.46 >=0.20	0.28 >=0.20
0.59 >=0.20	0.02 >=0.20
0.08 >=0.20	0.27 >=0.20
0.63 >=0.20	0.95 >=0.20
0.91 >=0.20	0.81 >=0.20
0.96 >=0.20	0.89 >=0.20
0.13 >=0.20	0.46 >=0.20
0.35 >=0.20	0.64 >=0.20
0.06 >=0.20	0.07 >=0.20
0.88 >=0.20	0.44 >=0.20
0.09 >=0.20	0.24 >=0.20
0.07 >=0.20	0.63 >=0.20
0.76 >=0.20	0.98 >=0.20
0.32 >=0.20	0.34 >=0.20
0.88 >=0.20	0.97 >=0.20
1 >=0.20	0.9 >=0.20
0.14 >=0.20	0.29 >=0.20
0.62 >=0.20	0.93 >=0.20
0.85 >=0.20	0.92 >=0.20
0.18 >=0.20	0.86 >=0.20
0.09 >=0.20	0.23 >=0.20
0.98 >=0.20	0.87 >=0.20
0.68 >=0.20	0.04 >=0.20
0.96 >=0.20	0.96 >=0.20
0.99 >=0.20	0.4 >=0.20
0.79 >=0.20	0.69 >=0.20
0.91 >=0.20	0.36 >=0.20
0.98 >=0.20	0.74 >=0.20
1 >=0.20	0.34 >=0.20
0.99 >=0.20	0.21 >=0.20
0.99 >=0.20	0.89 >=0.20
0.94 >=0.20	0.8 >=0.20
0.65 >=0.20	0.03 >=0.20
0.92 >=0.20	0.65 >=0.20
0.95 >=0.20	0.16 >=0.20
1 >=0.20	0.95 >=0.20

0.45 >=0.20	0.27 >=0.20
0.91 >=0.20	0.79 >=0.20
0.99 >=0.20	0.75 >=0.20
0.68 >=0.20	0.75 >=0.20
0.14 >=0.20	0.89 >=0.20
0.57 >=0.20	0.19 >=0.20
1 >=0.20	0.76 >=0.20
0.99 >=0.20	0.97 >=0.20
0.97 >=0.20	0.51 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.21 >=0.20
0.85 >=0.20	0.7 >=0.20
0.39 >=0.20	1 >=0.20
0.85 >=0.20	0.95 >=0.20
0.85 >=0.20	0.97 >=0.20
0.99 >=0.20	0.49 >=0.20
0.56 >=0.20	0.38 >=0.20
0.04 >=0.20	0.18 >=0.20
0.08 >=0.20	0.95 >=0.20
0.26 >=0.20	0.85 >=0.20
0.16 >=0.20	0.98 >=0.20
0.68 >=0.20	0.69 >=0.20
0.58 >=0.20	0.62 >=0.20
0.81 >=0.20	0.76 >=0.20
0.22 >=0.20	0.8 >=0.20
0.26 >=0.20	0.79 >=0.20
0.18 >=0.20	0.76 >=0.20
0.38 >=0.20	1 >=0.20
0.17 >=0.20	0.54 >=0.20
0.09 >=0.20	0.22 >=0.20
0.15 >=0.20	0.05 >=0.20
0.24 >=0.20	0.7 >=0.20
0.5 >=0.20	0.85 >=0.20
0.11 >=0.20	0.44 >=0.20
0.5 >=0.20	0.93 >=0.20
0.62 >=0.20	0.99 >=0.20
0.61 >=0.20	1 >=0.20
0.8 >=0.20	0.64 >=0.20
0.19 >=0.20	0.93 >=0.20
0.3 >=0.20	0.43 >=0.20
0.04 >=0.20	0.48 >=0.20
0.76 >=0.20	0.62 >=0.20
0.99 >=0.20	0.96 >=0.20
0.05 >=0.20	0.65 >=0.20
0.16 >=0.20	0.49 >=0.20
0.07 >=0.20	0.43 >=0.20
0.07 >=0.20	0.35 >=0.20

0.99 >=0.20	0.8 >=0.20
0.08 >=0.20	0.66 >=0.20
0.39 >=0.20	0.47 >=0.20
0.95 >=0.20	0.75 >=0.20
0.97 >=0.20	0.65 >=0.20
0.18 >=0.20	0.62 >=0.20
0.93 >=0.20	0.91 >=0.20
0.99 >=0.20	0.41 >=0.20
1 >=0.20	1 >=0.20
0.9 >=0.20	0.88 >=0.20
1 >=0.20	0.99 >=0.20
0.21 >=0.20	0.43 >=0.20
0.21 >=0.20	0.43 >=0.20
0.11 >=0.20	0.79 >=0.20
0.23 >=0.20	0.85 >=0.20
0.45 >=0.20	0.99 >=0.20
0.74 >=0.20	0.58 >=0.20
0.85 >=0.20	0.68 >=0.20
0.75 >=0.20	0.58 >=0.20
0.54 >=0.20	0.24 >=0.20
0.89 >=0.20	1 >=0.20
0.13 >=0.20	0.22 >=0.20
0.93 >=0.20	0.72 >=0.20
0.33 >=0.20	1 >=0.20
0.35 >=0.20	0.04 >=0.20
0.92 >=0.20	0.4 >=0.20
0.14 >=0.20	0.1 >=0.20
0.6 >=0.20	0.43 >=0.20
0.29 >=0.20	1 >=0.20
0.25 >=0.20	1 >=0.20
0.32 >=0.20	1 >=0.20
0.09 >=0.20	0.65 >=0.20
0.28 >=0.20	0.43 >=0.20
0.07 >=0.20	0.55 >=0.20
0.31 >=0.20	1 >=0.20
0.25 >=0.20	1 >=0.20
0.11 >=0.20	0.2 >=0.20
0.21 >=0.20	1 >=0.20
0.06 >=0.20	0.93 >=0.20
0.86 >=0.20	0.63 >=0.20
0.32 >=0.20	0.63 >=0.20
0.06 >=0.20	0.21 >=0.20
0.04 >=0.20	0.42 >=0.20
0.82 >=0.20	0.28 >=0.20
0.61 >=0.20	0.07 >=0.20
0.92 >=0.20	0.41 >=0.20
0.22 >=0.20	0.24 >=0.20

0.97 >=0.20	0.99 >=0.20
0.96 >=0.20	0.99 >=0.20
0.16 >=0.20	0.45 >=0.20
0.19 >=0.20	0.74 >=0.20
0.37 >=0.20	0.84 >=0.20
0.92 >=0.20	0.57 >=0.20
0.98 >=0.20	0.99 >=0.20
0.99 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
0.9 >=0.20	0.98 >=0.20
0.96 >=0.20	0.72 >=0.20
0.7 >=0.20	0.32 >=0.20
0.98 >=0.20	0.84 >=0.20
0.32 >=0.20	0.8 >=0.20
0.04 >=0.20	0.44 >=0.20
0.74 >=0.20	0.95 >=0.20
0.74 >=0.20	0.95 >=0.20
0.76 >=0.20	0.5 >=0.20
0.98 >=0.20	0.77 >=0.20
0.31 >=0.20	0.4 >=0.20
0.79 >=0.20	0.75 >=0.20
1 >=0.20	0.89 >=0.20
0.16 >=0.20	0.99 >=0.20
0.41 >=0.20	1 >=0.20
0.31 >=0.20	0.98 >=0.20
0.35 >=0.20	1 >=0.20
0.28 >=0.20	0.99 >=0.20
0.46 >=0.20	1 >=0.20
1 >=0.20	0.89 >=0.20
0.83 >=0.20	0.88 >=0.20
1 >=0.20	1 >=0.20
0.9 >=0.20	0.66 >=0.20
0.13 >=0.20	0.2 >=0.20
0.41 >=0.20	0.71 >=0.20
0.39 >=0.20	0.92 >=0.20
0.72 >=0.20	1 >=0.20
0.12 >=0.20	0.13 >=0.20
0.3 >=0.20	1 >=0.20
0.45 >=0.20	0.68 >=0.20
0.05 >=0.20	0.04 >=0.20
0.5 >=0.20	0.83 >=0.20
0.4 >=0.20	0.16 >=0.20
0.71 >=0.20	0.98 >=0.20
0.04 >=0.20	0.16 >=0.20
0.34 >=0.20	0.46 >=0.20
0.65 >=0.20	0.66 >=0.20
0.17 >=0.20	0.13 >=0.20

0.64	>=0.20	0.78	>=0.20
0.2	>=0.20	0.03	>=0.20
0.45	>=0.20	0.3	>=0.20
0.33	>=0.20	0.11	>=0.20
0.23	>=0.20	0.04	>=0.20
0.39	>=0.20	0.48	>=0.20
0.33	>=0.20	0.11	>=0.20
0.97	>=0.20	0.47	>=0.20
0.75	>=0.20	0.29	>=0.20
1	>=0.20	0.55	>=0.20
0.7	>=0.20	0.14	>=0.20
1	>=0.20	0.91	>=0.20
0.21	>=0.20	0.33	>=0.20
1	>=0.20	1	>=0.20
0.95	>=0.20	0.73	>=0.20
0.55	>=0.20	0.12	>=0.20
0.81	>=0.20	0.35	>=0.20
0.87	>=0.20	0.7	>=0.20
0.83	>=0.20	0.62	>=0.20
0.7	>=0.20	0.49	>=0.20
0.2	>=0.20	0.21	>=0.20
0.98	>=0.20	0.98	>=0.20
0.23	>=0.20	0.63	>=0.20
0.7	>=0.20	0.91	>=0.20
0.36	>=0.20	0.19	>=0.20
0.82	>=0.20	0.71	>=0.20
0.49	>=0.20	0.47	>=0.20
0.95	>=0.20	0.92	>=0.20
0.35	>=0.20	0.05	>=0.20
0.08	>=0.20	0.11	>=0.20
0.1	>=0.20	0.05	>=0.20
0.15	>=0.20	0.54	>=0.20
0.63	>=0.20	0.73	>=0.20
0.39	>=0.20	0.37	>=0.20
0.48	>=0.20	0.86	>=0.20
0.04	>=0.20	0.16	>=0.20
0.37	>=0.20	0.25	>=0.20
0.39	>=0.20	0.61	>=0.20
0.05	>=0.20	0.18	>=0.20
0.06	>=0.20	0.39	>=0.20
0.26	>=0.20	0.95	>=0.20
0.98	>=0.20	0.91	>=0.20
0.82	>=0.20	0.61	>=0.20
0.18	>=0.20	0.86	>=0.20
0.12	>=0.20	0.26	>=0.20
0.24	>=0.20	0.28	>=0.20
0.5	>=0.20	1	>=0.20

0.48 >=0.20	0.63 >=0.20
0.07 >=0.20	0.28 >=0.20
0.98 >=0.20	0.95 >=0.20
0.19 >=0.20	0.29 >=0.20
0.25 >=0.20	0.63 >=0.20
0.39 >=0.20	0.06 >=0.20
1 >=0.20	1 >=0.20
0.9 >=0.20	1 >=0.20
0.88 >=0.20	0.99 >=0.20
0.52 >=0.20	0.96 >=0.20
0.17 >=0.20	0.18 >=0.20
0.46 >=0.20	0.21 >=0.20
0.1 >=0.20	0.3 >=0.20
0.37 >=0.20	0.77 >=0.20
0.04 >=0.20	0.21 >=0.20
0.69 >=0.20	0.66 >=0.20
0.09 >=0.20	0.67 >=0.20
0.99 >=0.20	0.57 >=0.20
0.17 >=0.20	0.46 >=0.20
0.42 >=0.20	0.09 >=0.20
0.68 >=0.20	0.83 >=0.20
0.8 >=0.20	0.24 >=0.20
1 >=0.20	0.97 >=0.20
0.98 >=0.20	0.97 >=0.20
0.46 >=0.20	1 >=0.20
0.19 >=0.20	0.25 >=0.20
0.11 >=0.20	0.11 >=0.20
0.15 >=0.20	0.34 >=0.20
0.43 >=0.20	0.07 >=0.20
0.73 >=0.20	0.05 >=0.20
0.93 >=0.20	0.88 >=0.20
1 >=0.20	1 >=0.20
0.38 >=0.20	0.33 >=0.20
0.92 >=0.20	0.38 >=0.20
0.97 >=0.20	0.8 >=0.20
0.12 >=0.20	0.59 >=0.20
0.07 >=0.20	0.21 >=0.20
1 >=0.20	0.82 >=0.20
0.45 >=0.20	0.45 >=0.20
0.79 >=0.20	0.61 >=0.20
0.81 >=0.20	0.15 >=0.20
0.65 >=0.20	0.97 >=0.20
1 >=0.20	0.95 >=0.20
0.99 >=0.20	0.59 >=0.20
0.66 >=0.20	0.14 >=0.20
0.25 >=0.20	0.22 >=0.20
1 >=0.20	0.85 >=0.20

0.42 >=0.20	0.21 >=0.20
0.07 >=0.20	0.19 >=0.20
0.97 >=0.20	0.41 >=0.20
0.98 >=0.20	0.54 >=0.20
0.99 >=0.20	0.53 >=0.20
0.97 >=0.20	0.46 >=0.20
0.97 >=0.20	0.53 >=0.20
0.93 >=0.20	0.45 >=0.20
0.06 >=0.20	0.47 >=0.20
0.97 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.79 >=0.20
0.94 >=0.20	0.69 >=0.20
0.34 >=0.20	0.91 >=0.20
0.13 >=0.20	0.53 >=0.20
0.99 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
0.89 >=0.20	0.49 >=0.20
0.83 >=0.20	0.25 >=0.20
0.87 >=0.20	0.74 >=0.20
0.98 >=0.20	0.88 >=0.20
1 >=0.20	0.5 >=0.20
0.76 >=0.20	0.36 >=0.20
0.18 >=0.20	0.04 >=0.20
0.06 >=0.20	0.17 >=0.20
0.6 >=0.20	0.79 >=0.20
0.95 >=0.20	0.4 >=0.20
0.34 >=0.20	0.7 >=0.20
0.92 >=0.20	0.84 >=0.20
0.95 >=0.20	0.95 >=0.20
0.58 >=0.20	0.93 >=0.20
0.06 >=0.20	0.18 >=0.20
0.88 >=0.20	0.98 >=0.20
0.61 >=0.20	0.12 >=0.20
0.76 >=0.20	0.46 >=0.20
0.16 >=0.20	0.61 >=0.20
0.49 >=0.20	0.73 >=0.20
0.05 >=0.20	0.31 >=0.20
0.1 >=0.20	0.35 >=0.20
0.05 >=0.20	0.15 >=0.20
0.94 >=0.20	0.74 >=0.20
0.94 >=0.20	0.84 >=0.20
0.19 >=0.20	0.24 >=0.20
0.95 >=0.20	0.45 >=0.20
0.08 >=0.20	0.05 >=0.20
1 >=0.20	0.58 >=0.20
0.93 >=0.20	0.38 >=0.20

0.86	>=0.20	0.2	>=0.20
0.11	>=0.20	0.55	>=0.20
0.05	>=0.20	0.16	>=0.20
0.97	>=0.20	0.94	>=0.20
0.71	>=0.20	0.89	>=0.20
0.07	>=0.20	0.9	>=0.20
0.91	>=0.20	0.59	>=0.20
0.82	>=0.20	0.33	>=0.20
0.72	>=0.20	0.12	>=0.20
0.75	>=0.20	0.21	>=0.20
0.82	>=0.20	0.09	>=0.20
0.2	>=0.20	0.48	>=0.20
0.77	>=0.20	0.35	>=0.20
0.94	>=0.20	0.16	>=0.20
0.53	>=0.20	0.42	>=0.20
1	>=0.20	0.96	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
0.35	>=0.20	0.05	>=0.20
0.05	>=0.20	0.53	>=0.20
0.31	>=0.20	0.11	>=0.20
0.1	>=0.20	0.29	>=0.20
0.05	>=0.20	0.63	>=0.20
0.12	>=0.20	0.29	>=0.20
0.6	>=0.20	0.75	>=0.20
0.11	>=0.20	0.03	>=0.20
0.21	>=0.20	0.07	>=0.20
0.71	>=0.20	0.99	>=0.20
0.73	>=0.20	0.85	>=0.20
0.89	>=0.20	0.99	>=0.20
0.91	>=0.20	0.98	>=0.20
0.91	>=0.20	0.98	>=0.20
0.97	>=0.20	0.53	>=0.20
1	>=0.20	0.97	>=0.20
0.81	>=0.20	0.89	>=0.20
0.42	>=0.20	0.73	>=0.20
0.64	>=0.20	0.92	>=0.20
0.17	>=0.20	0.69	>=0.20
0.09	>=0.20	0.76	>=0.20
0.09	>=0.20	0.22	>=0.20
0.89	>=0.20	0.64	>=0.20
0.19	>=0.20	0.82	>=0.20
0.93	>=0.20	0.99	>=0.20
0.27	>=0.20	0.47	>=0.20
0.47	>=0.20	0.22	>=0.20
0.39	>=0.20	0.1	>=0.20

0.43 >=0.20	0.39 >=0.20
0.15 >=0.20	0.63 >=0.20
0.96 >=0.20	0.51 >=0.20
0.45 >=0.20	0.65 >=0.20
0.5 >=0.20	0.22 >=0.20
0.59 >=0.20	0.13 >=0.20
0.84 >=0.20	0.61 >=0.20
0.58 >=0.20	0.63 >=0.20
0.19 >=0.20	0.5 >=0.20
0.98 >=0.20	0.95 >=0.20
0.59 >=0.20	0.61 >=0.20
0.27 >=0.20	0.74 >=0.20
0.07 >=0.20	0.06 >=0.20
0.36 >=0.20	0.04 >=0.20
0.98 >=0.20	0.99 >=0.20
0.98 >=0.20	0.82 >=0.20
0.11 >=0.20	0.06 >=0.20
0.85 >=0.20	0.18 >=0.20
0.79 >=0.20	0.56 >=0.20
1 >=0.20	0.94 >=0.20
0.3 >=0.20	0.1 >=0.20
0.57 >=0.20	0.58 >=0.20
0.92 >=0.20	0.75 >=0.20
0.99 >=0.20	0.98 >=0.20
0.99 >=0.20	0.34 >=0.20
0.98 >=0.20	0.95 >=0.20
0.07 >=0.20	0.54 >=0.20
0.99 >=0.20	0.92 >=0.20
0.5 >=0.20	0.81 >=0.20
0.96 >=0.20	0.49 >=0.20
0.72 >=0.20	0.5 >=0.20
0.51 >=0.20	0.06 >=0.20
0.14 >=0.20	0.25 >=0.20
0.13 >=0.20	0.57 >=0.20
0.99 >=0.20	0.23 >=0.20
0.99 >=0.20	1 >=0.20
0.45 >=0.20	0.73 >=0.20
0.97 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.96 >=0.20
0.33 >=0.20	0.78 >=0.20
0.68 >=0.20	0.72 >=0.20
0.09 >=0.20	0.22 >=0.20
0.75 >=0.20	0.98 >=0.20
0.73 >=0.20	0.99 >=0.20
0.65 >=0.20	0.28 >=0.20

0.38	>=0.20	0.19	>=0.20
0.67	>=0.20	0.68	>=0.20
0.66	>=0.20	0.9	>=0.20
0.81	>=0.20	0.85	>=0.20
1	>=0.20	0.92	>=0.20
0.07	>=0.20	0.66	>=0.20
0.23	>=0.20	0.77	>=0.20
0.04	>=0.20	0.92	>=0.20
0.99	>=0.20	0.98	>=0.20
0.59	>=0.20	0.94	>=0.20
0.67	>=0.20	0.99	>=0.20
0.27	>=0.20	0.93	>=0.20
0.29	>=0.20	0.28	>=0.20
0.22	>=0.20	0.83	>=0.20
0.92	>=0.20	0.45	>=0.20
0.64	>=0.20	0.33	>=0.20
0.96	>=0.20	0.88	>=0.20
0.99	>=0.20	0.92	>=0.20
0.87	>=0.20	0.55	>=0.20
0.51	>=0.20	0.27	>=0.20
0.78	>=0.20	0.25	>=0.20
0.81	>=0.20	0.38	>=0.20
0.22	>=0.20	0.41	>=0.20
0.93	>=0.20	0.38	>=0.20
0.82	>=0.20	0.41	>=0.20
0.53	>=0.20	0.28	>=0.20
0.91	>=0.20	0.21	>=0.20
0.78	>=0.20	0.1	>=0.20
1	>=0.20	1	>=0.20
0.89	>=0.20	0.67	>=0.20
0.87	>=0.20	0.96	>=0.20
0.85	>=0.20	0.74	>=0.20
0.75	>=0.20	0.8	>=0.20
0.99	>=0.20	0.77	>=0.20
0.95	>=0.20	0.46	>=0.20
0.29	>=0.20	0.22	>=0.20
0.96	>=0.20	0.97	>=0.20
1	>=0.20	1	>=0.20
0.61	>=0.20	0.38	>=0.20
0.99	>=0.20	0.84	>=0.20
0.39	>=0.20	0.09	>=0.20
0.91	>=0.20	0.76	>=0.20
0.92	>=0.20	0.96	>=0.20
0.81	>=0.20	0.38	>=0.20
0.67	>=0.20	0.6	>=0.20
0.96	>=0.20	0.38	>=0.20
0.2	>=0.20	0.34	>=0.20

1 >=0.20	0.98 >=0.20
0.35 >=0.20	0.8 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
0.88 >=0.20	0.5 >=0.20
0.32 >=0.20	0.31 >=0.20
0.29 >=0.20	0.51 >=0.20
0.33 >=0.20	0.89 >=0.20
0.99 >=0.20	0.81 >=0.20
0.75 >=0.20	0.97 >=0.20
0.09 >=0.20	0.13 >=0.20
0.3 >=0.20	0.81 >=0.20
0.39 >=0.20	1 >=0.20
0.98 >=0.20	0.94 >=0.20
0.14 >=0.20	0.38 >=0.20
0.98 >=0.20	0.84 >=0.20
1 >=0.20	0.95 >=0.20
0.04 >=0.20	0.13 >=0.20
0.76 >=0.20	0.23 >=0.20
0.54 >=0.20	1 >=0.20
0.94 >=0.20	0.96 >=0.20
0.06 >=0.20	0.29 >=0.20
0.69 >=0.20	0.7 >=0.20
0.49 >=0.20	0.06 >=0.20
0.49 >=0.20	0.99 >=0.20
0.06 >=0.20	0.23 >=0.20
0.18 >=0.20	0.15 >=0.20
0.36 >=0.20	0.98 >=0.20
0.23 >=0.20	0.79 >=0.20
0.19 >=0.20	0.74 >=0.20
0.57 >=0.20	0.98 >=0.20
0.24 >=0.20	0.36 >=0.20
0.37 >=0.20	0.97 >=0.20
0.51 >=0.20	0.97 >=0.20
0.1 >=0.20	0.44 >=0.20
0.48 >=0.20	0.86 >=0.20
0.32 >=0.20	0.74 >=0.20
0.62 >=0.20	0.96 >=0.20
0.96 >=0.20	0.85 >=0.20
0.95 >=0.20	0.86 >=0.20
0.1 >=0.20	0.36 >=0.20
0.17 >=0.20	0.35 >=0.20
0.72 >=0.20	0.93 >=0.20
0.29 >=0.20	0.65 >=0.20
0.36 >=0.20	0.66 >=0.20
0.04 >=0.20	0.21 >=0.20
0.19 >=0.20	0.43 >=0.20

0.95 >=0.20	0.94 >=0.20
0.91 >=0.20	0.77 >=0.20
0.99 >=0.20	0.96 >=0.20
0.5 >=0.20	0.94 >=0.20
0.15 >=0.20	0.51 >=0.20
0.54 >=0.20	0.95 >=0.20
0.7 >=0.20	0.84 >=0.20
0.44 >=0.20	0.94 >=0.20
0.66 >=0.20	0.88 >=0.20
0.41 >=0.20	0.68 >=0.20
0.96 >=0.20	0.64 >=0.20
0.91 >=0.20	0.97 >=0.20
0.94 >=0.20	0.23 >=0.20
1 >=0.20	1 >=0.20
0.49 >=0.20	0.2 >=0.20
0.8 >=0.20	0.58 >=0.20
0.43 >=0.20	0.26 >=0.20
0.84 >=0.20	0.2 >=0.20
0.05 >=0.20	0.62 >=0.20
0.64 >=0.20	0.9 >=0.20
0.35 >=0.20	0.79 >=0.20
0.94 >=0.20	0.95 >=0.20
0.13 >=0.20	0.92 >=0.20
0.48 >=0.20	0.84 >=0.20
0.48 >=0.20	0.34 >=0.20
0.89 >=0.20	0.99 >=0.20
0.34 >=0.20	0.97 >=0.20
0.33 >=0.20	0.98 >=0.20
0.94 >=0.20	0.7 >=0.20
0.8 >=0.20	0.49 >=0.20
0.73 >=0.20	0.91 >=0.20
0.73 >=0.20	0.98 >=0.20
0.2 >=0.20	0.09 >=0.20
0.74 >=0.20	0.8 >=0.20
0.98 >=0.20	0.92 >=0.20
0.73 >=0.20	0.81 >=0.20
0.87 >=0.20	0.86 >=0.20
0.84 >=0.20	0.17 >=0.20
0.98 >=0.20	1 >=0.20
0.76 >=0.20	0.54 >=0.20
0.68 >=0.20	0.54 >=0.20
0.99 >=0.20	1 >=0.20
0.63 >=0.20	0.56 >=0.20
0.97 >=0.20	0.67 >=0.20
0.97 >=0.20	0.67 >=0.20
1 >=0.20	0.99 >=0.20
0.91 >=0.20	0.92 >=0.20

0.91 >=0.20	0.92 >=0.20
0.52 >=0.20	0.83 >=0.20
1 >=0.20	0.98 >=0.20
0.19 >=0.20	0.79 >=0.20
0.21 >=0.20	0.68 >=0.20
0.12 >=0.20	0.94 >=0.20
1 >=0.20	0.83 >=0.20
1 >=0.20	0.25 >=0.20
0.77 >=0.20	0.99 >=0.20
0.3 >=0.20	0.08 >=0.20
0.81 >=0.20	0.92 >=0.20
0.29 >=0.20	0.07 >=0.20
0.99 >=0.20	0.81 >=0.20
0.22 >=0.20	0.03 >=0.20
0.91 >=0.20	0.74 >=0.20
0.86 >=0.20	0.39 >=0.20
0.05 >=0.20	0.94 >=0.20
0.69 >=0.20	0.08 >=0.20
0.72 >=0.20	0.67 >=0.20
0.94 >=0.20	0.7 >=0.20
0.9 >=0.20	0.45 >=0.20
0.89 >=0.20	0.44 >=0.20
0.98 >=0.20	0.89 >=0.20
0.1 >=0.20	0.88 >=0.20
0.13 >=0.20	0.62 >=0.20
0.39 >=0.20	1 >=0.20
0.71 >=0.20	0.98 >=0.20
0.83 >=0.20	0.97 >=0.20
0.12 >=0.20	0.58 >=0.20
0.75 >=0.20	0.96 >=0.20
0.79 >=0.20	0.99 >=0.20
0.52 >=0.20	0.38 >=0.20
0.57 >=0.20	0.22 >=0.20
0.31 >=0.20	0.06 >=0.20
0.75 >=0.20	0.33 >=0.20
0.91 >=0.20	0.99 >=0.20
0.99 >=0.20	0.85 >=0.20
0.98 >=0.20	0.84 >=0.20
0.93 >=0.20	0.96 >=0.20
0.87 >=0.20	0.72 >=0.20
0.68 >=0.20	0.27 >=0.20
0.94 >=0.20	0.82 >=0.20
0.31 >=0.20	0.58 >=0.20
0.7 >=0.20	0.61 >=0.20
0.51 >=0.20	0.32 >=0.20
0.19 >=0.20	0.82 >=0.20
0.33 >=0.20	0.08 >=0.20

0.15 >=0.20	0.51 >=0.20
0.3 >=0.20	0.71 >=0.20
0.08 >=0.20	0.23 >=0.20
0.4 >=0.20	0.85 >=0.20
0.11 >=0.20	0.59 >=0.20
0.92 >=0.20	0.35 >=0.20
0.65 >=0.20	0.62 >=0.20
0.46 >=0.20	0.98 >=0.20
0.34 >=0.20	0.94 >=0.20
0.98 >=0.20	0.99 >=0.20
0.77 >=0.20	0.99 >=0.20
0.39 >=0.20	0.99 >=0.20
0.15 >=0.20	0.92 >=0.20
0.83 >=0.20	0.14 >=0.20
0.87 >=0.20	0.71 >=0.20
0.43 >=0.20	0.45 >=0.20
0.64 >=0.20	0.16 >=0.20
0.47 >=0.20	0.85 >=0.20
0.55 >=0.20	0.04 >=0.20
0.41 >=0.20	0.93 >=0.20
0.34 >=0.20	0.95 >=0.20
0.65 >=0.20	0.09 >=0.20
0.76 >=0.20	0.78 >=0.20
0.29 >=0.20	0.93 >=0.20
0.97 >=0.20	0.07 >=0.20
0.26 >=0.20	0.08 >=0.20
0.92 >=0.20	0.69 >=0.20
0.61 >=0.20	0.86 >=0.20
0.9 >=0.20	0.96 >=0.20
0.34 >=0.20	0.95 >=0.20
0.72 >=0.20	0.78 >=0.20
0.59 >=0.20	0.35 >=0.20
0.49 >=0.20	0.35 >=0.20
0.99 >=0.20	0.35 >=0.20
0.91 >=0.20	0.87 >=0.20
0.82 >=0.20	0.98 >=0.20
0.76 >=0.20	0.78 >=0.20
0.9 >=0.20	0.67 >=0.20
0.21 >=0.20	0.15 >=0.20
0.99 >=0.20	0.56 >=0.20
0.7 >=0.20	0.84 >=0.20
0.99 >=0.20	0.76 >=0.20
0.89 >=0.20	0.96 >=0.20
0.61 >=0.20	0.98 >=0.20
0.64 >=0.20	0.94 >=0.20
0.64 >=0.20	0.94 >=0.20
1 >=0.20	0.97 >=0.20

0.98 >=0.20	0.97 >=0.20
0.98 >=0.20	0.62 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
0.23 >=0.20	0.67 >=0.20
0.29 >=0.20	0.81 >=0.20
0.9 >=0.20	0.45 >=0.20
0.87 >=0.20	0.42 >=0.20
0.63 >=0.20	0.95 >=0.20
0.99 >=0.20	1 >=0.20
0.92 >=0.20	0.7 >=0.20
0.98 >=0.20	1 >=0.20
0.67 >=0.20	0.69 >=0.20
0.61 >=0.20	0.63 >=0.20
0.87 >=0.20	0.37 >=0.20
0.99 >=0.20	0.68 >=0.20
1 >=0.20	0.27 >=0.20
1 >=0.20	0.44 >=0.20
0.99 >=0.20	0.68 >=0.20
0.99 >=0.20	0.74 >=0.20
0.99 >=0.20	1 >=0.20
0.82 >=0.20	0.86 >=0.20
0.48 >=0.20	0.2 >=0.20
0.84 >=0.20	0.27 >=0.20
0.89 >=0.20	0.6 >=0.20
0.21 >=0.20	0.98 >=0.20
1 >=0.20	0.69 >=0.20
0.84 >=0.20	0.97 >=0.20
0.3 >=0.20	0.92 >=0.20
0.39 >=0.20	0.09 >=0.20
0.28 >=0.20	0.91 >=0.20
0.32 >=0.20	0.93 >=0.20
0.54 >=0.20	0.27 >=0.20
0.77 >=0.20	0.45 >=0.20
0.59 >=0.20	0.49 >=0.20
0.39 >=0.20	0.39 >=0.20
0.34 >=0.20	0.59 >=0.20
0.73 >=0.20	0.75 >=0.20
0.22 >=0.20	0.57 >=0.20
0.48 >=0.20	0.18 >=0.20
0.7 >=0.20	0.86 >=0.20
0.6 >=0.20	0.75 >=0.20
0.81 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	1 >=0.20
0.76 >=0.20	0.91 >=0.20
0.63 >=0.20	0.87 >=0.20

0.84 >=0.20	0.9 >=0.20
0.55 >=0.20	0.99 >=0.20
0.3 >=0.20	0.94 >=0.20
0.69 >=0.20	0.84 >=0.20
1 >=0.20	0.94 >=0.20
0.49 >=0.20	0.1 >=0.20
0.88 >=0.20	0.35 >=0.20
1 >=0.20	1 >=0.20
0.29 >=0.20	0.41 >=0.20
0.17 >=0.20	0.91 >=0.20
0.33 >=0.20	0.94 >=0.20
0.54 >=0.20	0.65 >=0.20
0.29 >=0.20	0.92 >=0.20
0.26 >=0.20	0.87 >=0.20
0.99 >=0.20	0.69 >=0.20
0.87 >=0.20	0.58 >=0.20
0.29 >=0.20	0.67 >=0.20
0.63 >=0.20	0.74 >=0.20
1 >=0.20	0.99 >=0.20
0.96 >=0.20	0.97 >=0.20
0.62 >=0.20	0.74 >=0.20
0.84 >=0.20	0.17 >=0.20
0.76 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.95 >=0.20	0.99 >=0.20
0.95 >=0.20	0.99 >=0.20
0.04 >=0.20	0.47 >=0.20
0.93 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.04 >=0.20	0.06 >=0.20
0.3 >=0.20	0.05 >=0.20
0.55 >=0.20	0.21 >=0.20
0.62 >=0.20	0.89 >=0.20
0.5 >=0.20	0.18 >=0.20
0.08 >=0.20	0.13 >=0.20
0.4 >=0.20	0.23 >=0.20
0.1 >=0.20	0.25 >=0.20
0.75 >=0.20	0.19 >=0.20
0.61 >=0.20	0.21 >=0.20
0.74 >=0.20	0.27 >=0.20
0.98 >=0.20	0.61 >=0.20

0.35 >=0.20	0.6 >=0.20
0.25 >=0.20	0.25 >=0.20
0.7 >=0.20	0.98 >=0.20
0.9 >=0.20	0.92 >=0.20
0.51 >=0.20	0.39 >=0.20
0.16 >=0.20	0.42 >=0.20
0.88 >=0.20	0.82 >=0.20
0.1 >=0.20	0.81 >=0.20
1 >=0.20	0.98 >=0.20
0.69 >=0.20	0.66 >=0.20
1 >=0.20	0.78 >=0.20
0.63 >=0.20	0.69 >=0.20
0.28 >=0.20	0.35 >=0.20
0.96 >=0.20	0.92 >=0.20
0.68 >=0.20	0.75 >=0.20
1 >=0.20	0.91 >=0.20
0.84 >=0.20	0.92 >=0.20
0.04 >=0.20	0.33 >=0.20
0.97 >=0.20	0.48 >=0.20
0.87 >=0.20	0.74 >=0.20
0.78 >=0.20	0.31 >=0.20
0.93 >=0.20	0.98 >=0.20
0.99 >=0.20	0.95 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.21 >=0.20	0.55 >=0.20
0.08 >=0.20	0.98 >=0.20
0.96 >=0.20	0.65 >=0.20
0.83 >=0.20	0.5 >=0.20
0.91 >=0.20	0.29 >=0.20
0.5 >=0.20	0.31 >=0.20
0.66 >=0.20	0.6 >=0.20
0.8 >=0.20	0.96 >=0.20
0.74 >=0.20	0.89 >=0.20
0.34 >=0.20	0.95 >=0.20
0.83 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.45 >=0.20	0.28 >=0.20
0.17 >=0.20	0.39 >=0.20
1 >=0.20	1 >=0.20
0.17 >=0.20	0.14 >=0.20
1 >=0.20	1 >=0.20
0.32 >=0.20	0.99 >=0.20
0.39 >=0.20	0.37 >=0.20
0.92 >=0.20	0.93 >=0.20
0.94 >=0.20	0.92 >=0.20
0.81 >=0.20	0.65 >=0.20

0.06 >=0.20	0.32 >=0.20
0.88 >=0.20	0.72 >=0.20
0.99 >=0.20	0.95 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	0.63 >=0.20
0.99 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
0.93 >=0.20	0.6 >=0.20
0.97 >=0.20	0.92 >=0.20
0.73 >=0.20	0.27 >=0.20
0.86 >=0.20	0.45 >=0.20
0.99 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.07 >=0.20	0.04 >=0.20
0.37 >=0.20	0.47 >=0.20
0.81 >=0.20	0.19 >=0.20
0.84 >=0.20	0.76 >=0.20
0.7 >=0.20	0.4 >=0.20
0.05 >=0.20	0.35 >=0.20
0.53 >=0.20	0.26 >=0.20
1 >=0.20	0.33 >=0.20
1 >=0.20	0.69 >=0.20
0.98 >=0.20	0.52 >=0.20
0.82 >=0.20	0.98 >=0.20
0.99 >=0.20	0.96 >=0.20
0.99 >=0.20	0.96 >=0.20
0.83 >=0.20	0.4 >=0.20
0.96 >=0.20	0.91 >=0.20
0.99 >=0.20	0.78 >=0.20
0.98 >=0.20	0.78 >=0.20
0.72 >=0.20	0.69 >=0.20
0.68 >=0.20	0.62 >=0.20
0.21 >=0.20	0.71 >=0.20
0.4 >=0.20	0.92 >=0.20
0.3 >=0.20	0.75 >=0.20
0.93 >=0.20	0.68 >=0.20
1 >=0.20	1 >=0.20
0.9 >=0.20	0.88 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.28 >=0.20
0.88 >=0.20	0.76 >=0.20
0.94 >=0.20	0.85 >=0.20
0.27 >=0.20	0.34 >=0.20
0.98 >=0.20	0.98 >=0.20

0.76 >=0.20	0.11 >=0.20
0.78 >=0.20	0.49 >=0.20
0.41 >=0.20	0.62 >=0.20
0.58 >=0.20	1 >=0.20
0.95 >=0.20	0.35 >=0.20
0.47 >=0.20	0.11 >=0.20
0.41 >=0.20	0.16 >=0.20
0.99 >=0.20	0.53 >=0.20
0.83 >=0.20	1 >=0.20
0.66 >=0.20	0.98 >=0.20
0.28 >=0.20	0.5 >=0.20
0.12 >=0.20	0.82 >=0.20
0.23 >=0.20	0.48 >=0.20
0.2 >=0.20	0.88 >=0.20
0.71 >=0.20	0.51 >=0.20
0.99 >=0.20	0.99 >=0.20
0.56 >=0.20	0.62 >=0.20
0.95 >=0.20	0.27 >=0.20
0.36 >=0.20	0.54 >=0.20
0.96 >=0.20	0.6 >=0.20
0.34 >=0.20	0.66 >=0.20
0.91 >=0.20	0.84 >=0.20
1 >=0.20	0.52 >=0.20
0.79 >=0.20	0.96 >=0.20
0.99 >=0.20	0.35 >=0.20
0.73 >=0.20	0.98 >=0.20
0.27 >=0.20	0.34 >=0.20
0.05 >=0.20	0.55 >=0.20
0.88 >=0.20	0.91 >=0.20
0.85 >=0.20	0.92 >=0.20
0.73 >=0.20	0.98 >=0.20
0.93 >=0.20	0.9 >=0.20
0.06 >=0.20	0.15 >=0.20
0.05 >=0.20	0.16 >=0.20
0.86 >=0.20	0.83 >=0.20
0.93 >=0.20	0.98 >=0.20
0.99 >=0.20	1 >=0.20
0.98 >=0.20	0.93 >=0.20
0.98 >=0.20	0.63 >=0.20
0.97 >=0.20	0.94 >=0.20
0.76 >=0.20	0.99 >=0.20
0.27 >=0.20	0.87 >=0.20
0.86 >=0.20	1 >=0.20
0.49 >=0.20	0.06 >=0.20
0.88 >=0.20	0.58 >=0.20
0.98 >=0.20	0.64 >=0.20
0.31 >=0.20	0.36 >=0.20

0.47 >=0.20	0.39 >=0.20
0.85 >=0.20	0.99 >=0.20
0.98 >=0.20	0.72 >=0.20
0.74 >=0.20	0.26 >=0.20
0.82 >=0.20	0.83 >=0.20
1 >=0.20	0.91 >=0.20
0.88 >=0.20	0.84 >=0.20
0.95 >=0.20	0.5 >=0.20
0.87 >=0.20	0.7 >=0.20
0.67 >=0.20	0.79 >=0.20
1 >=0.20	0.95 >=0.20
1 >=0.20	0.99 >=0.20
0.93 >=0.20	0.77 >=0.20
0.99 >=0.20	0.9 >=0.20
0.97 >=0.20	0.81 >=0.20
0.9 >=0.20	0.73 >=0.20
0.89 >=0.20	0.85 >=0.20
0.9 >=0.20	0.87 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.19 >=0.20
0.7 >=0.20	0.23 >=0.20
0.52 >=0.20	0.11 >=0.20
0.1 >=0.20	0.07 >=0.20
0.32 >=0.20	0.4 >=0.20
0.51 >=0.20	0.33 >=0.20
0.71 >=0.20	0.7 >=0.20
0.32 >=0.20	0.59 >=0.20
0.04 >=0.20	0.59 >=0.20
0.15 >=0.20	0.64 >=0.20
0.09 >=0.20	0.71 >=0.20
0.04 >=0.20	0.3 >=0.20
0.11 >=0.20	0.65 >=0.20
0.14 >=0.20	0.75 >=0.20
0.21 >=0.20	0.45 >=0.20
0.48 >=0.20	0.87 >=0.20
0.14 >=0.20	0.81 >=0.20
0.11 >=0.20	0.61 >=0.20
0.11 >=0.20	0.75 >=0.20
0.11 >=0.20	0.75 >=0.20
0.05 >=0.20	0.49 >=0.20
0.12 >=0.20	0.53 >=0.20
0.22 >=0.20	0.67 >=0.20
0.12 >=0.20	0.46 >=0.20
0.11 >=0.20	0.71 >=0.20
0.04 >=0.20	0.39 >=0.20
0.16 >=0.20	0.82 >=0.20

0.32 >=0.20	0.87 >=0.20
0.09 >=0.20	0.71 >=0.20
0.1 >=0.20	0.61 >=0.20
0.21 >=0.20	0.83 >=0.20
0.67 >=0.20	0.47 >=0.20
0.71 >=0.20	0.88 >=0.20
0.18 >=0.20	0.17 >=0.20
0.72 >=0.20	0.55 >=0.20
0.95 >=0.20	0.04 >=0.20
0.64 >=0.20	0.11 >=0.20
0.94 >=0.20	0.7 >=0.20
0.44 >=0.20	0.25 >=0.20
0.43 >=0.20	0.79 >=0.20
0.61 >=0.20	0.28 >=0.20
0.66 >=0.20	0.53 >=0.20
0.87 >=0.20	0.73 >=0.20
0.99 >=0.20	0.69 >=0.20
0.17 >=0.20	0.8 >=0.20
0.87 >=0.20	0.41 >=0.20
0.19 >=0.20	0.11 >=0.20
1 >=0.20	1 >=0.20
0.94 >=0.20	0.18 >=0.20
0.62 >=0.20	0.15 >=0.20
0.4 >=0.20	0.72 >=0.20
0.55 >=0.20	0.57 >=0.20
0.99 >=0.20	0.95 >=0.20
0.71 >=0.20	0.38 >=0.20
0.76 >=0.20	0.88 >=0.20
0.98 >=0.20	0.82 >=0.20
0.22 >=0.20	0.77 >=0.20
0.21 >=0.20	0.89 >=0.20
0.19 >=0.20	0.66 >=0.20
0.07 >=0.20	0.72 >=0.20
0.12 >=0.20	0.79 >=0.20
0.58 >=0.20	0.91 >=0.20
0.56 >=0.20	0.92 >=0.20
0.95 >=0.20	0.96 >=0.20
0.99 >=0.20	0.83 >=0.20
0.12 >=0.20	0.79 >=0.20
0.58 >=0.20	0.91 >=0.20
0.56 >=0.20	0.92 >=0.20
0.96 >=0.20	0.97 >=0.20
0.96 >=0.20	0.96 >=0.20
0.75 >=0.20	0.58 >=0.20
0.67 >=0.20	0.61 >=0.20
0.88 >=0.20	0.73 >=0.20
0.61 >=0.20	0.55 >=0.20

0.82 >=0.20	0.57 >=0.20
0.51 >=0.20	0.58 >=0.20
0.57 >=0.20	0.75 >=0.20
0.61 >=0.20	0.42 >=0.20
0.48 >=0.20	0.61 >=0.20
0.19 >=0.20	0.09 >=0.20
0.63 >=0.20	0.69 >=0.20
0.26 >=0.20	0.74 >=0.20
0.36 >=0.20	0.36 >=0.20
0.21 >=0.20	0.37 >=0.20
0.55 >=0.20	0.69 >=0.20
0.04 >=0.20	0.03 >=0.20
0.35 >=0.20	0.96 >=0.20
0.39 >=0.20	0.3 >=0.20
0.08 >=0.20	0.03 >=0.20
0.74 >=0.20	0.99 >=0.20
0.34 >=0.20	0.34 >=0.20
0.32 >=0.20	0.34 >=0.20
1 >=0.20	0.99 >=0.20
0.97 >=0.20	0.99 >=0.20
0.53 >=0.20	0.42 >=0.20
0.66 >=0.20	0.09 >=0.20
0.67 >=0.20	0.15 >=0.20
1 >=0.20	1 >=0.20
0.62 >=0.20	0.98 >=0.20
0.15 >=0.20	0.56 >=0.20
0.96 >=0.20	0.92 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.98 >=0.20
0.81 >=0.20	0.95 >=0.20
0.4 >=0.20	0.89 >=0.20
0.16 >=0.20	0.73 >=0.20
1 >=0.20	0.89 >=0.20
0.74 >=0.20	0.93 >=0.20
0.42 >=0.20	0.44 >=0.20
0.33 >=0.20	0.97 >=0.20
0.96 >=0.20	0.91 >=0.20
0.98 >=0.20	0.83 >=0.20
1 >=0.20	0.92 >=0.20
0.94 >=0.20	0.54 >=0.20
0.86 >=0.20	0.44 >=0.20
0.71 >=0.20	0.74 >=0.20
0.81 >=0.20	1 >=0.20

0.96 >=0.20	0.99 >=0.20
0.36 >=0.20	0.71 >=0.20
0.05 >=0.20	0.83 >=0.20
0.19 >=0.20	0.95 >=0.20
0.42 >=0.20	0.96 >=0.20
0.96 >=0.20	0.65 >=0.20
0.56 >=0.20	0.92 >=0.20
0.46 >=0.20	0.91 >=0.20
0.69 >=0.20	1 >=0.20
0.99 >=0.20	0.91 >=0.20
1 >=0.20	0.96 >=0.20
0.12 >=0.20	0.19 >=0.20
1 >=0.20	0.86 >=0.20
0.55 >=0.20	0.51 >=0.20
0.83 >=0.20	0.51 >=0.20
0.76 >=0.20	0.99 >=0.20
0.13 >=0.20	0.65 >=0.20
0.13 >=0.20	0.99 >=0.20
0.17 >=0.20	1 >=0.20
0.93 >=0.20	0.92 >=0.20
0.99 >=0.20	0.92 >=0.20
1 >=0.20	0.94 >=0.20
0.98 >=0.20	0.87 >=0.20
0.95 >=0.20	0.37 >=0.20
1 >=0.20	0.92 >=0.20
0.37 >=0.20	0.96 >=0.20
0.6 >=0.20	0.18 >=0.20
1 >=0.20	0.98 >=0.20
0.46 >=0.20	0.47 >=0.20
0.76 >=0.20	0.23 >=0.20
1 >=0.20	0.88 >=0.20
0.2 >=0.20	0.12 >=0.20
1 >=0.20	0.86 >=0.20
0.97 >=0.20	0.9 >=0.20
0.92 >=0.20	0.99 >=0.20
0.12 >=0.20	0.17 >=0.20
0.63 >=0.20	0.53 >=0.20
0.97 >=0.20	0.62 >=0.20
0.71 >=0.20	0.2 >=0.20
0.58 >=0.20	0.5 >=0.20
1 >=0.20	0.9 >=0.20
0.68 >=0.20	0.93 >=0.20
0.99 >=0.20	0.85 >=0.20
0.15 >=0.20	0.34 >=0.20
0.13 >=0.20	0.16 >=0.20
0.31 >=0.20	0.07 >=0.20
0.2 >=0.20	0.26 >=0.20

0.36 >=0.20	0.77 >=0.20
0.86 >=0.20	0.96 >=0.20
0.11 >=0.20	0.08 >=0.20
0.97 >=0.20	0.29 >=0.20
0.98 >=0.20	0.16 >=0.20
0.98 >=0.20	0.81 >=0.20
0.96 >=0.20	0.73 >=0.20
0.46 >=0.20	1 >=0.20
0.53 >=0.20	0.52 >=0.20
0.11 >=0.20	0.31 >=0.20
0.11 >=0.20	0.31 >=0.20
0.11 >=0.20	0.31 >=0.20
0.97 >=0.20	0.23 >=0.20
0.45 >=0.20	0.9 >=0.20
0.23 >=0.20	0.16 >=0.20
0.36 >=0.20	0.31 >=0.20
0.55 >=0.20	0.67 >=0.20
0.6 >=0.20	0.88 >=0.20
0.13 >=0.20	0.31 >=0.20
0.11 >=0.20	0.8 >=0.20
0.23 >=0.20	1 >=0.20
0.55 >=0.20	0.12 >=0.20
1 >=0.20	1 >=0.20
0.04 >=0.20	0.33 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
0.06 >=0.20	0.61 >=0.20
1 >=0.20	0.98 >=0.20
0.55 >=0.20	0.67 >=0.20
1 >=0.20	1 >=0.20
0.81 >=0.20	0.35 >=0.20
0.36 >=0.20	0.8 >=0.20
0.24 >=0.20	0.99 >=0.20
0.29 >=0.20	0.67 >=0.20
0.71 >=0.20	0.75 >=0.20
0.97 >=0.20	0.59 >=0.20
0.95 >=0.20	0.82 >=0.20
0.45 >=0.20	0.7 >=0.20
0.47 >=0.20	0.18 >=0.20
0.97 >=0.20	0.96 >=0.20
0.1 >=0.20	0.42 >=0.20
0.1 >=0.20	0.18 >=0.20
0.06 >=0.20	0.5 >=0.20
0.09 >=0.20	0.71 >=0.20
0.42 >=0.20	0.67 >=0.20
0.19 >=0.20	0.59 >=0.20
0.6 >=0.20	0.68 >=0.20

0.19 >=0.20	0.85 >=0.20
0.58 >=0.20	0.62 >=0.20
0.11 >=0.20	0.78 >=0.20
0.11 >=0.20	0.69 >=0.20
0.08 >=0.20	0.75 >=0.20
0.04 >=0.20	0.16 >=0.20
0.29 >=0.20	0.45 >=0.20
0.95 >=0.20	0.75 >=0.20
0.08 >=0.20	0.68 >=0.20
0.07 >=0.20	0.66 >=0.20
1 >=0.20	0.95 >=0.20
0.57 >=0.20	0.77 >=0.20
0.68 >=0.20	0.03 >=0.20
0.75 >=0.20	0.42 >=0.20
0.68 >=0.20	0.8 >=0.20
0.2 >=0.20	0.15 >=0.20
0.89 >=0.20	0.93 >=0.20
0.35 >=0.20	0.09 >=0.20
1 >=0.20	0.97 >=0.20
0.27 >=0.20	0.04 >=0.20
1 >=0.20	0.89 >=0.20
0.05 >=0.20	0.31 >=0.20
1 >=0.20	0.89 >=0.20
0.28 >=0.20	0.79 >=0.20
0.5 >=0.20	0.85 >=0.20
0.1 >=0.20	0.96 >=0.20
0.21 >=0.20	0.92 >=0.20
0.21 >=0.20	0.99 >=0.20
0.12 >=0.20	0.75 >=0.20
0.06 >=0.20	0.61 >=0.20
0.07 >=0.20	0.72 >=0.20
0.87 >=0.20	0.61 >=0.20
0.05 >=0.20	0.82 >=0.20
0.98 >=0.20	0.26 >=0.20
0.7 >=0.20	0.25 >=0.20
1 >=0.20	0.82 >=0.20
0.39 >=0.20	0.98 >=0.20
0.12 >=0.20	0.95 >=0.20
0.3 >=0.20	0.98 >=0.20
0.68 >=0.20	0.3 >=0.20
0.97 >=0.20	0.48 >=0.20
0.77 >=0.20	0.92 >=0.20
1 >=0.20	0.97 >=0.20
0.48 >=0.20	0.54 >=0.20
0.61 >=0.20	0.41 >=0.20
0.62 >=0.20	1 >=0.20
0.36 >=0.20	0.1 >=0.20

0.54 >=0.20	0.2 >=0.20
0.91 >=0.20	0.52 >=0.20
0.75 >=0.20	0.21 >=0.20
0.97 >=0.20	1 >=0.20
0.3 >=0.20	0.62 >=0.20
0.8 >=0.20	0.78 >=0.20
0.82 >=0.20	0.88 >=0.20
0.35 >=0.20	0.43 >=0.20
0.41 >=0.20	0.91 >=0.20
0.94 >=0.20	0.99 >=0.20
0.99 >=0.20	0.99 >=0.20
0.9 >=0.20	0.09 >=0.20
0.07 >=0.20	0.66 >=0.20
0.75 >=0.20	0.29 >=0.20
0.4 >=0.20	0.96 >=0.20
0.16 >=0.20	0.65 >=0.20
0.89 >=0.20	0.07 >=0.20
0.16 >=0.20	0.65 >=0.20
0.12 >=0.20	0.4 >=0.20
0.23 >=0.20	0.9 >=0.20
0.99 >=0.20	0.96 >=0.20
1 >=0.20	0.89 >=0.20
0.16 >=0.20	0.96 >=0.20
0.35 >=0.20	0.72 >=0.20
0.05 >=0.20	0.75 >=0.20
0.18 >=0.20	0.05 >=0.20
0.23 >=0.20	0.47 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.14 >=0.20	0.75 >=0.20
0.51 >=0.20	0.99 >=0.20
0.14 >=0.20	0.95 >=0.20
1 >=0.20	0.19 >=0.20
0.13 >=0.20	0.98 >=0.20
0.05 >=0.20	0.92 >=0.20
0.25 >=0.20	0.98 >=0.20
0.95 >=0.20	0.99 >=0.20
0.13 >=0.20	0.98 >=0.20
0.86 >=0.20	0.36 >=0.20
1 >=0.20	0.4 >=0.20
0.76 >=0.20	0.86 >=0.20
0.91 >=0.20	0.27 >=0.20
0.31 >=0.20	0.81 >=0.20
0.23 >=0.20	0.6 >=0.20
0.11 >=0.20	0.95 >=0.20
0.29 >=0.20	0.53 >=0.20
0.09 >=0.20	0.28 >=0.20

1 >=0.20	1 >=0.20
0.3 >=0.20	0.34 >=0.20
0.99 >=0.20	0.97 >=0.20
0.99 >=0.20	0.6 >=0.20
0.08 >=0.20	0.28 >=0.20
0.75 >=0.20	0.13 >=0.20
0.99 >=0.20	0.91 >=0.20
0.06 >=0.20	0.71 >=0.20
0.16 >=0.20	0.09 >=0.20
0.27 >=0.20	0.74 >=0.20
0.28 >=0.20	0.79 >=0.20
0.36 >=0.20	0.78 >=0.20
0.17 >=0.20	0.98 >=0.20
0.05 >=0.20	0.75 >=0.20
0.5 >=0.20	0.8 >=0.20
0.04 >=0.20	0.88 >=0.20
1 >=0.20	0.68 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	0.94 >=0.20
1 >=0.20	0.92 >=0.20
1 >=0.20	0.87 >=0.20
1 >=0.20	0.89 >=0.20
1 >=0.20	0.89 >=0.20
0.97 >=0.20	0.95 >=0.20
0.44 >=0.20	0.92 >=0.20
0.99 >=0.20	0.76 >=0.20
0.17 >=0.20	0.45 >=0.20
0.16 >=0.20	0.52 >=0.20
0.31 >=0.20	0.81 >=0.20
0.16 >=0.20	0.52 >=0.20
0.43 >=0.20	0.56 >=0.20
0.43 >=0.20	0.56 >=0.20
0.47 >=0.20	0.84 >=0.20
0.23 >=0.20	0.6 >=0.20
0.54 >=0.20	0.84 >=0.20
0.89 >=0.20	0.71 >=0.20
0.99 >=0.20	0.64 >=0.20
0.9 >=0.20	0.81 >=0.20
0.98 >=0.20	0.73 >=0.20
1 >=0.20	0.99 >=0.20
0.95 >=0.20	0.54 >=0.20
0.97 >=0.20	0.81 >=0.20
0.99 >=0.20	0.84 >=0.20
0.94 >=0.20	0.27 >=0.20
1 >=0.20	0.91 >=0.20
0.98 >=0.20	0.71 >=0.20
0.93 >=0.20	0.7 >=0.20

0.99 >=0.20	0.98 >=0.20
0.58 >=0.20	0.59 >=0.20
0.89 >=0.20	0.07 >=0.20
0.45 >=0.20	0.61 >=0.20
0.08 >=0.20	0.51 >=0.20
0.16 >=0.20	0.86 >=0.20
0.22 >=0.20	0.99 >=0.20
0.69 >=0.20	0.95 >=0.20
0.98 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.08 >=0.20	0.18 >=0.20
0.27 >=0.20	0.98 >=0.20
0.27 >=0.20	0.98 >=0.20
0.16 >=0.20	0.26 >=0.20
0.36 >=0.20	0.26 >=0.20
0.49 >=0.20	0.18 >=0.20
0.85 >=0.20	0.99 >=0.20
0.07 >=0.20	0.71 >=0.20
0.14 >=0.20	0.84 >=0.20
0.88 >=0.20	0.76 >=0.20
0.94 >=0.20	0.59 >=0.20
0.95 >=0.20	0.57 >=0.20
0.56 >=0.20	0.67 >=0.20
0.39 >=0.20	0.19 >=0.20
0.84 >=0.20	0.38 >=0.20
0.35 >=0.20	0.43 >=0.20
0.93 >=0.20	0.49 >=0.20
0.95 >=0.20	0.71 >=0.20
0.7 >=0.20	0.87 >=0.20
0.42 >=0.20	0.9 >=0.20
0.52 >=0.20	0.59 >=0.20
0.08 >=0.20	0.28 >=0.20
0.17 >=0.20	0.45 >=0.20
0.33 >=0.20	0.79 >=0.20
0.21 >=0.20	0.99 >=0.20
0.21 >=0.20	0.99 >=0.20
0.8 >=0.20	0.39 >=0.20
0.05 >=0.20	0.54 >=0.20
0.1 >=0.20	0.42 >=0.20
0.68 >=0.20	0.81 >=0.20
0.47 >=0.20	0.19 >=0.20
0.07 >=0.20	0.53 >=0.20
0.07 >=0.20	0.55 >=0.20
0.33 >=0.20	0.73 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	0.95 >=0.20

0.5 >=0.20	0.15 >=0.20
0.68 >=0.20	0.81 >=0.20
0.81 >=0.20	0.78 >=0.20
0.99 >=0.20	0.64 >=0.20
0.97 >=0.20	0.98 >=0.20
0.59 >=0.20	0.26 >=0.20
1 >=0.20	1 >=0.20
0.14 >=0.20	0.35 >=0.20
0.14 >=0.20	0.92 >=0.20
0.47 >=0.20	0.92 >=0.20
0.22 >=0.20	0.93 >=0.20
0.05 >=0.20	0.12 >=0.20
0.53 >=0.20	0.37 >=0.20
0.72 >=0.20	0.25 >=0.20
0.15 >=0.20	0.23 >=0.20
0.8 >=0.20	0.39 >=0.20
1 >=0.20	0.91 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
0.09 >=0.20	0.18 >=0.20
0.2 >=0.20	0.27 >=0.20
0.99 >=0.20	0.77 >=0.20
0.99 >=0.20	0.77 >=0.20
0.19 >=0.20	0.59 >=0.20
0.56 >=0.20	0.51 >=0.20
0.72 >=0.20	1 >=0.20
0.45 >=0.20	0.9 >=0.20
0.99 >=0.20	0.85 >=0.20
0.2 >=0.20	0.96 >=0.20
0.28 >=0.20	0.94 >=0.20
0.95 >=0.20	1 >=0.20
0.75 >=0.20	0.94 >=0.20
0.75 >=0.20	0.94 >=0.20
0.46 >=0.20	0.54 >=0.20
0.34 >=0.20	1 >=0.20
0.31 >=0.20	0.16 >=0.20
0.75 >=0.20	0.24 >=0.20
0.94 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
0.97 >=0.20	0.98 >=0.20
0.06 >=0.20	0.88 >=0.20
0.06 >=0.20	0.72 >=0.20
0.12 >=0.20	0.3 >=0.20
0.06 >=0.20	0.41 >=0.20
0.04 >=0.20	0.19 >=0.20
0.05 >=0.20	0.92 >=0.20

0.63 >=0.20	0.57 >=0.20
0.2 >=0.20	0.81 >=0.20
0.63 >=0.20	0.92 >=0.20
0.14 >=0.20	0.99 >=0.20
0.4 >=0.20	1 >=0.20
0.55 >=0.20	0.82 >=0.20
0.39 >=0.20	0.45 >=0.20
0.54 >=0.20	0.96 >=0.20
0.93 >=0.20	0.96 >=0.20
0.98 >=0.20	0.99 >=0.20
0.87 >=0.20	0.61 >=0.20
0.22 >=0.20	0.27 >=0.20
0.23 >=0.20	0.19 >=0.20
0.54 >=0.20	0.21 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	0.99 >=0.20
0.07 >=0.20	0.44 >=0.20
0.09 >=0.20	0.72 >=0.20
1 >=0.20	0.3 >=0.20
0.39 >=0.20	0.27 >=0.20
0.85 >=0.20	0.62 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.33 >=0.20	0.12 >=0.20
0.26 >=0.20	0.25 >=0.20
0.53 >=0.20	0.26 >=0.20
0.94 >=0.20	0.29 >=0.20
0.98 >=0.20	0.92 >=0.20
0.13 >=0.20	0.13 >=0.20
0.17 >=0.20	0.71 >=0.20
0.17 >=0.20	0.71 >=0.20
0.28 >=0.20	0.79 >=0.20
0.96 >=0.20	0.85 >=0.20
0.94 >=0.20	0.29 >=0.20
0.95 >=0.20	0.58 >=0.20
0.26 >=0.20	0.61 >=0.20
0.78 >=0.20	0.54 >=0.20
0.99 >=0.20	1 >=0.20
0.24 >=0.20	0.5 >=0.20
0.43 >=0.20	0.67 >=0.20
0.12 >=0.20	0.74 >=0.20
0.73 >=0.20	0.86 >=0.20
0.92 >=0.20	0.98 >=0.20
1 >=0.20	0.82 >=0.20
0.07 >=0.20	0.75 >=0.20
0.73 >=0.20	0.3 >=0.20

0.85 >=0.20	0.38 >=0.20
0.59 >=0.20	0.7 >=0.20
0.96 >=0.20	0.66 >=0.20
0.12 >=0.20	0.5 >=0.20
0.12 >=0.20	0.5 >=0.20
0.86 >=0.20	0.27 >=0.20
0.6 >=0.20	0.49 >=0.20
0.62 >=0.20	0.43 >=0.20
0.99 >=0.20	0.97 >=0.20
0.08 >=0.20	0.28 >=0.20
0.08 >=0.20	0.28 >=0.20
0.09 >=0.20	0.22 >=0.20
0.53 >=0.20	0.92 >=0.20
0.38 >=0.20	0.69 >=0.20
0.26 >=0.20	0.76 >=0.20
0.29 >=0.20	0.11 >=0.20
0.94 >=0.20	0.51 >=0.20
0.06 >=0.20	0.45 >=0.20
1 >=0.20	0.95 >=0.20
0.55 >=0.20	0.97 >=0.20
0.62 >=0.20	0.77 >=0.20
0.97 >=0.20	0.12 >=0.20
0.99 >=0.20	0.75 >=0.20
0.23 >=0.20	0.07 >=0.20
0.87 >=0.20	0.8 >=0.20
0.86 >=0.20	0.73 >=0.20
0.86 >=0.20	0.68 >=0.20
0.85 >=0.20	0.83 >=0.20
0.39 >=0.20	0.59 >=0.20
0.99 >=0.20	0.95 >=0.20
0.96 >=0.20	0.73 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	0.99 >=0.20
0.98 >=0.20	0.98 >=0.20
0.28 >=0.20	0.94 >=0.20
0.28 >=0.20	0.94 >=0.20
0.87 >=0.20	0.99 >=0.20
0.29 >=0.20	0.7 >=0.20
1 >=0.20	1 >=0.20
0.55 >=0.20	0.67 >=0.20
1 >=0.20	1 >=0.20
0.82 >=0.20	0.88 >=0.20
0.94 >=0.20	0.81 >=0.20
0.43 >=0.20	0.68 >=0.20
0.08 >=0.20	0.09 >=0.20
0.24 >=0.20	0.96 >=0.20
0.23 >=0.20	0.96 >=0.20

0.8 >=0.20	0.39 >=0.20
0.97 >=0.20	0.64 >=0.20
0.39 >=0.20	0.77 >=0.20
0.84 >=0.20	0.9 >=0.20
0.14 >=0.20	0.41 >=0.20
0.9 >=0.20	0.97 >=0.20
0.09 >=0.20	0.33 >=0.20
0.07 >=0.20	0.17 >=0.20
0.59 >=0.20	0.14 >=0.20
0.35 >=0.20	0.06 >=0.20
0.98 >=0.20	0.94 >=0.20
0.97 >=0.20	1 >=0.20
0.77 >=0.20	0.92 >=0.20
0.49 >=0.20	0.54 >=0.20
0.94 >=0.20	0.71 >=0.20
0.41 >=0.20	0.37 >=0.20
0.08 >=0.20	0.68 >=0.20
0.97 >=0.20	0.92 >=0.20
0.16 >=0.20	0.78 >=0.20
0.09 >=0.20	0.66 >=0.20
0.05 >=0.20	0.71 >=0.20
0.12 >=0.20	0.88 >=0.20
0.25 >=0.20	0.57 >=0.20
1 >=0.20	0.89 >=0.20
0.91 >=0.20	0.82 >=0.20
1 >=0.20	0.94 >=0.20
0.29 >=0.20	0.68 >=0.20
0.19 >=0.20	0.85 >=0.20
0.09 >=0.20	0.8 >=0.20
0.11 >=0.20	0.83 >=0.20
0.68 >=0.20	0.24 >=0.20
0.36 >=0.20	0.39 >=0.20
1 >=0.20	0.86 >=0.20
0.63 >=0.20	0.57 >=0.20
0.08 >=0.20	0.8 >=0.20
0.34 >=0.20	0.98 >=0.20
0.38 >=0.20	0.99 >=0.20
0.38 >=0.20	0.99 >=0.20
0.95 >=0.20	0.82 >=0.20
0.97 >=0.20	0.76 >=0.20
0.66 >=0.20	0.74 >=0.20
0.98 >=0.20	0.81 >=0.20
0.43 >=0.20	0.89 >=0.20
0.11 >=0.20	0.22 >=0.20
0.33 >=0.20	0.44 >=0.20
1 >=0.20	0.82 >=0.20
0.99 >=0.20	0.76 >=0.20

0.19 >=0.20	0.79 >=0.20
1 >=0.20	0.81 >=0.20
0.56 >=0.20	0.45 >=0.20
0.99 >=0.20	0.72 >=0.20
0.13 >=0.20	0.81 >=0.20
0.16 >=0.20	0.79 >=0.20
0.33 >=0.20	0.79 >=0.20
0.17 >=0.20	0.7 >=0.20
0.33 >=0.20	0.79 >=0.20
0.16 >=0.20	0.52 >=0.20
0.33 >=0.20	0.79 >=0.20
0.33 >=0.20	0.79 >=0.20
0.33 >=0.20	0.79 >=0.20
0.13 >=0.20	0.54 >=0.20
0.75 >=0.20	0.94 >=0.20
0.13 >=0.20	0.54 >=0.20
0.25 >=0.20	0.8 >=0.20
0.59 >=0.20	0.97 >=0.20
0.57 >=0.20	0.96 >=0.20
0.21 >=0.20	0.63 >=0.20
0.42 >=0.20	0.63 >=0.20
0.11 >=0.20	0.89 >=0.20
0.12 >=0.20	0.69 >=0.20
0.13 >=0.20	0.55 >=0.20
0.41 >=0.20	0.17 >=0.20
0.8 >=0.20	0.49 >=0.20
0.99 >=0.20	0.8 >=0.20
0.92 >=0.20	0.26 >=0.20
0.95 >=0.20	0.99 >=0.20
0.94 >=0.20	0.94 >=0.20
1 >=0.20	0.66 >=0.20
0.79 >=0.20	0.69 >=0.20
0.97 >=0.20	0.65 >=0.20
0.84 >=0.20	0.47 >=0.20
0.97 >=0.20	0.78 >=0.20
0.68 >=0.20	0.12 >=0.20
0.85 >=0.20	0.49 >=0.20
1 >=0.20	0.19 >=0.20
1 >=0.20	0.73 >=0.20
0.62 >=0.20	0.08 >=0.20
0.66 >=0.20	0.12 >=0.20
0.99 >=0.20	0.73 >=0.20
0.98 >=0.20	0.81 >=0.20
1 >=0.20	0.99 >=0.20
0.66 >=0.20	0.35 >=0.20
0.23 >=0.20	0.47 >=0.20
0.95 >=0.20	0.76 >=0.20

0.8 >=0.20	0.94 >=0.20
0.86 >=0.20	0.65 >=0.20
0.04 >=0.20	0.05 >=0.20
0.99 >=0.20	0.85 >=0.20
0.06 >=0.20	0.72 >=0.20
0.45 >=0.20	0.79 >=0.20
0.3 >=0.20	0.79 >=0.20
0.07 >=0.20	0.6 >=0.20
0.9 >=0.20	0.99 >=0.20
0.07 >=0.20	0.75 >=0.20
0.98 >=0.20	0.88 >=0.20
0.06 >=0.20	0.88 >=0.20
0.47 >=0.20	0.89 >=0.20
0.11 >=0.20	0.24 >=0.20
0.81 >=0.20	0.41 >=0.20
0.63 >=0.20	0.26 >=0.20
0.66 >=0.20	0.67 >=0.20
0.22 >=0.20	0.12 >=0.20
0.99 >=0.20	0.93 >=0.20
0.17 >=0.20	0.45 >=0.20
0.09 >=0.20	0.22 >=0.20
0.85 >=0.20	0.93 >=0.20
0.19 >=0.20	0.95 >=0.20
0.59 >=0.20	0.98 >=0.20
0.08 >=0.20	0.27 >=0.20
0.06 >=0.20	0.47 >=0.20
0.9 >=0.20	0.42 >=0.20
0.75 >=0.20	0.99 >=0.20
0.2 >=0.20	0.64 >=0.20
0.95 >=0.20	0.37 >=0.20
0.98 >=0.20	0.66 >=0.20
0.38 >=0.20	0.05 >=0.20
0.06 >=0.20	0.05 >=0.20
0.17 >=0.20	0.14 >=0.20
0.14 >=0.20	0.06 >=0.20
0.07 >=0.20	0.64 >=0.20
0.17 >=0.20	0.08 >=0.20
0.95 >=0.20	0.57 >=0.20
0.91 >=0.20	0.67 >=0.20
0.05 >=0.20	0.19 >=0.20
0.15 >=0.20	0.86 >=0.20
0.15 >=0.20	0.65 >=0.20
0.3 >=0.20	0.34 >=0.20
0.22 >=0.20	0.73 >=0.20
0.49 >=0.20	0.87 >=0.20
0.62 >=0.20	0.98 >=0.20
0.08 >=0.20	0.1 >=0.20

0.99 >=0.20	0.99 >=0.20
0.15 >=0.20	0.1 >=0.20
0.7 >=0.20	0.75 >=0.20
0.05 >=0.20	0.33 >=0.20
0.06 >=0.20	0.05 >=0.20
0.07 >=0.20	0.83 >=0.20
0.09 >=0.20	0.68 >=0.20
0.09 >=0.20	0.68 >=0.20
1 >=0.20	1 >=0.20
0.35 >=0.20	0.95 >=0.20
0.1 >=0.20	0.71 >=0.20
0.48 >=0.20	0.32 >=0.20
0.43 >=0.20	0.84 >=0.20
1 >=0.20	1 >=0.20
0.1 >=0.20	0.43 >=0.20
0.13 >=0.20	0.67 >=0.20
0.07 >=0.20	0.05 >=0.20
0.09 >=0.20	0.19 >=0.20
0.88 >=0.20	0.72 >=0.20
1 >=0.20	1 >=0.20
0.72 >=0.20	0.16 >=0.20
0.88 >=0.20	0.72 >=0.20
0.5 >=0.20	0.6 >=0.20
0.87 >=0.20	0.69 >=0.20
0.79 >=0.20	0.26 >=0.20
0.9 >=0.20	1 >=0.20
0.9 >=0.20	1 >=0.20
0.15 >=0.20	0.99 >=0.20
0.55 >=0.20	0.99 >=0.20
0.06 >=0.20	0.4 >=0.20
0.65 >=0.20	0.5 >=0.20
0.4 >=0.20	0.32 >=0.20
0.94 >=0.20	0.16 >=0.20
0.76 >=0.20	0.84 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
0.97 >=0.20	0.83 >=0.20
1 >=0.20	0.6 >=0.20
0.89 >=0.20	0.17 >=0.20
0.72 >=0.20	0.66 >=0.20
0.57 >=0.20	0.31 >=0.20
0.05 >=0.20	0.9 >=0.20
1 >=0.20	0.89 >=0.20
0.99 >=0.20	0.73 >=0.20
0.78 >=0.20	0.69 >=0.20
0.95 >=0.20	0.98 >=0.20
0.96 >=0.20	0.98 >=0.20

0.68 >=0.20	0.96 >=0.20
0.67 >=0.20	0.95 >=0.20
0.47 >=0.20	0.97 >=0.20
0.63 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.56 >=0.20	0.37 >=0.20
1 >=0.20	0.54 >=0.20
0.43 >=0.20	0.93 >=0.20
0.41 >=0.20	0.99 >=0.20
0.44 >=0.20	0.99 >=0.20
1 >=0.20	0.93 >=0.20
0.8 >=0.20	0.49 >=0.20
1 >=0.20	0.97 >=0.20
0.85 >=0.20	0.94 >=0.20
0.83 >=0.20	0.9 >=0.20
0.72 >=0.20	0.99 >=0.20
1 >=0.20	0.91 >=0.20
0.81 >=0.20	0.92 >=0.20
0.91 >=0.20	0.37 >=0.20
0.42 >=0.20	0.17 >=0.20
0.38 >=0.20	0.03 >=0.20
0.82 >=0.20	0.71 >=0.20
0.81 >=0.20	0.83 >=0.20
0.99 >=0.20	0.43 >=0.20
0.96 >=0.20	0.4 >=0.20
0.3 >=0.20	0.19 >=0.20
0.84 >=0.20	0.41 >=0.20
0.82 >=0.20	0.51 >=0.20
1 >=0.20	0.82 >=0.20
0.51 >=0.20	0.74 >=0.20
0.38 >=0.20	0.22 >=0.20
0.75 >=0.20	0.99 >=0.20
0.61 >=0.20	0.94 >=0.20
0.91 >=0.20	0.3 >=0.20
0.63 >=0.20	0.4 >=0.20
0.94 >=0.20	1 >=0.20
0.78 >=0.20	0.22 >=0.20
0.56 >=0.20	0.15 >=0.20
0.12 >=0.20	0.07 >=0.20
0.92 >=0.20	0.54 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.89 >=0.20
1 >=0.20	0.87 >=0.20
1 >=0.20	0.98 >=0.20

1	>=0.20	0.77	>=0.20
0.44	>=0.20	0.58	>=0.20
0.69	>=0.20	0.42	>=0.20
0.57	>=0.20	0.46	>=0.20
0.74	>=0.20	0.78	>=0.20
0.96	>=0.20	0.92	>=0.20
0.95	>=0.20	0.93	>=0.20
0.98	>=0.20	0.73	>=0.20
0.31	>=0.20	0.5	>=0.20
1	>=0.20	0.57	>=0.20
0.19	>=0.20	0.99	>=0.20
0.19	>=0.20	0.99	>=0.20
1	>=0.20	0.89	>=0.20
0.94	>=0.20	0.71	>=0.20
0.72	>=0.20	0.4	>=0.20
0.91	>=0.20	0.15	>=0.20
0.89	>=0.20	0.99	>=0.20
0.99	>=0.20	0.69	>=0.20
1	>=0.20	0.9	>=0.20
1	>=0.20	0.89	>=0.20
0.43	>=0.20	0.45	>=0.20
0.89	>=0.20	0.66	>=0.20
0.15	>=0.20	0.94	>=0.20
0.22	>=0.20	0.94	>=0.20
0.99	>=0.20	0.96	>=0.20
0.89	>=0.20	0.87	>=0.20
0.63	>=0.20	0.16	>=0.20
0.99	>=0.20	0.78	>=0.20
0.13	>=0.20	0.66	>=0.20
0.74	>=0.20	0.98	>=0.20
0.76	>=0.20	0.95	>=0.20
0.58	>=0.20	0.95	>=0.20
0.08	>=0.20	0.95	>=0.20
0.8	>=0.20	0.11	>=0.20
0.82	>=0.20	0.81	>=0.20
0.77	>=0.20	0.97	>=0.20
0.55	>=0.20	0.99	>=0.20
0.77	>=0.20	0.87	>=0.20
0.77	>=0.20	0.87	>=0.20
1	>=0.20	0.95	>=0.20
0.99	>=0.20	0.81	>=0.20
0.99	>=0.20	0.73	>=0.20
0.71	>=0.20	0.39	>=0.20
0.04	>=0.20	0.42	>=0.20
0.11	>=0.20	0.68	>=0.20
0.21	>=0.20	0.8	>=0.20
0.39	>=0.20	0.66	>=0.20

0.11 >=0.20	0.78 >=0.20
0.87 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.72 >=0.20	0.66 >=0.20
0.82 >=0.20	0.96 >=0.20
0.54 >=0.20	0.81 >=0.20
0.89 >=0.20	0.91 >=0.20
0.68 >=0.20	0.89 >=0.20
0.95 >=0.20	0.24 >=0.20
0.59 >=0.20	0.99 >=0.20
0.81 >=0.20	0.81 >=0.20
0.49 >=0.20	0.9 >=0.20
0.83 >=0.20	1 >=0.20
0.18 >=0.20	0.99 >=0.20
0.79 >=0.20	0.91 >=0.20
1 >=0.20	0.99 >=0.20
0.41 >=0.20	0.05 >=0.20
0.7 >=0.20	0.27 >=0.20
0.37 >=0.20	0.15 >=0.20
0.06 >=0.20	0.04 >=0.20
0.92 >=0.20	0.82 >=0.20
0.88 >=0.20	0.99 >=0.20
0.92 >=0.20	0.59 >=0.20
0.97 >=0.20	0.91 >=0.20
0.91 >=0.20	0.58 >=0.20
0.99 >=0.20	0.88 >=0.20
0.91 >=0.20	0.76 >=0.20
1 >=0.20	1 >=0.20
0.83 >=0.20	0.59 >=0.20
0.98 >=0.20	0.9 >=0.20
0.96 >=0.20	0.59 >=0.20
0.79 >=0.20	0.87 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
0.33 >=0.20	0.84 >=0.20
0.75 >=0.20	1 >=0.20
0.53 >=0.20	0.89 >=0.20
0.21 >=0.20	0.24 >=0.20
0.7 >=0.20	0.65 >=0.20
0.89 >=0.20	0.55 >=0.20
0.98 >=0.20	0.78 >=0.20
0.89 >=0.20	1 >=0.20
0.26 >=0.20	0.95 >=0.20
0.93 >=0.20	0.76 >=0.20
0.94 >=0.20	0.78 >=0.20
1 >=0.20	0.78 >=0.20
0.53 >=0.20	0.48 >=0.20

0.42	>=0.20	0.83	>=0.20
0.67	>=0.20	0.67	>=0.20
0.73	>=0.20	0.53	>=0.20
0.87	>=0.20	0.83	>=0.20
0.61	>=0.20	0.47	>=0.20
0.94	>=0.20	0.96	>=0.20
0.88	>=0.20	0.28	>=0.20
0.84	>=0.20	0.19	>=0.20
0.23	>=0.20	0.67	>=0.20
0.22	>=0.20	0.56	>=0.20
0.14	>=0.20	0.4	>=0.20
0.04	>=0.20	0.31	>=0.20
0.77	>=0.20	1	>=0.20
0.34	>=0.20	0.8	>=0.20
0.3	>=0.20	0.43	>=0.20
0.99	>=0.20	0.83	>=0.20
0.86	>=0.20	0.43	>=0.20
0.25	>=0.20	0.99	>=0.20
0.11	>=0.20	0.85	>=0.20
0.22	>=0.20	0.94	>=0.20
0.99	>=0.20	0.95	>=0.20
0.92	>=0.20	0.99	>=0.20
0.94	>=0.20	1	>=0.20
0.64	>=0.20	0.98	>=0.20
0.86	>=0.20	0.97	>=0.20
0.75	>=0.20	0.82	>=0.20
0.34	>=0.20	0.95	>=0.20
0.17	>=0.20	0.89	>=0.20
0.64	>=0.20	0.03	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
0.96	>=0.20	0.99	>=0.20
0.99	>=0.20	0.99	>=0.20
0.16	>=0.20	0.03	>=0.20
0.23	>=0.20	0.43	>=0.20
1	>=0.20	0.83	>=0.20
0.35	>=0.20	0.67	>=0.20
0.71	>=0.20	0.41	>=0.20
0.6	>=0.20	0.07	>=0.20
0.62	>=0.20	0.36	>=0.20
0.67	>=0.20	0.97	>=0.20
0.54	>=0.20	0.97	>=0.20
0.56	>=0.20	0.1	>=0.20
0.57	>=0.20	0.87	>=0.20
0.37	>=0.20	0.96	>=0.20
0.8	>=0.20	0.04	>=0.20

1 >=0.20	1 >=0.20
1 >=0.20	0.95 >=0.20
0.52 >=0.20	0.8 >=0.20
0.9 >=0.20	0.86 >=0.20
0.59 >=0.20	0.99 >=0.20
0.54 >=0.20	0.88 >=0.20
0.15 >=0.20	0.05 >=0.20
0.66 >=0.20	0.14 >=0.20
0.52 >=0.20	0.21 >=0.20
0.9 >=0.20	0.09 >=0.20
0.65 >=0.20	0.71 >=0.20
0.64 >=0.20	0.51 >=0.20
0.55 >=0.20	0.47 >=0.20
0.97 >=0.20	0.87 >=0.20
1 >=0.20	1 >=0.20
0.84 >=0.20	0.87 >=0.20
1 >=0.20	0.99 >=0.20
0.97 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
0.92 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
0.31 >=0.20	0.36 >=0.20
0.33 >=0.20	0.94 >=0.20
0.09 >=0.20	0.93 >=0.20
0.76 >=0.20	0.92 >=0.20
0.58 >=0.20	0.88 >=0.20
0.99 >=0.20	0.62 >=0.20
0.68 >=0.20	0.44 >=0.20
0.1 >=0.20	0.61 >=0.20
0.98 >=0.20	0.27 >=0.20
0.99 >=0.20	0.99 >=0.20
0.88 >=0.20	0.77 >=0.20
0.94 >=0.20	0.94 >=0.20
0.96 >=0.20	0.32 >=0.20
0.89 >=0.20	0.68 >=0.20
0.51 >=0.20	0.25 >=0.20
0.93 >=0.20	0.52 >=0.20
0.57 >=0.20	0.96 >=0.20
0.73 >=0.20	0.98 >=0.20
0.73 >=0.20	0.98 >=0.20
1 >=0.20	0.95 >=0.20
1 >=0.20	0.8 >=0.20
1 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.97 >=0.20
1 >=0.20	0.93 >=0.20

1 >=0.20	1 >=0.20
0.7 >=0.20	0.9 >=0.20
0.53 >=0.20	0.99 >=0.20
0.88 >=0.20	1 >=0.20
0.54 >=0.20	0.95 >=0.20
1 >=0.20	0.61 >=0.20
0.33 >=0.20	0.94 >=0.20
0.93 >=0.20	0.65 >=0.20
0.99 >=0.20	0.81 >=0.20
0.97 >=0.20	0.82 >=0.20
0.99 >=0.20	0.68 >=0.20
0.71 >=0.20	1 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
0.51 >=0.20	0.57 >=0.20
0.96 >=0.20	0.83 >=0.20
0.93 >=0.20	0.99 >=0.20
0.98 >=0.20	0.54 >=0.20
0.99 >=0.20	0.46 >=0.20
0.94 >=0.20	0.56 >=0.20
0.87 >=0.20	0.35 >=0.20
0.88 >=0.20	0.32 >=0.20
0.88 >=0.20	0.32 >=0.20
0.94 >=0.20	0.48 >=0.20
0.99 >=0.20	0.93 >=0.20
0.44 >=0.20	0.42 >=0.20
0.99 >=0.20	0.29 >=0.20
0.41 >=0.20	0.3 >=0.20
1 >=0.20	1 >=0.20
0.28 >=0.20	0.47 >=0.20
0.99 >=0.20	0.98 >=0.20
0.77 >=0.20	0.79 >=0.20
0.54 >=0.20	0.95 >=0.20
0.84 >=0.20	1 >=0.20
0.73 >=0.20	0.33 >=0.20
0.71 >=0.20	0.8 >=0.20
0.83 >=0.20	1 >=0.20
0.23 >=0.20	0.12 >=0.20
0.05 >=0.20	0.36 >=0.20
0.54 >=0.20	0.54 >=0.20
0.42 >=0.20	0.94 >=0.20
0.05 >=0.20	0.44 >=0.20
0.97 >=0.20	0.82 >=0.20
0.28 >=0.20	0.5 >=0.20
0.28 >=0.20	0.5 >=0.20
0.76 >=0.20	0.34 >=0.20
0.76 >=0.20	0.27 >=0.20

0.86 >=0.20	0.03 >=0.20
0.81 >=0.20	0.4 >=0.20
0.37 >=0.20	0.58 >=0.20
0.08 >=0.20	0.68 >=0.20
0.34 >=0.20	1 >=0.20
0.87 >=0.20	0.98 >=0.20
0.65 >=0.20	0.68 >=0.20
0.67 >=0.20	0.55 >=0.20
0.64 >=0.20	0.66 >=0.20
0.56 >=0.20	0.24 >=0.20
0.93 >=0.20	0.23 >=0.20
0.91 >=0.20	0.66 >=0.20
0.96 >=0.20	0.6 >=0.20
0.87 >=0.20	0.86 >=0.20
0.63 >=0.20	0.22 >=0.20
0.82 >=0.20	0.39 >=0.20
0.3 >=0.20	0.04 >=0.20
0.62 >=0.20	0.91 >=0.20
0.96 >=0.20	0.93 >=0.20
0.62 >=0.20	0.58 >=0.20
0.18 >=0.20	0.47 >=0.20
0.93 >=0.20	0.32 >=0.20
1 >=0.20	1 >=0.20
0.81 >=0.20	0.74 >=0.20
0.36 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.98 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.99 >=0.20	0.68 >=0.20
0.98 >=0.20	0.8 >=0.20
0.69 >=0.20	0.89 >=0.20
0.88 >=0.20	0.93 >=0.20
0.62 >=0.20	0.87 >=0.20
0.9 >=0.20	0.93 >=0.20
0.83 >=0.20	1 >=0.20
0.24 >=0.20	0.96 >=0.20
0.54 >=0.20	0.88 >=0.20
0.22 >=0.20	0.86 >=0.20
0.98 >=0.20	0.97 >=0.20
0.46 >=0.20	0.56 >=0.20
0.07 >=0.20	0.11 >=0.20
0.61 >=0.20	0.82 >=0.20
0.92 >=0.20	1 >=0.20
0.85 >=0.20	0.68 >=0.20

0.64 >=0.20	0.85 >=0.20
0.51 >=0.20	0.84 >=0.20
0.95 >=0.20	0.38 >=0.20
0.99 >=0.20	0.97 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
0.12 >=0.20	0.06 >=0.20
0.34 >=0.20	0.5 >=0.20
0.21 >=0.20	0.98 >=0.20
0.3 >=0.20	0.78 >=0.20
0.38 >=0.20	0.96 >=0.20
0.31 >=0.20	0.93 >=0.20
0.11 >=0.20	0.31 >=0.20
0.98 >=0.20	0.59 >=0.20
0.81 >=0.20	0.59 >=0.20
0.1 >=0.20	0.03 >=0.20
0.67 >=0.20	0.35 >=0.20
0.15 >=0.20	0.47 >=0.20
0.18 >=0.20	0.49 >=0.20
0.46 >=0.20	0.79 >=0.20
0.99 >=0.20	0.8 >=0.20
0.88 >=0.20	0.15 >=0.20
0.88 >=0.20	0.15 >=0.20
0.4 >=0.20	0.23 >=0.20
0.18 >=0.20	0.06 >=0.20
0.99 >=0.20	0.81 >=0.20
0.97 >=0.20	0.72 >=0.20
0.31 >=0.20	0.02 >=0.20
1 >=0.20	0.94 >=0.20
0.97 >=0.20	0.69 >=0.20
0.45 >=0.20	0.47 >=0.20
0.99 >=0.20	0.99 >=0.20
0.97 >=0.20	0.98 >=0.20
0.97 >=0.20	0.88 >=0.20
0.95 >=0.20	0.8 >=0.20
0.35 >=0.20	0.97 >=0.20
0.61 >=0.20	1 >=0.20
0.84 >=0.20	0.58 >=0.20
0.39 >=0.20	0.88 >=0.20
0.18 >=0.20	0.53 >=0.20
0.96 >=0.20	0.77 >=0.20
0.96 >=0.20	0.76 >=0.20
0.98 >=0.20	0.83 >=0.20
0.99 >=0.20	0.52 >=0.20
0.96 >=0.20	0.97 >=0.20
1 >=0.20	0.56 >=0.20

0.71 >=0.20	0.57 >=0.20
0.71 >=0.20	0.04 >=0.20
0.88 >=0.20	0.93 >=0.20
0.71 >=0.20	0.03 >=0.20
0.54 >=0.20	0.96 >=0.20
0.46 >=0.20	0.7 >=0.20
0.64 >=0.20	0.9 >=0.20
0.58 >=0.20	0.87 >=0.20
0.99 >=0.20	1 >=0.20
0.97 >=0.20	0.65 >=0.20
0.75 >=0.20	0.98 >=0.20
0.78 >=0.20	0.43 >=0.20
0.77 >=0.20	1 >=0.20
0.62 >=0.20	0.8 >=0.20
0.82 >=0.20	0.79 >=0.20
0.8 >=0.20	0.28 >=0.20
0.13 >=0.20	0.19 >=0.20
0.51 >=0.20	0.93 >=0.20
1 >=0.20	0.72 >=0.20
0.89 >=0.20	0.86 >=0.20
0.46 >=0.20	0.97 >=0.20
0.78 >=0.20	0.41 >=0.20
0.04 >=0.20	0.54 >=0.20
0.11 >=0.20	0.12 >=0.20
0.99 >=0.20	0.28 >=0.20
0.72 >=0.20	0.83 >=0.20
0.04 >=0.20	0.42 >=0.20
0.29 >=0.20	0.18 >=0.20
0.1 >=0.20	0.23 >=0.20
0.11 >=0.20	0.84 >=0.20
0.52 >=0.20	0.96 >=0.20
0.81 >=0.20	0.53 >=0.20
0.71 >=0.20	0.63 >=0.20
0.19 >=0.20	0.73 >=0.20
0.32 >=0.20	0.83 >=0.20
0.88 >=0.20	0.83 >=0.20
0.24 >=0.20	0.87 >=0.20
0.77 >=0.20	0.15 >=0.20
0.86 >=0.20	0.92 >=0.20
0.66 >=0.20	0.84 >=0.20
0.07 >=0.20	0.02 >=0.20
0.95 >=0.20	0.99 >=0.20
0.83 >=0.20	0.77 >=0.20
0.88 >=0.20	0.65 >=0.20
0.74 >=0.20	0.69 >=0.20
0.04 >=0.20	0.65 >=0.20
0.31 >=0.20	0.05 >=0.20

0.31 >=0.20	0.64 >=0.20
0.66 >=0.20	0.63 >=0.20
0.67 >=0.20	0.86 >=0.20
0.75 >=0.20	0.98 >=0.20
0.08 >=0.20	0.54 >=0.20
0.4 >=0.20	1 >=0.20
0.72 >=0.20	0.91 >=0.20
0.41 >=0.20	0.97 >=0.20
0.09 >=0.20	0.42 >=0.20
0.99 >=0.20	0.96 >=0.20
0.96 >=0.20	1 >=0.20
0.05 >=0.20	0.29 >=0.20
0.86 >=0.20	0.74 >=0.20
0.79 >=0.20	0.83 >=0.20
0.12 >=0.20	0.15 >=0.20
1 >=0.20	1 >=0.20
0.59 >=0.20	0.69 >=0.20
0.69 >=0.20	0.52 >=0.20
0.42 >=0.20	0.69 >=0.20
0.23 >=0.20	0.56 >=0.20
0.51 >=0.20	0.79 >=0.20
0.04 >=0.20	0.09 >=0.20
0.24 >=0.20	0.24 >=0.20
0.18 >=0.20	0.06 >=0.20
1 >=0.20	1 >=0.20
0.31 >=0.20	0.8 >=0.20
0.99 >=0.20	0.72 >=0.20
0.28 >=0.20	0.97 >=0.20
0.37 >=0.20	0.93 >=0.20
0.15 >=0.20	0.94 >=0.20
0.08 >=0.20	0.95 >=0.20
0.09 >=0.20	0.97 >=0.20
0.06 >=0.20	0.87 >=0.20
0.38 >=0.20	0.11 >=0.20
0.87 >=0.20	0.56 >=0.20
0.95 >=0.20	0.92 >=0.20
0.43 >=0.20	0.72 >=0.20
0.59 >=0.20	0.41 >=0.20
0.96 >=0.20	0.57 >=0.20
0.91 >=0.20	0.83 >=0.20
0.82 >=0.20	0.64 >=0.20
0.96 >=0.20	0.86 >=0.20
0.6 >=0.20	0.53 >=0.20
0.15 >=0.20	0.16 >=0.20
0.99 >=0.20	0.86 >=0.20
0.81 >=0.20	0.38 >=0.20
1 >=0.20	0.94 >=0.20

0.88 >=0.20	0.54 >=0.20
1 >=0.20	0.96 >=0.20
0.3 >=0.20	0.21 >=0.20
0.43 >=0.20	0.52 >=0.20
1 >=0.20	0.67 >=0.20
0.98 >=0.20	0.76 >=0.20
0.12 >=0.20	0.78 >=0.20
0.07 >=0.20	0.93 >=0.20
0.14 >=0.20	0.41 >=0.20
0.04 >=0.20	0.85 >=0.20
0.07 >=0.20	0.94 >=0.20
0.4 >=0.20	0.79 >=0.20
0.12 >=0.20	0.79 >=0.20
0.35 >=0.20	0.8 >=0.20
0.34 >=0.20	0.81 >=0.20
0.95 >=0.20	0.94 >=0.20
0.88 >=0.20	0.9 >=0.20
0.75 >=0.20	0.96 >=0.20
0.48 >=0.20	0.86 >=0.20
0.64 >=0.20	0.79 >=0.20
0.08 >=0.20	0.9 >=0.20
0.34 >=0.20	0.47 >=0.20
0.4 >=0.20	0.21 >=0.20
0.06 >=0.20	0.27 >=0.20
0.57 >=0.20	0.26 >=0.20
1 >=0.20	0.95 >=0.20
0.71 >=0.20	0.96 >=0.20
0.25 >=0.20	0.69 >=0.20
0.58 >=0.20	0.7 >=0.20
0.41 >=0.20	0.61 >=0.20
0.93 >=0.20	0.07 >=0.20
0.93 >=0.20	0.07 >=0.20
0.09 >=0.20	0.26 >=0.20
0.97 >=0.20	0.97 >=0.20
0.7 >=0.20	0.54 >=0.20
0.5 >=0.20	0.84 >=0.20
0.34 >=0.20	0.83 >=0.20
0.33 >=0.20	0.13 >=0.20
0.1 >=0.20	0.77 >=0.20
0.21 >=0.20	0.18 >=0.20
0.55 >=0.20	0.78 >=0.20
0.15 >=0.20	0.92 >=0.20
0.15 >=0.20	0.55 >=0.20
0.26 >=0.20	0.23 >=0.20
0.04 >=0.20	0.48 >=0.20
0.23 >=0.20	0.65 >=0.20
0.09 >=0.20	0.87 >=0.20

0.35 >=0.20	0.7 >=0.20
0.23 >=0.20	0.86 >=0.20
0.15 >=0.20	0.57 >=0.20
0.51 >=0.20	0.88 >=0.20
0.9 >=0.20	0.59 >=0.20
0.86 >=0.20	0.78 >=0.20
0.96 >=0.20	0.87 >=0.20
0.74 >=0.20	0.98 >=0.20
0.65 >=0.20	0.05 >=0.20
0.97 >=0.20	0.92 >=0.20
0.98 >=0.20	0.98 >=0.20
0.93 >=0.20	0.78 >=0.20
0.92 >=0.20	0.93 >=0.20
0.64 >=0.20	0.41 >=0.20
0.87 >=0.20	0.89 >=0.20
0.93 >=0.20	0.78 >=0.20
0.12 >=0.20	0.6 >=0.20
0.11 >=0.20	0.44 >=0.20
0.11 >=0.20	0.44 >=0.20
0.04 >=0.20	0.48 >=0.20
0.67 >=0.20	0.24 >=0.20
0.33 >=0.20	0.56 >=0.20
1 >=0.20	0.48 >=0.20
0.5 >=0.20	0.62 >=0.20
0.94 >=0.20	0.37 >=0.20
0.36 >=0.20	0.68 >=0.20
0.97 >=0.20	0.83 >=0.20
0.17 >=0.20	0.4 >=0.20
0.05 >=0.20	0.22 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	0.93 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.24 >=0.20
0.74 >=0.20	0.79 >=0.20
0.41 >=0.20	0.24 >=0.20
0.28 >=0.20	0.98 >=0.20
0.4 >=0.20	0.99 >=0.20
0.25 >=0.20	0.98 >=0.20
0.24 >=0.20	1 >=0.20
0.28 >=0.20	0.59 >=0.20
0.05 >=0.20	0.19 >=0.20
0.06 >=0.20	0.16 >=0.20
0.39 >=0.20	0.44 >=0.20
1 >=0.20	1 >=0.20
0.07 >=0.20	0.35 >=0.20
0.09 >=0.20	0.1 >=0.20

0.1 >=0.20	0.36 >=0.20
0.39 >=0.20	0.86 >=0.20
0.32 >=0.20	0.46 >=0.20
0.05 >=0.20	0.13 >=0.20
0.16 >=0.20	0.37 >=0.20
0.19 >=0.20	0.71 >=0.20
0.76 >=0.20	0.76 >=0.20
0.91 >=0.20	0.48 >=0.20
0.04 >=0.20	0.14 >=0.20
0.08 >=0.20	0.29 >=0.20
0.24 >=0.20	0.69 >=0.20
0.34 >=0.20	0.62 >=0.20
0.2 >=0.20	0.61 >=0.20
0.06 >=0.20	0.36 >=0.20
0.37 >=0.20	0.47 >=0.20
0.64 >=0.20	0.92 >=0.20
0.65 >=0.20	0.64 >=0.20
0.69 >=0.20	0.97 >=0.20
0.61 >=0.20	0.86 >=0.20
0.47 >=0.20	0.69 >=0.20
0.6 >=0.20	0.8 >=0.20
0.12 >=0.20	0.62 >=0.20
0.12 >=0.20	0.5 >=0.20
0.26 >=0.20	0.57 >=0.20
0.47 >=0.20	0.54 >=0.20
0.35 >=0.20	0.92 >=0.20
0.46 >=0.20	0.8 >=0.20
0.26 >=0.20	0.5 >=0.20
0.95 >=0.20	0.63 >=0.20
0.07 >=0.20	0.38 >=0.20
0.19 >=0.20	0.63 >=0.20
0.18 >=0.20	0.65 >=0.20
0.1 >=0.20	0.2 >=0.20
0.63 >=0.20	0.94 >=0.20
0.08 >=0.20	0.7 >=0.20
0.76 >=0.20	0.42 >=0.20
0.12 >=0.20	0.92 >=0.20
0.08 >=0.20	0.56 >=0.20
0.71 >=0.20	0.8 >=0.20
0.07 >=0.20	0.37 >=0.20
0.36 >=0.20	0.91 >=0.20
0.4 >=0.20	0.87 >=0.20
0.05 >=0.20	0.2 >=0.20
0.05 >=0.20	0.2 >=0.20
0.08 >=0.20	0.07 >=0.20
0.8 >=0.20	0.41 >=0.20
0.52 >=0.20	0.57 >=0.20

0.84	>=0.20	0.77	>=0.20
0.53	>=0.20	0.66	>=0.20
0.07	>=0.20	0.15	>=0.20
0.32	>=0.20	0.55	>=0.20
0.38	>=0.20	0.85	>=0.20
0.34	>=0.20	1	>=0.20
0.14	>=0.20	0.3	>=0.20
0.2	>=0.20	0.79	>=0.20
0.1	>=0.20	0.16	>=0.20
0.17	>=0.20	0.39	>=0.20
0.43	>=0.20	0.83	>=0.20
0.13	>=0.20	0.09	>=0.20
0.96	>=0.20	0.7	>=0.20
0.99	>=0.20	0.85	>=0.20
0.97	>=0.20	0.43	>=0.20
0.94	>=0.20	0.29	>=0.20
0.35	>=0.20	0.16	>=0.20
0.11	>=0.20	0.48	>=0.20
0.12	>=0.20	0.21	>=0.20
0.07	>=0.20	0.32	>=0.20
0.16	>=0.20	0.37	>=0.20
0.8	>=0.20	0.99	>=0.20
0.78	>=0.20	0.93	>=0.20
0.84	>=0.20	0.44	>=0.20
0.69	>=0.20	0.31	>=0.20
0.86	>=0.20	1	>=0.20
0.42	>=0.20	0.09	>=0.20
0.06	>=0.20	0.91	>=0.20
0.05	>=0.20	0.89	>=0.20
0.04	>=0.20	0.93	>=0.20
0.14	>=0.20	0.28	>=0.20
0.04	>=0.20	0.25	>=0.20
0.27	>=0.20	0.21	>=0.20
0.06	>=0.20	0.25	>=0.20
0.05	>=0.20	0.1	>=0.20
0.2	>=0.20	0.23	>=0.20
0.67	>=0.20	0.85	>=0.20
1	>=0.20	0.99	>=0.20
0.89	>=0.20	0.89	>=0.20
0.94	>=0.20	0.69	>=0.20
0.74	>=0.20	0.19	>=0.20
0.9	>=0.20	0.72	>=0.20
0.53	>=0.20	0.27	>=0.20
0.27	>=0.20	0.35	>=0.20
0.31	>=0.20	0.14	>=0.20
0.9	>=0.20	0.81	>=0.20
0.48	>=0.20	0.27	>=0.20

0.92 >=0.20	0.78 >=0.20
0.04 >=0.20	0.93 >=0.20
0.04 >=0.20	0.96 >=0.20
0.82 >=0.20	0.69 >=0.20
0.68 >=0.20	0.53 >=0.20
0.98 >=0.20	0.99 >=0.20
0.95 >=0.20	0.92 >=0.20
0.94 >=0.20	0.83 >=0.20
0.44 >=0.20	0.81 >=0.20
0.18 >=0.20	0.54 >=0.20
0.97 >=0.20	0.79 >=0.20
0.91 >=0.20	0.18 >=0.20
0.84 >=0.20	0.76 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	0.96 >=0.20
0.67 >=0.20	0.53 >=0.20
0.88 >=0.20	0.66 >=0.20
0.5 >=0.20	0.79 >=0.20
0.97 >=0.20	0.3 >=0.20
0.58 >=0.20	0.87 >=0.20
0.53 >=0.20	0.57 >=0.20
0.21 >=0.20	0.77 >=0.20
1 >=0.20	0.97 >=0.20
0.98 >=0.20	0.99 >=0.20
0.94 >=0.20	0.73 >=0.20
0.88 >=0.20	0.98 >=0.20
0.9 >=0.20	0.98 >=0.20
0.34 >=0.20	0.7 >=0.20
0.09 >=0.20	0.27 >=0.20
0.65 >=0.20	0.41 >=0.20
0.51 >=0.20	0.2 >=0.20
0.38 >=0.20	0.7 >=0.20
0.98 >=0.20	0.87 >=0.20
0.49 >=0.20	0.41 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.09 >=0.20	0.04 >=0.20
0.58 >=0.20	0.46 >=0.20
0.07 >=0.20	0.13 >=0.20
0.91 >=0.20	0.51 >=0.20
0.99 >=0.20	0.23 >=0.20
0.71 >=0.20	0.97 >=0.20
0.59 >=0.20	0.99 >=0.20
0.05 >=0.20	0.17 >=0.20
0.96 >=0.20	0.4 >=0.20
0.62 >=0.20	0.12 >=0.20
0.96 >=0.20	0.56 >=0.20

0.99 >=0.20	0.83 >=0.20
0.81 >=0.20	0.51 >=0.20
0.35 >=0.20	0.46 >=0.20
0.19 >=0.20	0.98 >=0.20
0.28 >=0.20	0.34 >=0.20
0.08 >=0.20	0.03 >=0.20
0.4 >=0.20	0.81 >=0.20
0.12 >=0.20	0.23 >=0.20
0.04 >=0.20	0.19 >=0.20
0.5 >=0.20	0.2 >=0.20
0.17 >=0.20	0.14 >=0.20
0.99 >=0.20	0.52 >=0.20
0.29 >=0.20	0.11 >=0.20
0.48 >=0.20	0.27 >=0.20
0.99 >=0.20	0.81 >=0.20
1 >=0.20	0.99 >=0.20
0.98 >=0.20	0.69 >=0.20
0.28 >=0.20	1 >=0.20
0.84 >=0.20	0.81 >=0.20
0.74 >=0.20	0.97 >=0.20
0.98 >=0.20	0.57 >=0.20
0.89 >=0.20	0.61 >=0.20
0.56 >=0.20	0.81 >=0.20
0.97 >=0.20	0.98 >=0.20
0.91 >=0.20	0.71 >=0.20
0.12 >=0.20	0.32 >=0.20
0.83 >=0.20	0.83 >=0.20
1 >=0.20	1 >=0.20
0.97 >=0.20	1 >=0.20
0.97 >=0.20	0.99 >=0.20
0.93 >=0.20	1 >=0.20
0.93 >=0.20	0.99 >=0.20
0.86 >=0.20	1 >=0.20
0.97 >=0.20	0.98 >=0.20
0.93 >=0.20	0.99 >=0.20
0.89 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
0.99 >=0.20	0.99 >=0.20
0.53 >=0.20	0.12 >=0.20
0.14 >=0.20	0.17 >=0.20
0.96 >=0.20	0.99 >=0.20

0.99 >=0.20	1 >=0.20
0.08 >=0.20	0.27 >=0.20
0.93 >=0.20	0.28 >=0.20
0.73 >=0.20	0.67 >=0.20
0.86 >=0.20	0.47 >=0.20
0.94 >=0.20	0.45 >=0.20
0.86 >=0.20	0.95 >=0.20
1 >=0.20	0.98 >=0.20
0.89 >=0.20	0.69 >=0.20
0.68 >=0.20	0.85 >=0.20
0.34 >=0.20	0.32 >=0.20
0.14 >=0.20	0.28 >=0.20
0.05 >=0.20	0.18 >=0.20
0.04 >=0.20	0.21 >=0.20
0.04 >=0.20	0.12 >=0.20
0.39 >=0.20	0.1 >=0.20
0.27 >=0.20	0.15 >=0.20
0.78 >=0.20	0.76 >=0.20
0.73 >=0.20	0.67 >=0.20
0.78 >=0.20	0.76 >=0.20
0.78 >=0.20	0.76 >=0.20
0.17 >=0.20	0.45 >=0.20
0.43 >=0.20	0.86 >=0.20
0.69 >=0.20	1 >=0.20
0.97 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.82 >=0.20	0.23 >=0.20
0.65 >=0.20	0.3 >=0.20
0.39 >=0.20	1 >=0.20
0.54 >=0.20	1 >=0.20
0.84 >=0.20	1 >=0.20
0.7 >=0.20	0.99 >=0.20
0.07 >=0.20	0.26 >=0.20
0.83 >=0.20	0.92 >=0.20
0.23 >=0.20	0.66 >=0.20
0.33 >=0.20	0.06 >=0.20
1 >=0.20	0.99 >=0.20
0.66 >=0.20	0.3 >=0.20
0.05 >=0.20	0.38 >=0.20
0.53 >=0.20	0.13 >=0.20
1 >=0.20	1 >=0.20
0.93 >=0.20	0.76 >=0.20
0.85 >=0.20	0.68 >=0.20
0.4 >=0.20	0.21 >=0.20
0.98 >=0.20	0.73 >=0.20
0.94 >=0.20	0.44 >=0.20

0.75 >=0.20	0.19 >=0.20
0.13 >=0.20	0.47 >=0.20
0.22 >=0.20	0.06 >=0.20
0.16 >=0.20	0.52 >=0.20
0.9 >=0.20	0.55 >=0.20
0.65 >=0.20	0.74 >=0.20
0.97 >=0.20	0.98 >=0.20
0.07 >=0.20	0.75 >=0.20
0.32 >=0.20	0.2 >=0.20
0.98 >=0.20	0.92 >=0.20
0.95 >=0.20	0.66 >=0.20
0.84 >=0.20	0.73 >=0.20
0.59 >=0.20	0.78 >=0.20
0.41 >=0.20	0.83 >=0.20
0.75 >=0.20	0.88 >=0.20
0.99 >=0.20	1 >=0.20
0.92 >=0.20	0.92 >=0.20
0.91 >=0.20	0.77 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	0.63 >=0.20
0.88 >=0.20	0.8 >=0.20
0.97 >=0.20	0.99 >=0.20
0.81 >=0.20	0.7 >=0.20
0.77 >=0.20	0.93 >=0.20
0.97 >=0.20	0.96 >=0.20
0.55 >=0.20	0.7 >=0.20
0.67 >=0.20	0.06 >=0.20
0.42 >=0.20	0.13 >=0.20
1 >=0.20	0.97 >=0.20
0.47 >=0.20	0.21 >=0.20
0.06 >=0.20	0.49 >=0.20
0.78 >=0.20	0.3 >=0.20
0.58 >=0.20	0.91 >=0.20
0.3 >=0.20	0.53 >=0.20
0.95 >=0.20	0.41 >=0.20
0.07 >=0.20	0.26 >=0.20
0.22 >=0.20	0.77 >=0.20
0.22 >=0.20	0.76 >=0.20
0.22 >=0.20	0.76 >=0.20
0.22 >=0.20	0.77 >=0.20
0.22 >=0.20	0.76 >=0.20
0.22 >=0.20	0.76 >=0.20
0.22 >=0.20	0.76 >=0.20
0.73 >=0.20	0.61 >=0.20
0.82 >=0.20	0.07 >=0.20
0.77 >=0.20	0.94 >=0.20
0.94 >=0.20	0.64 >=0.20

0.97 >=0.20	0.69 >=0.20
0.99 >=0.20	0.95 >=0.20
0.89 >=0.20	0.67 >=0.20
0.63 >=0.20	0.79 >=0.20
0.43 >=0.20	0.44 >=0.20
0.53 >=0.20	0.98 >=0.20
1 >=0.20	0.92 >=0.20
0.5 >=0.20	0.12 >=0.20
0.26 >=0.20	0.49 >=0.20
0.12 >=0.20	0.22 >=0.20
0.95 >=0.20	0.94 >=0.20
0.84 >=0.20	0.96 >=0.20
0.4 >=0.20	0.99 >=0.20
0.97 >=0.20	0.96 >=0.20
0.99 >=0.20	0.9 >=0.20
0.73 >=0.20	0.94 >=0.20
0.34 >=0.20	1 >=0.20
0.94 >=0.20	0.23 >=0.20
1 >=0.20	0.5 >=0.20
0.53 >=0.20	0.99 >=0.20
0.95 >=0.20	0.51 >=0.20
0.94 >=0.20	1 >=0.20
0.99 >=0.20	0.62 >=0.20
0.99 >=0.20	0.73 >=0.20
0.69 >=0.20	0.52 >=0.20
0.97 >=0.20	0.81 >=0.20
0.89 >=0.20	0.84 >=0.20
0.94 >=0.20	0.22 >=0.20
0.94 >=0.20	0.91 >=0.20
0.68 >=0.20	0.91 >=0.20
0.17 >=0.20	0.03 >=0.20
0.04 >=0.20	0.17 >=0.20
0.96 >=0.20	0.99 >=0.20
0.49 >=0.20	0.27 >=0.20
0.7 >=0.20	0.97 >=0.20
0.96 >=0.20	0.42 >=0.20
0.45 >=0.20	0.37 >=0.20
0.3 >=0.20	0.21 >=0.20
0.91 >=0.20	0.58 >=0.20
0.97 >=0.20	0.81 >=0.20
0.41 >=0.20	0.58 >=0.20
0.61 >=0.20	0.96 >=0.20
0.09 >=0.20	0.05 >=0.20
0.09 >=0.20	0.05 >=0.20
1 >=0.20	0.99 >=0.20
0.95 >=0.20	0.42 >=0.20
0.55 >=0.20	0.59 >=0.20

0.5	>=0.20	0.64	>=0.20
0.91	>=0.20	0.85	>=0.20
0.84	>=0.20	0.44	>=0.20
0.58	>=0.20	0.84	>=0.20
0.31	>=0.20	0.23	>=0.20
0.99	>=0.20	0.52	>=0.20
0.94	>=0.20	0.58	>=0.20
0.92	>=0.20	0.75	>=0.20
0.6	>=0.20	0.91	>=0.20
0.89	>=0.20	0.99	>=0.20
0.28	>=0.20	0.42	>=0.20
0.99	>=0.20	0.87	>=0.20
0.96	>=0.20	0.99	>=0.20
0.94	>=0.20	0.89	>=0.20
0.99	>=0.20	0.97	>=0.20
0.87	>=0.20	0.44	>=0.20
0.77	>=0.20	0.24	>=0.20
0.93	>=0.20	0.35	>=0.20
1	>=0.20	0.96	>=0.20
0.99	>=0.20	0.58	>=0.20
0.55	>=0.20	0.3	>=0.20
0.99	>=0.20	0.98	>=0.20
0.17	>=0.20	0.81	>=0.20
0.99	>=0.20	0.99	>=0.20
0.83	>=0.20	0.75	>=0.20
0.49	>=0.20	0.26	>=0.20
0.7	>=0.20	0.81	>=0.20
0.31	>=0.20	0.56	>=0.20
0.45	>=0.20	0.58	>=0.20
0.14	>=0.20	0.8	>=0.20
0.33	>=0.20	0.07	>=0.20
0.78	>=0.20	0.24	>=0.20
0.26	>=0.20	0.21	>=0.20
0.35	>=0.20	0.96	>=0.20
0.97	>=0.20	0.47	>=0.20
0.99	>=0.20	0.69	>=0.20
0.33	>=0.20	0.32	>=0.20
0.99	>=0.20	0.99	>=0.20
0.78	>=0.20	0.4	>=0.20
0.96	>=0.20	0.46	>=0.20
0.99	>=0.20	0.58	>=0.20
0.75	>=0.20	0.31	>=0.20
0.91	>=0.20	0.75	>=0.20
0.97	>=0.20	0.48	>=0.20
0.91	>=0.20	0.55	>=0.20
1	>=0.20	0.99	>=0.20
0.99	>=0.20	0.54	>=0.20

0.5	>=0.20	0.82	>=0.20
0.28	>=0.20	0.13	>=0.20
0.17	>=0.20	0.83	>=0.20
0.98	>=0.20	0.39	>=0.20
0.98	>=0.20	0.47	>=0.20
0.08	>=0.20	0.75	>=0.20
0.08	>=0.20	0.75	>=0.20
0.5	>=0.20	0.34	>=0.20
0.35	>=0.20	0.39	>=0.20
1	>=0.20	0.6	>=0.20
0.84	>=0.20	0.27	>=0.20
0.18	>=0.20	0.03	>=0.20
0.73	>=0.20	0.79	>=0.20
0.83	>=0.20	0.89	>=0.20
0.98	>=0.20	0.95	>=0.20
0.98	>=0.20	0.97	>=0.20
0.99	>=0.20	0.87	>=0.20
0.72	>=0.20	0.65	>=0.20
0.97	>=0.20	0.99	>=0.20
0.93	>=0.20	0.99	>=0.20
0.37	>=0.20	0.92	>=0.20
0.14	>=0.20	0.41	>=0.20
0.16	>=0.20	0.41	>=0.20
0.08	>=0.20	0.5	>=0.20
0.2	>=0.20	0.46	>=0.20
0.08	>=0.20	0.63	>=0.20
0.94	>=0.20	0.7	>=0.20
0.66	>=0.20	0.31	>=0.20
0.74	>=0.20	0.65	>=0.20
0.72	>=0.20	0.8	>=0.20
0.14	>=0.20	0.54	>=0.20
0.18	>=0.20	0.28	>=0.20
0.15	>=0.20	0.16	>=0.20
0.04	>=0.20	0.14	>=0.20
0.07	>=0.20	0.19	>=0.20
0.09	>=0.20	0.28	>=0.20
0.71	>=0.20	0.97	>=0.20
0.35	>=0.20	0.35	>=0.20
0.04	>=0.20	0.58	>=0.20
1	>=0.20	1	>=0.20
0.08	>=0.20	0.05	>=0.20
0.05	>=0.20	0.05	>=0.20
0.18	>=0.20	0.09	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20

0.79 >=0.20	0.71 >=0.20
1 >=0.20	1 >=0.20
0.14 >=0.20	0.58 >=0.20
0.89 >=0.20	1 >=0.20
1 >=0.20	0.77 >=0.20
0.46 >=0.20	0.32 >=0.20
0.11 >=0.20	0.3 >=0.20
0.36 >=0.20	0.31 >=0.20
1 >=0.20	0.98 >=0.20
0.7 >=0.20	0.99 >=0.20
0.44 >=0.20	0.94 >=0.20
0.7 >=0.20	0.99 >=0.20
0.17 >=0.20	0.84 >=0.20
0.64 >=0.20	1 >=0.20
0.43 >=0.20	1 >=0.20
0.64 >=0.20	1 >=0.20
0.99 >=0.20	0.82 >=0.20
0.96 >=0.20	0.59 >=0.20
0.97 >=0.20	0.7 >=0.20
0.94 >=0.20	0.77 >=0.20
0.83 >=0.20	0.37 >=0.20
0.38 >=0.20	0.13 >=0.20
0.96 >=0.20	1 >=0.20
0.54 >=0.20	0.24 >=0.20
0.9 >=0.20	0.59 >=0.20
0.69 >=0.20	0.3 >=0.20
0.54 >=0.20	0.7 >=0.20
0.47 >=0.20	0.83 >=0.20
0.31 >=0.20	0.52 >=0.20
0.38 >=0.20	1 >=0.20
0.39 >=0.20	1 >=0.20
0.87 >=0.20	0.75 >=0.20
0.97 >=0.20	0.78 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.96 >=0.20
0.73 >=0.20	0.4 >=0.20
0.66 >=0.20	0.65 >=0.20
0.28 >=0.20	0.98 >=0.20
0.52 >=0.20	0.79 >=0.20
0.84 >=0.20	0.99 >=0.20
0.82 >=0.20	0.99 >=0.20
0.83 >=0.20	0.96 >=0.20
0.22 >=0.20	0.59 >=0.20
0.16 >=0.20	0.64 >=0.20
0.04 >=0.20	0.3 >=0.20
0.14 >=0.20	0.12 >=0.20
0.61 >=0.20	0.85 >=0.20

0.04 >=0.20	0.41 >=0.20
0.12 >=0.20	0.45 >=0.20
0.39 >=0.20	0.9 >=0.20
0.98 >=0.20	0.71 >=0.20
0.98 >=0.20	0.71 >=0.20
0.4 >=0.20	0.44 >=0.20
1 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
0.99 >=0.20	0.98 >=0.20
0.83 >=0.20	0.88 >=0.20
0.71 >=0.20	1 >=0.20
0.7 >=0.20	1 >=0.20
0.7 >=0.20	0.91 >=0.20
0.69 >=0.20	0.99 >=0.20
0.72 >=0.20	0.94 >=0.20
0.96 >=0.20	0.97 >=0.20
0.87 >=0.20	0.95 >=0.20
0.07 >=0.20	0.7 >=0.20
0.69 >=0.20	1 >=0.20
0.39 >=0.20	0.97 >=0.20
0.96 >=0.20	1 >=0.20
0.83 >=0.20	0.13 >=0.20
0.23 >=0.20	0.66 >=0.20
0.15 >=0.20	0.94 >=0.20
0.83 >=0.20	0.38 >=0.20
0.13 >=0.20	0.42 >=0.20
0.4 >=0.20	0.46 >=0.20
1 >=0.20	1 >=0.20
0.86 >=0.20	0.7 >=0.20
0.97 >=0.20	0.98 >=0.20
1 >=0.20	0.87 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.92 >=0.20
0.24 >=0.20	0.79 >=0.20
0.16 >=0.20	0.58 >=0.20
0.96 >=0.20	0.48 >=0.20
0.24 >=0.20	0.15 >=0.20
0.22 >=0.20	0.58 >=0.20
0.64 >=0.20	0.25 >=0.20
0.69 >=0.20	0.05 >=0.20
0.27 >=0.20	0.68 >=0.20
0.51 >=0.20	0.32 >=0.20
0.75 >=0.20	0.76 >=0.20
0.1 >=0.20	0.39 >=0.20
0.85 >=0.20	0.65 >=0.20

0.04 >=0.20	0.12 >=0.20
0.67 >=0.20	0.45 >=0.20
0.68 >=0.20	0.59 >=0.20
0.66 >=0.20	0.95 >=0.20
0.91 >=0.20	0.49 >=0.20
0.8 >=0.20	0.93 >=0.20
0.81 >=0.20	0.39 >=0.20
0.71 >=0.20	0.81 >=0.20
0.96 >=0.20	0.99 >=0.20
0.25 >=0.20	0.16 >=0.20
0.5 >=0.20	0.87 >=0.20
0.99 >=0.20	1 >=0.20
0.16 >=0.20	0.19 >=0.20
0.85 >=0.20	0.98 >=0.20
0.99 >=0.20	0.68 >=0.20
0.98 >=0.20	0.32 >=0.20
0.98 >=0.20	0.7 >=0.20
0.99 >=0.20	0.45 >=0.20
0.1 >=0.20	0.28 >=0.20
0.11 >=0.20	0.08 >=0.20
0.37 >=0.20	0.44 >=0.20
0.97 >=0.20	0.81 >=0.20
0.92 >=0.20	0.86 >=0.20
0.97 >=0.20	1 >=0.20
0.08 >=0.20	0.57 >=0.20
0.35 >=0.20	0.11 >=0.20
0.51 >=0.20	0.82 >=0.20
0.34 >=0.20	0.58 >=0.20
0.53 >=0.20	0.83 >=0.20
0.28 >=0.20	0.82 >=0.20
0.3 >=0.20	0.6 >=0.20
0.97 >=0.20	0.57 >=0.20
0.97 >=0.20	0.65 >=0.20
0.96 >=0.20	0.33 >=0.20
0.64 >=0.20	0.95 >=0.20
0.99 >=0.20	1 >=0.20
0.9 >=0.20	0.98 >=0.20
0.99 >=0.20	0.91 >=0.20
0.89 >=0.20	0.99 >=0.20
0.84 >=0.20	0.95 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	0.81 >=0.20
0.98 >=0.20	0.97 >=0.20
0.99 >=0.20	0.99 >=0.20
1 >=0.20	0.99 >=0.20
0.56 >=0.20	0.93 >=0.20
0.44 >=0.20	0.24 >=0.20

0.83 >=0.20	1 >=0.20
0.92 >=0.20	0.92 >=0.20
0.26 >=0.20	0.58 >=0.20
0.06 >=0.20	0.21 >=0.20
0.49 >=0.20	0.25 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.94 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	0.94 >=0.20
0.06 >=0.20	0.56 >=0.20
0.85 >=0.20	0.45 >=0.20
0.58 >=0.20	0.5 >=0.20
0.25 >=0.20	0.45 >=0.20
0.95 >=0.20	0.99 >=0.20
0.07 >=0.20	0.2 >=0.20
1 >=0.20	1 >=0.20
0.17 >=0.20	0.25 >=0.20
0.43 >=0.20	0.34 >=0.20
0.66 >=0.20	0.43 >=0.20
0.05 >=0.20	0.09 >=0.20
0.33 >=0.20	0.66 >=0.20
0.48 >=0.20	0.45 >=0.20
0.7 >=0.20	0.66 >=0.20
0.62 >=0.20	0.48 >=0.20
0.7 >=0.20	0.24 >=0.20
0.34 >=0.20	0.5 >=0.20
0.2 >=0.20	0.65 >=0.20
0.15 >=0.20	0.59 >=0.20
0.04 >=0.20	0.57 >=0.20
0.04 >=0.20	0.17 >=0.20
0.06 >=0.20	0.13 >=0.20
0.06 >=0.20	0.06 >=0.20
1 >=0.20	0.99 >=0.20
0.23 >=0.20	0.51 >=0.20
0.93 >=0.20	0.63 >=0.20
0.91 >=0.20	0.79 >=0.20
0.99 >=0.20	0.99 >=0.20
0.59 >=0.20	0.38 >=0.20
0.99 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.89 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.96 >=0.20	1 >=0.20
0.91 >=0.20	0.99 >=0.20

1 >=0.20	1 >=0.20
0.99 >=0.20	1 >=0.20
0.98 >=0.20	0.99 >=0.20
0.81 >=0.20	0.87 >=0.20
0.7 >=0.20	0.91 >=0.20
1 >=0.20	1 >=0.20
0.85 >=0.20	0.93 >=0.20
0.91 >=0.20	1 >=0.20
0.91 >=0.20	1 >=0.20
0.95 >=0.20	1 >=0.20
0.78 >=0.20	0.64 >=0.20
0.73 >=0.20	0.88 >=0.20
0.46 >=0.20	0.7 >=0.20
0.91 >=0.20	1 >=0.20
0.64 >=0.20	0.88 >=0.20
0.79 >=0.20	0.64 >=0.20
0.92 >=0.20	0.72 >=0.20
0.97 >=0.20	0.81 >=0.20
0.97 >=0.20	0.78 >=0.20
0.99 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.92 >=0.20	0.94 >=0.20
0.81 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
0.64 >=0.20	0.79 >=0.20
0.17 >=0.20	0.66 >=0.20
0.75 >=0.20	0.7 >=0.20
1 >=0.20	0.91 >=0.20
0.44 >=0.20	0.51 >=0.20
0.94 >=0.20	0.93 >=0.20
0.68 >=0.20	0.98 >=0.20
0.43 >=0.20	0.27 >=0.20
0.75 >=0.20	0.4 >=0.20
0.49 >=0.20	0.51 >=0.20
0.86 >=0.20	0.89 >=0.20
0.58 >=0.20	0.85 >=0.20
0.92 >=0.20	1 >=0.20
0.63 >=0.20	0.99 >=0.20
0.59 >=0.20	0.82 >=0.20
0.34 >=0.20	0.91 >=0.20
0.98 >=0.20	0.98 >=0.20
0.92 >=0.20	0.99 >=0.20
0.41 >=0.20	0.28 >=0.20
0.9 >=0.20	0.62 >=0.20
0.7 >=0.20	0.55 >=0.20
0.42 >=0.20	0.82 >=0.20
0.81 >=0.20	0.36 >=0.20

0.16 >=0.20	0.61 >=0.20
0.25 >=0.20	0.68 >=0.20
0.34 >=0.20	0.39 >=0.20
0.58 >=0.20	0.88 >=0.20
0.53 >=0.20	0.2 >=0.20
0.1 >=0.20	0.85 >=0.20
0.35 >=0.20	0.85 >=0.20
0.1 >=0.20	0.77 >=0.20
0.5 >=0.20	0.57 >=0.20
0.85 >=0.20	0.87 >=0.20
0.48 >=0.20	0.56 >=0.20
0.61 >=0.20	0.68 >=0.20
0.78 >=0.20	0.49 >=0.20
0.52 >=0.20	0.37 >=0.20
0.45 >=0.20	0.73 >=0.20
0.87 >=0.20	0.91 >=0.20
0.28 >=0.20	0.34 >=0.20
0.61 >=0.20	0.54 >=0.20
1 >=0.20	1 >=0.20
0.86 >=0.20	0.9 >=0.20
0.13 >=0.20	0.7 >=0.20
0.82 >=0.20	0.87 >=0.20
0.64 >=0.20	1 >=0.20
0.93 >=0.20	0.66 >=0.20
0.95 >=0.20	0.73 >=0.20
0.14 >=0.20	0.72 >=0.20
0.14 >=0.20	0.72 >=0.20
0.26 >=0.20	0.9 >=0.20
0.26 >=0.20	0.9 >=0.20
0.26 >=0.20	0.9 >=0.20
0.91 >=0.20	0.99 >=0.20
0.38 >=0.20	0.08 >=0.20
0.18 >=0.20	0.63 >=0.20
0.81 >=0.20	0.6 >=0.20
0.87 >=0.20	0.11 >=0.20
0.25 >=0.20	0.65 >=0.20
0.72 >=0.20	0.23 >=0.20
0.97 >=0.20	0.98 >=0.20
0.76 >=0.20	1 >=0.20
0.31 >=0.20	0.53 >=0.20
0.98 >=0.20	0.76 >=0.20
0.89 >=0.20	0.45 >=0.20
0.96 >=0.20	0.46 >=0.20
0.72 >=0.20	0.47 >=0.20
0.24 >=0.20	0.28 >=0.20
0.83 >=0.20	0.62 >=0.20
0.12 >=0.20	0.52 >=0.20

0.57 >=0.20	0.73 >=0.20
0.58 >=0.20	0.83 >=0.20
1 >=0.20	0.32 >=0.20
1 >=0.20	0.81 >=0.20
0.99 >=0.20	0.29 >=0.20
0.31 >=0.20	0.88 >=0.20
0.77 >=0.20	0.27 >=0.20
0.21 >=0.20	0.47 >=0.20
0.84 >=0.20	0.49 >=0.20
0.68 >=0.20	0.27 >=0.20
0.82 >=0.20	0.84 >=0.20
0.63 >=0.20	0.86 >=0.20
0.87 >=0.20	0.96 >=0.20
0.19 >=0.20	0.93 >=0.20
0.1 >=0.20	0.85 >=0.20
0.17 >=0.20	0.99 >=0.20
0.23 >=0.20	1 >=0.20
0.11 >=0.20	0.8 >=0.20
0.13 >=0.20	0.95 >=0.20
0.09 >=0.20	0.85 >=0.20
0.41 >=0.20	0.93 >=0.20
0.52 >=0.20	0.85 >=0.20
0.69 >=0.20	0.85 >=0.20
0.57 >=0.20	0.89 >=0.20
0.38 >=0.20	0.99 >=0.20
0.23 >=0.20	0.97 >=0.20
1 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
0.18 >=0.20	0.86 >=0.20
0.04 >=0.20	0.21 >=0.20
0.68 >=0.20	0.96 >=0.20
1 >=0.20	1 >=0.20
0.24 >=0.20	0.74 >=0.20
0.97 >=0.20	0.98 >=0.20
0.82 >=0.20	0.93 >=0.20
0.72 >=0.20	0.16 >=0.20
0.13 >=0.20	0.92 >=0.20
0.15 >=0.20	0.42 >=0.20
0.88 >=0.20	0.16 >=0.20
0.82 >=0.20	0.35 >=0.20
0.18 >=0.20	0.04 >=0.20
0.32 >=0.20	0.23 >=0.20
0.56 >=0.20	0.13 >=0.20
0.82 >=0.20	0.21 >=0.20
0.38 >=0.20	0.36 >=0.20
0.55 >=0.20	0.15 >=0.20
0.61 >=0.20	0.51 >=0.20

0.99 >=0.20	0.85 >=0.20
0.27 >=0.20	0.08 >=0.20
0.34 >=0.20	0.45 >=0.20
0.11 >=0.20	0.07 >=0.20
1 >=0.20	0.8 >=0.20
0.15 >=0.20	0.07 >=0.20
0.39 >=0.20	0.05 >=0.20
0.9 >=0.20	0.48 >=0.20
0.84 >=0.20	0.74 >=0.20
0.19 >=0.20	0.42 >=0.20
0.97 >=0.20	0.82 >=0.20
0.33 >=0.20	0.58 >=0.20
0.31 >=0.20	0.28 >=0.20
0.12 >=0.20	0.18 >=0.20
0.05 >=0.20	0.58 >=0.20
0.07 >=0.20	0.15 >=0.20
0.98 >=0.20	0.55 >=0.20
0.96 >=0.20	0.06 >=0.20
0.94 >=0.20	0.89 >=0.20
0.72 >=0.20	0.88 >=0.20
0.49 >=0.20	0.93 >=0.20
0.49 >=0.20	0.93 >=0.20
0.04 >=0.20	0.41 >=0.20
0.22 >=0.20	0.59 >=0.20
0.98 >=0.20	1 >=0.20
0.87 >=0.20	0.65 >=0.20
0.96 >=0.20	0.69 >=0.20
0.99 >=0.20	0.85 >=0.20
0.5 >=0.20	0.4 >=0.20
0.89 >=0.20	0.18 >=0.20
0.98 >=0.20	0.33 >=0.20
0.62 >=0.20	0.83 >=0.20
0.95 >=0.20	0.91 >=0.20
0.61 >=0.20	0.07 >=0.20
0.89 >=0.20	0.72 >=0.20
0.06 >=0.20	0.81 >=0.20
0.86 >=0.20	0.98 >=0.20
0.22 >=0.20	0.2 >=0.20
0.35 >=0.20	0.98 >=0.20
0.98 >=0.20	0.99 >=0.20
1 >=0.20	0.88 >=0.20
0.14 >=0.20	0.03 >=0.20
0.96 >=0.20	0.95 >=0.20
0.88 >=0.20	0.53 >=0.20
0.75 >=0.20	0.04 >=0.20
0.16 >=0.20	0.14 >=0.20
0.74 >=0.20	0.84 >=0.20

0.97 >=0.20	0.73 >=0.20
0.74 >=0.20	0.17 >=0.20
0.06 >=0.20	0.05 >=0.20
0.2 >=0.20	0.66 >=0.20
0.31 >=0.20	0.35 >=0.20
0.91 >=0.20	0.33 >=0.20
0.94 >=0.20	0.73 >=0.20
1 >=0.20	0.93 >=0.20
0.79 >=0.20	0.52 >=0.20
0.64 >=0.20	0.22 >=0.20
0.98 >=0.20	0.71 >=0.20
0.74 >=0.20	0.53 >=0.20
0.6 >=0.20	0.89 >=0.20
0.6 >=0.20	0.89 >=0.20
0.22 >=0.20	0.39 >=0.20
0.09 >=0.20	0.38 >=0.20
0.98 >=0.20	0.87 >=0.20
0.09 >=0.20	0.09 >=0.20
0.88 >=0.20	0.22 >=0.20
0.38 >=0.20	0.49 >=0.20
0.83 >=0.20	0.89 >=0.20
0.2 >=0.20	0.31 >=0.20
0.15 >=0.20	0.19 >=0.20
0.29 >=0.20	0.31 >=0.20
0.09 >=0.20	0.61 >=0.20
0.71 >=0.20	0.97 >=0.20
0.19 >=0.20	0.2 >=0.20
0.92 >=0.20	0.27 >=0.20
0.97 >=0.20	0.96 >=0.20
0.99 >=0.20	0.76 >=0.20
0.99 >=0.20	1 >=0.20
0.84 >=0.20	0.08 >=0.20
0.13 >=0.20	0.24 >=0.20
0.37 >=0.20	0.28 >=0.20
0.54 >=0.20	0.27 >=0.20
0.58 >=0.20	0.82 >=0.20
0.87 >=0.20	0.98 >=0.20
0.1 >=0.20	0.04 >=0.20
0.15 >=0.20	0.4 >=0.20
0.15 >=0.20	0.38 >=0.20
0.12 >=0.20	0.33 >=0.20
0.04 >=0.20	0.26 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.39 >=0.20
0.99 >=0.20	1 >=0.20
0.93 >=0.20	0.98 >=0.20
0.98 >=0.20	0.86 >=0.20

1 >=0.20	1 >=0.20
0.43 >=0.20	1 >=0.20
0.53 >=0.20	0.55 >=0.20
0.6 >=0.20	0.79 >=0.20
0.62 >=0.20	0.63 >=0.20
0.8 >=0.20	1 >=0.20
0.99 >=0.20	0.97 >=0.20
0.98 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
1 >=0.20	0.96 >=0.20
1 >=0.20	0.96 >=0.20
0.97 >=0.20	0.27 >=0.20
0.35 >=0.20	0.64 >=0.20
0.88 >=0.20	0.92 >=0.20
0.3 >=0.20	0.2 >=0.20
0.06 >=0.20	0.16 >=0.20
0.82 >=0.20	0.44 >=0.20
1 >=0.20	1 >=0.20
0.98 >=0.20	0.94 >=0.20
1 >=0.20	1 >=0.20
0.63 >=0.20	0.98 >=0.20
1 >=0.20	1 >=0.20
0.92 >=0.20	0.54 >=0.20
1 >=0.20	1 >=0.20
0.47 >=0.20	0.86 >=0.20
0.57 >=0.20	0.43 >=0.20
0.13 >=0.20	0.67 >=0.20
0.54 >=0.20	0.73 >=0.20
0.36 >=0.20	0.2 >=0.20
0.62 >=0.20	0.31 >=0.20
0.75 >=0.20	0.13 >=0.20
0.22 >=0.20	0.77 >=0.20
0.59 >=0.20	0.98 >=0.20
0.94 >=0.20	0.89 >=0.20
0.2 >=0.20	0.94 >=0.20
0.71 >=0.20	0.13 >=0.20
0.55 >=0.20	0.05 >=0.20
0.11 >=0.20	0.25 >=0.20
0.24 >=0.20	0.87 >=0.20
0.13 >=0.20	0.64 >=0.20
0.68 >=0.20	0.96 >=0.20
0.04 >=0.20	0.43 >=0.20
0.94 >=0.20	0.16 >=0.20
0.74 >=0.20	0.11 >=0.20
0.6 >=0.20	0.29 >=0.20
0.82 >=0.20	0.95 >=0.20
0.25 >=0.20	0.77 >=0.20

0.39	>=0.20	0.9	>=0.20
0.34	>=0.20	0.87	>=0.20
0.57	>=0.20	0.85	>=0.20
0.39	>=0.20	0.72	>=0.20
0.93	>=0.20	0.16	>=0.20
1	>=0.20	0.95	>=0.20
0.96	>=0.20	0.58	>=0.20
0.12	>=0.20	0.24	>=0.20
0.39	>=0.20	0.44	>=0.20
0.24	>=0.20	0.4	>=0.20
0.96	>=0.20	0.54	>=0.20
0.96	>=0.20	0.41	>=0.20
0.62	>=0.20	0.83	>=0.20
0.97	>=0.20	0.43	>=0.20
0.66	>=0.20	0.3	>=0.20
0.11	>=0.20	0.35	>=0.20
0.25	>=0.20	0.95	>=0.20
0.89	>=0.20	0.8	>=0.20
0.65	>=0.20	0.94	>=0.20
0.52	>=0.20	0.97	>=0.20
0.99	>=0.20	0.58	>=0.20
0.4	>=0.20	0.97	>=0.20
0.67	>=0.20	0.98	>=0.20
0.4	>=0.20	0.98	>=0.20
0.6	>=0.20	0.29	>=0.20
0.95	>=0.20	0.42	>=0.20
0.89	>=0.20	0.51	>=0.20
0.99	>=0.20	0.29	>=0.20
0.37	>=0.20	0.35	>=0.20
0.95	>=0.20	0.42	>=0.20
0.87	>=0.20	0.35	>=0.20
0.38	>=0.20	0.17	>=0.20
0.99	>=0.20	0.91	>=0.20
0.19	>=0.20	0.24	>=0.20
0.18	>=0.20	0.41	>=0.20
0.49	>=0.20	0.61	>=0.20
0.46	>=0.20	0.65	>=0.20
0.07	>=0.20	0.04	>=0.20
0.59	>=0.20	0.38	>=0.20
0.99	>=0.20	0.87	>=0.20
0.78	>=0.20	0.69	>=0.20
0.87	>=0.20	0.62	>=0.20
0.87	>=0.20	0.62	>=0.20
1	>=0.20	1	>=0.20
1	>=0.20	1	>=0.20
0.53	>=0.20	0.09	>=0.20
0.27	>=0.20	0.8	>=0.20

0.08 >=0.20	0.03 >=0.20
0.09 >=0.20	0.38 >=0.20
0.06 >=0.20	0.89 >=0.20
0.1 >=0.20	0.91 >=0.20
0.07 >=0.20	0.82 >=0.20
0.99 >=0.20	0.87 >=0.20
0.99 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.33 >=0.20	0.28 >=0.20
1 >=0.20	0.39 >=0.20
0.99 >=0.20	0.57 >=0.20
0.38 >=0.20	0.41 >=0.20
0.65 >=0.20	0.22 >=0.20
0.18 >=0.20	0.02 >=0.20
0.08 >=0.20	0.04 >=0.20
0.99 >=0.20	0.84 >=0.20
0.08 >=0.20	0.55 >=0.20
0.11 >=0.20	0.4 >=0.20
0.28 >=0.20	0.51 >=0.20
0.79 >=0.20	0.87 >=0.20
0.74 >=0.20	0.84 >=0.20
0.93 >=0.20	0.97 >=0.20
0.94 >=0.20	0.82 >=0.20
0.1 >=0.20	0.42 >=0.20
0.1 >=0.20	0.42 >=0.20
0.09 >=0.20	0.45 >=0.20
0.42 >=0.20	0.47 >=0.20
0.42 >=0.20	0.47 >=0.20
0.95 >=0.20	0.7 >=0.20
0.12 >=0.20	0.45 >=0.20
0.38 >=0.20	0.46 >=0.20
0.95 >=0.20	0.89 >=0.20
0.98 >=0.20	0.16 >=0.20
0.98 >=0.20	0.93 >=0.20
0.99 >=0.20	0.69 >=0.20
0.46 >=0.20	1 >=0.20
0.93 >=0.20	1 >=0.20
0.3 >=0.20	0.92 >=0.20
0.64 >=0.20	0.98 >=0.20
0.87 >=0.20	1 >=0.20
0.2 >=0.20	0.43 >=0.20
0.23 >=0.20	0.94 >=0.20
0.33 >=0.20	0.9 >=0.20
0.23 >=0.20	0.86 >=0.20
0.56 >=0.20	0.19 >=0.20

0.97 >=0.20	0.18 >=0.20
0.31 >=0.20	0.18 >=0.20
0.36 >=0.20	0.6 >=0.20
0.39 >=0.20	1 >=0.20
0.22 >=0.20	0.78 >=0.20
0.21 >=0.20	0.33 >=0.20
0.13 >=0.20	0.8 >=0.20
0.1 >=0.20	0.13 >=0.20
0.24 >=0.20	0.2 >=0.20
0.39 >=0.20	0.59 >=0.20
0.99 >=0.20	0.78 >=0.20
0.72 >=0.20	0.96 >=0.20
0.72 >=0.20	0.95 >=0.20
0.65 >=0.20	0.34 >=0.20
0.26 >=0.20	0.27 >=0.20
0.74 >=0.20	0.96 >=0.20
0.96 >=0.20	0.94 >=0.20
0.7 >=0.20	0.61 >=0.20
0.92 >=0.20	0.88 >=0.20
0.95 >=0.20	0.82 >=0.20
0.79 >=0.20	0.74 >=0.20
0.98 >=0.20	0.89 >=0.20
0.72 >=0.20	0.83 >=0.20
0.97 >=0.20	0.6 >=0.20
0.83 >=0.20	0.62 >=0.20
0.14 >=0.20	0.13 >=0.20
1 >=0.20	0.97 >=0.20
0.66 >=0.20	0.52 >=0.20
0.96 >=0.20	0.58 >=0.20
0.96 >=0.20	0.91 >=0.20
1 >=0.20	1 >=0.20
0.4 >=0.20	0.56 >=0.20
0.09 >=0.20	0.51 >=0.20
0.82 >=0.20	0.88 >=0.20
0.97 >=0.20	0.76 >=0.20
0.88 >=0.20	0.98 >=0.20
0.16 >=0.20	0.31 >=0.20
0.78 >=0.20	0.63 >=0.20
0.73 >=0.20	0.42 >=0.20
0.5 >=0.20	0.98 >=0.20
0.26 >=0.20	0.64 >=0.20
0.8 >=0.20	0.55 >=0.20
0.99 >=0.20	0.83 >=0.20
0.78 >=0.20	0.82 >=0.20
0.29 >=0.20	0.94 >=0.20
0.95 >=0.20	0.81 >=0.20
0.92 >=0.20	0.66 >=0.20

0.19 >=0.20	0.95 >=0.20
0.11 >=0.20	0.29 >=0.20
0.83 >=0.20	0.94 >=0.20
0.98 >=0.20	0.9 >=0.20
0.16 >=0.20	0.57 >=0.20
0.89 >=0.20	0.99 >=0.20
0.95 >=0.20	0.8 >=0.20
0.09 >=0.20	0.35 >=0.20
0.98 >=0.20	0.75 >=0.20
0.8 >=0.20	0.45 >=0.20
0.89 >=0.20	0.88 >=0.20
0.18 >=0.20	0.05 >=0.20
0.7 >=0.20	0.96 >=0.20
0.12 >=0.20	0.63 >=0.20
0.31 >=0.20	0.82 >=0.20
0.97 >=0.20	0.97 >=0.20
0.98 >=0.20	0.84 >=0.20
0.95 >=0.20	0.75 >=0.20
0.15 >=0.20	0.73 >=0.20
0.34 >=0.20	0.75 >=0.20
0.09 >=0.20	0.89 >=0.20
0.95 >=0.20	0.55 >=0.20
0.83 >=0.20	0.58 >=0.20
0.57 >=0.20	0.4 >=0.20
0.88 >=0.20	0.55 >=0.20
0.85 >=0.20	0.66 >=0.20
1 >=0.20	0.97 >=0.20
0.98 >=0.20	0.95 >=0.20
0.41 >=0.20	0.57 >=0.20
1 >=0.20	0.91 >=0.20
0.89 >=0.20	0.83 >=0.20
0.57 >=0.20	0.37 >=0.20
0.2 >=0.20	0.72 >=0.20
0.08 >=0.20	0.27 >=0.20
0.33 >=0.20	0.76 >=0.20
0.22 >=0.20	0.68 >=0.20
0.97 >=0.20	0.75 >=0.20
0.26 >=0.20	0.6 >=0.20
0.26 >=0.20	0.21 >=0.20
0.04 >=0.20	0.39 >=0.20
0.83 >=0.20	0.75 >=0.20
0.75 >=0.20	0.93 >=0.20
0.05 >=0.20	0.15 >=0.20
0.98 >=0.20	0.96 >=0.20
0.28 >=0.20	0.08 >=0.20
0.08 >=0.20	0.56 >=0.20
0.95 >=0.20	0.93 >=0.20

0.97 >=0.20	0.81 >=0.20
0.5 >=0.20	0.69 >=0.20
0.73 >=0.20	0.6 >=0.20
0.83 >=0.20	0.55 >=0.20
0.58 >=0.20	0.72 >=0.20
0.74 >=0.20	0.98 >=0.20
0.35 >=0.20	0.86 >=0.20
0.13 >=0.20	0.12 >=0.20
0.13 >=0.20	0.12 >=0.20
0.11 >=0.20	0.31 >=0.20
0.98 >=0.20	0.42 >=0.20
0.15 >=0.20	0.06 >=0.20
0.75 >=0.20	0.38 >=0.20
0.76 >=0.20	0.54 >=0.20
0.72 >=0.20	0.71 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.81 >=0.20	0.57 >=0.20
0.87 >=0.20	0.44 >=0.20
0.92 >=0.20	0.91 >=0.20
0.67 >=0.20	0.3 >=0.20
0.82 >=0.20	0.86 >=0.20
0.73 >=0.20	0.35 >=0.20
0.05 >=0.20	0.11 >=0.20
0.33 >=0.20	0.64 >=0.20
0.18 >=0.20	0.7 >=0.20
0.06 >=0.20	0.11 >=0.20
0.95 >=0.20	0.93 >=0.20
0.3 >=0.20	0.28 >=0.20
1 >=0.20	1 >=0.20
0.64 >=0.20	0.9 >=0.20
0.98 >=0.20	0.95 >=0.20
1 >=0.20	0.99 >=0.20
0.92 >=0.20	0.65 >=0.20
0.96 >=0.20	0.15 >=0.20
0.47 >=0.20	0.37 >=0.20
0.48 >=0.20	0.27 >=0.20
0.69 >=0.20	0.09 >=0.20
0.92 >=0.20	0.21 >=0.20
0.21 >=0.20	0.23 >=0.20
0.28 >=0.20	0.44 >=0.20
0.78 >=0.20	0.78 >=0.20
0.75 >=0.20	0.79 >=0.20
0.6 >=0.20	0.6 >=0.20
0.62 >=0.20	0.93 >=0.20
0.81 >=0.20	0.5 >=0.20
0.38 >=0.20	0.49 >=0.20

0.49 >=0.20	0.63 >=0.20
0.39 >=0.20	0.6 >=0.20
0.81 >=0.20	0.99 >=0.20
0.66 >=0.20	0.89 >=0.20
0.46 >=0.20	0.52 >=0.20
0.65 >=0.20	0.85 >=0.20
0.77 >=0.20	0.7 >=0.20
0.4 >=0.20	0.92 >=0.20
0.51 >=0.20	0.28 >=0.20
0.26 >=0.20	0.26 >=0.20
0.07 >=0.20	0.46 >=0.20
0.38 >=0.20	0.17 >=0.20
0.4 >=0.20	0.92 >=0.20
0.99 >=0.20	1 >=0.20
0.98 >=0.20	1 >=0.20
0.93 >=0.20	1 >=0.20
0.06 >=0.20	0.19 >=0.20
0.26 >=0.20	0.81 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.95 >=0.20	0.79 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
1 >=0.20	1 >=0.20
0.99 >=0.20	0.99 >=0.20
0.2 >=0.20	0.88 >=0.20
0.34 >=0.20	0.59 >=0.20
0.38 >=0.20	0.26 >=0.20
0.82 >=0.20	0.31 >=0.20
0.15 >=0.20	0.4 >=0.20
0.77 >=0.20	0.25 >=0.20
0.98 >=0.20	0.85 >=0.20
0.04 >=0.20	0.14 >=0.20
0.92 >=0.20	0.46 >=0.20
0.44 >=0.20	0.49 >=0.20
1 >=0.20	0.93 >=0.20
0.04 >=0.20	0.04 >=0.20
0.84 >=0.20	0.52 >=0.20
0.21 >=0.20	0.24 >=0.20
0.37 >=0.20	0.84 >=0.20
0.28 >=0.20	0.58 >=0.20
0.45 >=0.20	0.88 >=0.20
0.91 >=0.20	0.94 >=0.20

0.24 >=0.20	0.23 >=0.20
0.64 >=0.20	0.5 >=0.20
0.09 >=0.20	0.05 >=0.20
0.74 >=0.20	0.99 >=0.20
0.36 >=0.20	0.09 >=0.20
0.96 >=0.20	0.98 >=0.20
0.07 >=0.20	0.23 >=0.20
0.99 >=0.20	0.97 >=0.20
0.23 >=0.20	0.5 >=0.20
0.5 >=0.20	0.16 >=0.20
1 >=0.20	1 >=0.20
0.05 >=0.20	0.2 >=0.20
0.96 >=0.20	0.35 >=0.20
0.91 >=0.20	0.85 >=0.20
0.06 >=0.20	0.36 >=0.20
0.84 >=0.20	0.95 >=0.20
0.16 >=0.20	0.58 >=0.20
0.64 >=0.20	0.75 >=0.20
0.82 >=0.20	0.97 >=0.20
0.86 >=0.20	0.17 >=0.20
0.91 >=0.20	0.92 >=0.20
0.14 >=0.20	0.48 >=0.20
0.92 >=0.20	0.95 >=0.20
0.99 >=0.20	1 >=0.20
0.52 >=0.20	0.3 >=0.20
0.08 >=0.20	0.24 >=0.20
0.14 >=0.20	0.18 >=0.20
1 >=0.20	0.89 >=0.20
0.93 >=0.20	0.97 >=0.20
0.99 >=0.20	0.88 >=0.20
0.47 >=0.20	0.52 >=0.20
0.49 >=0.20	0.56 >=0.20
0.49 >=0.20	0.56 >=0.20
0.49 >=0.20	0.56 >=0.20
0.51 >=0.20	0.24 >=0.20
0.49 >=0.20	0.56 >=0.20
0.33 >=0.20	0.52 >=0.20
0.77 >=0.20	0.83 >=0.20
0.41 >=0.20	0.72 >=0.20
0.42 >=0.20	0.53 >=0.20
0.81 >=0.20	0.87 >=0.20
0.68 >=0.20	0.86 >=0.20
0.56 >=0.20	0.74 >=0.20
0.46 >=0.20	0.62 >=0.20
0.53 >=0.20	0.73 >=0.20
0.49 >=0.20	0.56 >=0.20
0.49 >=0.20	0.56 >=0.20

0.49 >=0.20	0.56 >=0.20
0.49 >=0.20	0.56 >=0.20
0.99 >=0.20	0.97 >=0.20
1 >=0.20	0.99 >=0.20
0.17 >=0.20	0.24 >=0.20
0.43 >=0.20	0.19 >=0.20
0.47 >=0.20	0.95 >=0.20
0.18 >=0.20	0.53 >=0.20
0.78 >=0.20	0.35 >=0.20
0.36 >=0.20	0.24 >=0.20
0.48 >=0.20	0.08 >=0.20
0.65 >=0.20	0.35 >=0.20
0.84 >=0.20	0.27 >=0.20
0.05 >=0.20	0.82 >=0.20
0.07 >=0.20	0.39 >=0.20
0.44 >=0.20	0.84 >=0.20
0.28 >=0.20	0.97 >=0.20
0.25 >=0.20	0.26 >=0.20
0.09 >=0.20	0.81 >=0.20
0.07 >=0.20	0.38 >=0.20
0.93 >=0.20	0.23 >=0.20
1 >=0.20	0.57 >=0.20
0.99 >=0.20	0.58 >=0.20
0.81 >=0.20	0.26 >=0.20
0.87 >=0.20	0.45 >=0.20
0.88 >=0.20	0.4 >=0.20
0.36 >=0.20	0.82 >=0.20
0.26 >=0.20	0.38 >=0.20
0.59 >=0.20	0.04 >=0.20
1 >=0.20	0.37 >=0.20
0.28 >=0.20	0.15 >=0.20
1 >=0.20	1 >=0.20
0.32 >=0.20	0.47 >=0.20
0.92 >=0.20	0.45 >=0.20
0.95 >=0.20	0.31 >=0.20
0.09 >=0.20	0.76 >=0.20
0.57 >=0.20	0.88 >=0.20
0.64 >=0.20	0.91 >=0.20
0.22 >=0.20	0.85 >=0.20
0.31 >=0.20	0.02 >=0.20
0.65 >=0.20	0.03 >=0.20
0.92 >=0.20	0.67 >=0.20
0.24 >=0.20	0.8 >=0.20
0.22 >=0.20	0.79 >=0.20
0.46 >=0.20	0.31 >=0.20
0.62 >=0.20	0.97 >=0.20
0.55 >=0.20	0.95 >=0.20

0.16	>=0.20	0.19	>=0.20
0.09	>=0.20	0.43	>=0.20
0.12	>=0.20	0.41	>=0.20
0.07	>=0.20	0.11	>=0.20
0.15	>=0.20	0.03	>=0.20
0.23	>=0.20	0.68	>=0.20
0.21	>=0.20	0.61	>=0.20
1	>=0.20	0.99	>=0.20
0.51	>=0.20	0.23	>=0.20
0.23	>=0.20	0.13	>=0.20
0.15	>=0.20	0.28	>=0.20
0.11	>=0.20	0.43	>=0.20
0.97	>=0.20	1	>=0.20
0.94	>=0.20	0.79	>=0.20
0.46	>=0.20	0.59	>=0.20
0.46	>=0.20	0.59	>=0.20
0.96	>=0.20	0.33	>=0.20
0.3	>=0.20	0.2	>=0.20
0.65	>=0.20	0.6	>=0.20
0.3	>=0.20	1	>=0.20
0.37	>=0.20	1	>=0.20
0.73	>=0.20	0.32	>=0.20
1	>=0.20	0.97	>=0.20

Web Table 16: Comparison of significant DEPICT tissue and cell type enrichments across the three traits H

MeSH term	Name	MeSH first level term
A11.436.348	Hepatocytes	Cells
A11.436	Epithelial Cells	Cells
A03.620	Liver	Digestive System
A10.165.114.830.500	Abdominal Fat	Tissues
A10.165.114.830.500.750	Subcutaneous Fat Abdominal	Tissues
A10.165.114	Adipose Tissue	Tissues
A10.165.114.830	Adipose Tissue White	Tissues
A10.165.114.830.750	Subcutaneous Fat	Tissues
A06.407.071.140	Adrenal Cortex	Endocrine System
A03.556.249.124	Ileum	Digestive System
A06.407.071	Adrenal Glands	Endocrine System
A15.378.316.580	Monocytes	Hemic and Immune Systems
A15.382.812	Mononuclear Phagocyte System	Hemic and Immune Systems
A11.627	Myeloid Cells	Cells
A15.382.680	Phagocytes	Hemic and Immune Systems
A03.556.124.684	Intestine Small	Digestive System
A15.378.316	Bone Marrow Cells	Hemic and Immune Systems
A15.378	Hematopoietic System	Hemic and Immune Systems
A11.066	Antigen Presenting Cells	Cells
A15.382.812.260	Dendritic Cells	Hemic and Immune Systems
A11.066	Antigen Presenting Cells	Cells
A15.382.812.522	Macrophages	Hemic and Immune Systems
A15.145.229.637.555	Leukocytes Mononuclear	Hemic and Immune Systems
A11.329.114	Adipocytes	Cells
A03.556.124	Intestines	Digestive System
A03.556.124.369	Intestinal Mucosa	Digestive System
A03.556.249.249.356	Colon	Digestive System
A03.556.249	Lower Gastrointestinal Tract	Digestive System
A03.556.249.249	Intestine Large	Digestive System
A11.118.637	Leukocytes	Cells
A15.145.300	Fetal Blood	Hemic and Immune Systems
A02.835.583.443.800.800	Synovial Fluid	Musculoskeletal System
A15.145.229	Blood Cells	Hemic and Immune Systems

IDL-C, LDL-C and TG. n.s.=not significant (FDR>0.05).

	HDL-C		LDL-C		TG	
MeSH second level term	**P-value**	**FDR**	**P-value**	**FDR**	**P-value**	**FDR**
Epithelial Cells	5.73E-05	**<0.01**	4.81E-09	**<0.01**	1.20E-06	**<0.01**
Epithelial Cells	1.41E-04	**<0.01**	4.40E-07	**<0.01**	2.94E-03	**<0.05**
Liver	9.57E-05	**<0.01**	2.21E-06	**<0.01**	5.93E-06	**<0.01**
Connective Tissue	8.36E-06	**<0.01**	n.s.	n.s.	8.29E-04	**<0.05**
Connective Tissue	8.36E-06	**<0.01**	n.s.	n.s.	8.29E-04	**<0.05**
Connective Tissue	1.04E-05	**<0.01**	n.s.	n.s.	1.60E-03	**<0.05**
Connective Tissue	2.76E-05	**<0.01**	n.s.	n.s.	2.53E-03	**<0.05**
Connective Tissue	2.76E-05	**<0.01**	n.s.	n.s.	2.53E-03	**<0.05**
Endocrine Glands	8.07E-05	**<0.01**	n.s.	n.s.	1.51E-03	**<0.05**
Gastrointestinal Tract	8.08E-05	**<0.01**	n.s.	n.s.	2.76E-04	**<0.01**
Endocrine Glands	1.17E-04	**<0.01**	n.s.	n.s.	1.26E-03	**<0.05**
Hematopoietic System	1.59E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Immune System	2.92E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Myeloid Cells	3.63E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Immune System	3.94E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Gastrointestinal Tract	1.13E-03	**<0.01**	n.s.	n.s.	5.66E-04	**<0.05**
Hematopoietic System	6.00E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Hematopoietic System	6.00E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Antigen-Presenting Cells	7.31E-04	**<0.01**	n.s.	n.s.	n.s.	n.s.
Immune System	7.31E-04	**<0.01**	1.18E-03	**<0.05**	n.s.	n.s.
Antigen-Presenting Cells	n.s.	n.s.	1.18E-03	**<0.05**	n.s.	n.s.
Immune System	1.56E-03	**<0.01**	n.s.	n.s.	n.s.	n.s.
Blood	n.s.	n.s.	1.81E-03	**<0.05**	n.s.	n.s.
Connective Tissue Cells	1.84E-03	**<0.01**	n.s.	n.s.	n.s.	n.s.
Gastrointestinal Tract	n.s.	n.s.	2.11E-03	**<0.05**	n.s.	n.s.
Gastrointestinal Tract	n.s.	n.s.	2.61E-03	**<0.05**	n.s.	n.s.
Gastrointestinal Tract	n.s.	n.s.	3.04E-03	**<0.05**	n.s.	n.s.
Gastrointestinal Tract	n.s.	n.s.	3.19E-03	**<0.05**	n.s.	n.s.
Gastrointestinal Tract	n.s.	n.s.	3.65E-03	**<0.05**	n.s.	n.s.
Blood Cells	n.s.	n.s.	3.90E-03	**<0.05**	n.s.	n.s.
Blood	n.s.	n.s.	4.10E-03	**<0.05**	n.s.	n.s.
Skeleton	4.32E-03	**<0.05**	n.s.	n.s.	n.s.	n.s.
Blood	n.s.	n.s.	5.12E-03	**<0.05**	n.s.	n.s.

Web Table 17: Look-up information for Coronary Artery Disease traits at the 147 most significant loci.

rsID	SNP	CHR	BP	CARDIoGRAMplusC4D CAD					CARDIoGR		
				A1	A2	EAF	Beta	P-value	A1	A2	EAF
rs9438905	1:25764177	1	25764177	G	A	0.51	-0.0098	2.93E-01	G	A	0.50
rs114165349	1:27021913	1	27021913	G	C	0.97	-0.0322	2.86E-01	C	G	0.03
rs4660303	1:40060473	1	40060473	G	A	0.81	-0.0199	9.87E-02	A	G	0.19
rs11591147	1:55505647	1	55505647	G	T	0.99	0.2565	7.47E-06	T	G	0.02
rs4495740	1:63124465	1	63124465	T	G	0.67	0.0132	1.77E-01	G	T	0.31
rs4847240	1:93817946	1	93817946	G	A	0.62	0.0060	5.30E-01	G	A	0.60
rs7528419	1:109817192	1	109817192	A	G	0.79	0.1145	1.97E-23	G	A	0.20
rs12753251	1:178529898	1	178529898	G	A	0.51	-0.0270	3.42E-03	A	G	0.47
rs1689788	1:182144422	1	182144422	T	C	0.68	-0.0109	2.67E-01	C	T	0.32
rs2642438	1:220970028	1	220970028	G	A	0.71	0.0076	4.79E-01	G	A	0.68
rs10127775	1:230295789	1	230295789	A	T	0.46	0.0308	1.22E-03	T	A	0.52
rs486142	1:234848609	1	234848609	A	G	0.56	0.0223	1.79E-02	A	G	0.55
rs201445483	2:17890087:ID	2	17890087	D	I	0.95	0.0046	8.39E-01	I	D	0.05
rs581411	2:21289432	2	21289432	A	G	0.81	0.0689	3.83E-08	A	G	0.75
rs4665972	2:27598097	2	27598097	C	T	0.60	0.0071	4.81E-01	C	T	0.57
rs1111336	2:28657896	2	28657896	A	C	0.78	0.0099	4.03E-01	C	A	0.20
rs4299376	2:44072576	2	44072576	T	G	0.68	-0.0508	1.21E-06	T	G	0.64
rs2111622	2:53984823	2	53984823	A	G	0.72	0.0094	3.77E-01	A	G	0.73
rs360804	2:62939397	2	62939397	G	A	0.69	0.0274	6.57E-03	A	G	0.31
rs55809639	2:118842801	2	118842801	T	A	0.91	0.0395	2.97E-02	A	T	0.08
rs7570971	2:135837906	2	135837906	A	C	0.44	0.0166	1.42E-01	A	C	0.47
rs1128249	2:165528624	2	165528624	G	T	0.63	0.0237	1.90E-02	T	G	0.37
rs10176901	2:169830661	2	169830661	A	G	0.58	-0.0119	2.17E-01	A	G	0.55
rs1047891	2:211540507	2	211540507	C	A	0.69	0.0254	1.85E-02	A	C	0.30
rs2972143	2:227116365	2	227116365	G	A	0.64	0.0362	3.84E-04	G	A	0.61
rs1584063	3:12266855	3	12266855	G	A	0.56	0.0139	1.38E-01	A	G	0.44
rs2013208	3:50129399	3	50129399	T	C	0.54	-0.0247	1.00E-02	T	C	0.53
rs1154988	3:135925191	3	135925191	A	T	0.76	0.0390	5.26E-04	A	T	0.73
rs17451107	3:156797609	3	156797609	T	C	0.61	-0.0140	1.46E-01	C	T	0.39
rs80080062	3:185812169	3	185812169	C	G	0.87	0.0119	3.86E-01	G	C	0.12
rs34311866	4:951947	4	951947	T	C	0.82	-0.0172	1.83E-01	C	T	0.17
rs13108218	4:3443931	4	3443931	G	A	0.59	-0.0100	3.22E-01	G	A	0.56
chr4:26050450:D	4:26050450:ID	4	26050450	I	D	0.84	-0.0072	5.90E-01	D	I	0.16
rs60695258	4:88022709	4	88022709	C	T	0.64	-0.0084	3.89E-01	T	C	0.36
rs13135092	4:103198082	4	103198082	A	G	0.94	0.0053	8.05E-01	G	A	0.07
rs143528679	4:124558378	4	124558378	G	A	0.95	0.0582	3.16E-01	G	A	0.93
rs72729610	4:154190965	4	154190965	A	G	0.86	-0.0137	3.19E-01	G	A	0.14
rs465002	5:55808475	5	55808475	T	C	0.70	0.0262	1.06E-02	T	C	0.67
chr5:74745529:D	5:74745529:ID	5	74745529	I	D	0.87	-0.0221	1.18E-01	D	I	0.12
rs56076449	5:132442190	5	132442190	T	G	0.76	0.0060	5.87E-01	G	T	0.23
rs10066168	5:156484218	5	156484218	T	C	0.83	0.0126	3.82E-01	T	C	0.80
rs2963472	5:157999022	5	157999022	G	A	0.76	-0.0061	5.65E-01	A	G	0.23
rs2235215	6:16131156	6	16131156	C	T	0.36	-0.0093	3.47E-01	C	T	0.36

rs41266779	6:26021872	6	26021872	C	T	0.93	0.0115	5.94E-01	T	C	0.06
rs2763981	6:31840021	6	31840021	A	T	0.73	0.0346	3.95E-03	A	T	0.71
rs6907508	6:34592090	6	34592090	A	G	0.89	-0.0480	2.21E-03	G	A	0.10
rs56144648	6:41988742	6	41988742	G	A	0.77	-0.0046	6.82E-01	A	G	0.23
rs11967262	6:43760327	6	43760327	C	G	0.49	-0.0386	8.61E-05	G	C	0.49
rs2749008	6:52626120	6	52626120	T	C	0.65	0.0126	2.01E-01	T	C	0.63
rs9496567	6:100602753	6	100602753	G	A	0.78	0.0041	7.32E-01	A	G	0.22
rs13210143	6:116389636	6	116389636	G	A	0.64	-0.0094	3.43E-01	A	G	0.36
rs9491694	6:127437100	6	127437100	T	A	0.71	-0.0093	3.54E-01	A	T	0.29
rs2908522	6:139835399	6	139835399	C	G	0.45	0.0071	4.61E-01	G	C	0.52
rs5014650	6:161099503	6	161099503	G	A	0.85	-0.0527	8.34E-05	A	G	0.15
chr7:1067762:D	7:1067762:ID	7	1067762	I	D	0.84	-0.0227	8.51E-02	D	I	0.15
rs836546	7:6479668	7	6479668	G	A	0.79	0.0370	1.45E-03	A	G	0.20
rs6461354	7:17914600	7	17914600	T	C	0.42	-0.0146	1.18E-01	T	C	0.42
rs66476925	7:21611399	7	21611399	G	C	0.81	-0.0164	1.66E-01	C	G	0.19
rs4722551	7:25991826	7	25991826	T	C	0.85	-0.0079	5.59E-01	C	T	0.14
rs217381	7:44606217	7	44606217	C	G	0.62	0.0203	3.83E-02	G	C	0.38
rs79624003	7:73012785	7	73012785	A	G	0.88	-0.0064	6.65E-01	G	A	0.11
rs4470970	7:80344361	7	80344361	G	A	0.87	-0.0185	4.86E-01	G	A	0.87
rs11762784	7:130424646	7	130424646	G	A	0.55	0.0188	4.86E-02	A	G	0.44
NA	7:137559799	7	137559799	NA	NA	NA	NA	NA	NA	NA	NA
rs2911971	8:6607634	8	6607634	G	C	0.62	-0.0057	5.54E-01	G	C	0.61
rs4841132	8:9183596	8	9183596	G	A	0.87	0.0001	9.93E-01	G	A	0.84
rs1090107	8:11632528	8	11632528	G	A	0.47	0.0007	9.47E-01	G	A	0.46
rs1495743	8:18273300	8	18273300	C	G	0.74	-0.0303	5.82E-03	C	G	0.70
rs287	8:19815556	8	19815556	A	G	0.76	0.0457	5.72E-05	G	A	0.23
rs56204645	8:55421769	8	55421769	T	C	0.80	-0.0296	9.34E-03	C	T	0.19
rs10957054	8:59336556	8	59336556	T	C	0.64	-0.0017	8.63E-01	T	C	0.62
rs2737216	8:116630079	8	116630079	T	A	0.59	-0.0103	2.80E-01	T	A	0.58
rs10955992	8:121872464	8	121872464	C	A	0.64	-0.0111	2.66E-01	C	A	0.62
rs2954021	8:126482077	8	126482077	G	A	0.50	-0.0443	1.48E-06	G	A	0.49
rs56960668	8:144300760	8	144300760	G	A	0.68	-0.0049	6.69E-01	A	G	0.30
rs1215112	9:15303583	9	15303583	A	G	0.85	-0.0259	7.65E-02	A	G	0.82
rs7035578	9:78745177	9	78745177	G	A	0.87	0.0122	4.17E-01	A	G	0.12
rs2575876	9:107665739	9	107665739	G	A	0.74	0.0251	1.68E-02	A	G	0.24
rs13284665	9:131513370	9	131513370	A	G	0.88	0.0050	7.71E-01	G	A	0.11
rs495828	9:136154867	9	136154867	G	T	0.79	-0.0726	1.29E-10	T	G	0.21
rs3802548	10:45952745	10	45952745	T	A	0.77	-0.0058	5.93E-01	A	T	0.23
rs41274050	10:52573772	10	52573772	T	C	0.01	0.0599	3.42E-01	T	C	0.01
rs10761716	10:64882300	10	64882300	C	G	0.55	-0.0150	1.09E-01	G	C	0.44
rs4418728	10:94839724	10	94839724	G	T	0.52	0.0382	8.16E-05	T	G	0.46
rs7096937	10:113950418	10	113950418	C	T	0.71	-0.0110	2.94E-01	C	T	0.68
rs7904973	10:124693587	10	124693587	T	G	0.55	0.0085	3.62E-01	T	G	0.54
rs2896635	11:13359745	11	13359745	A	T	0.64	0.0335	7.24E-04	A	T	0.61
rs10832961	11:18653957	11	18653957	G	C	0.70	0.0167	1.03E-01	G	C	0.67
rs10769254	11:47362465	11	47362465	G	C	0.77	-0.0049	6.70E-01	C	G	0.23
rs658118	11:49255042	11	49255042	C	T	0.88	0.0172	2.72E-01	T	C	0.11

rs11246533	11:51377255	11	51377255	C	T	0.88	0.0140	3.55E-01	T	C	0.12
rs11230661	11:55451313	11	55451313	G	A	0.81	0.0039	7.71E-01	A	G	0.18
rs174566	11:61592362	11	61592362	A	G	0.68	0.0221	2.79E-02	G	A	0.32
rs190528931	11:63911273	11	63911273	C	A	0.96	-0.0282	3.03E-01	A	C	0.04
rs1806895	11:75473715	11	75473715	T	C	0.88	-0.0118	4.11E-01	C	T	0.12
rs509728	11:116533167	11	116533167	G	C	0.96	-0.0379	1.22E-01	C	G	0.04
rs76970536	11:126250680	11	126250680	G	A	0.92	-0.0419	1.07E-02	A	G	0.08
chr12:7725904:D	12:7725904:ID	12	7725904	I	D	0.91	0.0001	9.98E-01	D	I	0.08
rs78459082	12:20442785	12	20442785	G	C	0.82	0.0017	8.89E-01	C	G	0.17
rs4898521	12:49755162	12	49755162	A	T	0.92	-0.0400	1.41E-01	A	T	0.88
rs540730	12:57807114	12	57807114	C	T	0.75	0.0060	6.05E-01	C	T	0.73
rs10744826	12:109965512	12	109965512	G	C	0.51	0.0056	5.45E-01	G	C	0.51
rs7310615	12:111865049	12	111865049	G	C	0.57	-0.0637	1.67E-09	G	C	0.55
rs2244608	12:121416988	12	121416988	A	G	0.65	-0.0476	1.02E-06	G	A	0.34
rs7298909	12:123830939	12	123830939	T	C	0.84	-0.0154	2.80E-01	T	C	0.82
rs57276302	12:125363987	12	125363987	C	A	0.87	-0.0024	8.67E-01	A	C	0.12
chr13:32976640:D	13:32976640:ID	13	32976640	I	D	0.65	0.0285	8.27E-03	D	I	0.34
rs7140110	13:114544024	13	114544024	C	T	0.30	0.0129	2.94E-01	C	T	0.29
rs6573778	14:24872209	14	24872209	C	T	0.55	-0.0013	8.98E-01	C	T	0.54
rs45490496	14:105272678	14	105272678	A	T	0.46	-0.0117	2.71E-01	T	A	0.53
rs28364406	15:42679423	15	42679423	C	T	0.98	-0.0512	1.72E-01	T	C	0.02
rs150844304	15:43726625	15	43726625	A	C	0.97	-0.0108	7.30E-01	C	A	0.03
rs28487964	15:44784375	15	44784375	T	A	0.98	-0.0550	1.26E-01	A	T	0.02
rs2043082	15:58674308	15	58674308	G	A	0.65	-0.0122	2.09E-01	A	G	0.34
rs76127683	15:63391362	15	63391362	C	G	0.74	-0.0019	8.69E-01	C	G	0.72
chr16:53822169:D	16:53822169:ID	16	53822169	I	D	0.63	-0.0284	3.74E-03	D	I	0.36
rs9989419	16:56985139	16	56985139	G	A	0.60	-0.0088	3.56E-01	G	A	0.58
NA	16:66944180	16	66944180	NA	NA	NA	NA	NA	NA	NA	NA
rs255056	16:68016185	16	68016185	G	C	0.84	-0.0083	5.11E-01	C	G	0.15
rs3794695	16:72097827	16	72097827	C	T	0.77	-0.0371	7.38E-04	T	C	0.22
rs2925979	16:81534790	16	81534790	C	T	0.68	-0.0164	1.12E-01	C	T	0.65
rs881844	17:37810218	17	37810218	C	G	0.35	0.0175	7.48E-02	G	C	0.62
rs149580368	17:41874745	17	41874745	C	A	0.98	-0.0841	5.13E-02	A	C	0.02
rs11870935	17:45732605	17	45732605	A	G	0.53	-0.0168	6.72E-02	A	G	0.51
rs8178824	17:64224775	17	64224775	C	T	0.97	-0.0370	3.09E-01	T	C	0.03
rs117753190	17:67136325	17	67136325	C	G	0.98	-0.0252	4.97E-01	G	C	0.02
rs8071884	17:76398058	17	76398058	G	C	0.60	-0.0066	4.89E-01	G	C	0.58
rs2156552	18:47181668	18	47181668	T	A	0.81	-0.0256	4.42E-02	T	A	0.79
rs58084604	18:57849429	18	57849429	C	T	0.74	-0.0557	1.14E-07	T	C	0.24
rs4804411	19:7222377	19	7222377	C	G	0.57	0.0075	4.18E-01	C	G	0.55
rs116843064	19:8429323	19	8429323	A	G	0.03	-0.1408	1.04E-03	A	G	0.02
rs143020224	19:11187324	19	11187324	C	G	0.89	0.1210	5.88E-13	G	C	0.10
rs2304128	19:19746151	19	19746151	G	T	0.92	0.0308	7.33E-02	T	G	0.08
rs57457691	19:33911705	19	33911705	C	T	0.58	-0.0246	9.37E-03	C	T	0.57
rs1531517	19:45242173	19	45242173	G	A	0.91	0.0225	1.66E-01	A	G	0.08
rs35866622	19:49218060	19	49218060	C	T	0.60	-0.0023	8.19E-01	T	C	0.39
rs28873836	19:52314655	19	52314655	G	C	0.74	0.0056	6.00E-01	C	G	0.25

rs367070	19:54800500	19	54800500	A	G	0.78	0.0081	5.09E-01	G	A	0.20
rs2328223	20:17845921	20	17845921	A	C	0.79	-0.0125	2.76E-01	C	A	0.20
rs4911477	20:33780985	20	33780985	T	C	0.60	-0.0014	8.88E-01	C	T	0.40
rs2050058	20:39906988	20	39906988	G	A	0.65	-0.0097	3.64E-01	A	G	0.35
rs1800961	20:43042364	20	43042364	C	T	0.97	0.0281	3.21E-01	T	C	0.03
rs6073958	20:44551855	20	44551855	T	C	0.80	0.0251	3.27E-02	C	T	0.19
rs6063050	20:45604240	20	45604240	T	C	0.74	0.0169	1.27E-01	C	T	0.25
rs235314	21:46271452	21	46271452	C	T	0.47	-0.0108	2.43E-01	T	C	0.51
rs7445	22:21977047	22	21977047	C	T	0.76	0.0098	3.67E-01	T	C	0.23
rs4820323	22:38599767	22	38599767	G	C	0.55	0.0015	8.77E-01	G	C	0.54

AMplusC4D MI	
Beta	P-value
-0.0176	8.72E-02
0.0221	5.10E-01
0.0192	1.50E-01
-0.3547	2.30E-07
-0.0065	5.43E-01
0.0042	6.90E-01
-0.1013	9.92E-16
0.0338	9.33E-04
0.0004	9.73E-01
0.0102	3.86E-01
-0.0251	1.78E-02
0.0222	3.25E-02
-0.0142	5.75E-01
0.0493	3.41E-04
0.0028	8.03E-01
-0.0097	4.58E-01
-0.0498	1.37E-05
0.0053	6.45E-01
-0.0315	4.19E-03
-0.0458	1.87E-02
0.0118	3.23E-01
-0.0107	3.22E-01
-0.0113	2.76E-01
-0.0111	3.39E-01
0.0345	1.56E-03
-0.0284	6.48E-03
-0.0212	4.67E-02
0.0390	1.85E-03
0.0159	1.38E-01
-0.0068	6.50E-01
0.0112	4.32E-01
-0.0114	3.09E-01
0.0205	1.64E-01
0.0152	1.64E-01
0.0012	9.60E-01
0.0600	3.85E-01
-0.0021	8.88E-01
0.0287	1.14E-02
0.0259	9.28E-02
-0.0107	3.87E-01
0.0096	5.48E-01
0.0030	7.97E-01
-0.0145	1.84E-01

-0.0026	9.14E-01
0.0402	2.20E-03
0.0519	2.82E-03
-0.0032	7.96E-01
0.0447	3.94E-05
0.0065	5.50E-01
0.0004	9.76E-01
0.0153	1.58E-01
0.0062	5.79E-01
-0.0041	6.99E-01
0.0420	4.49E-03
0.0078	5.92E-01
-0.0379	3.63E-03
-0.0160	1.22E-01
0.0152	2.54E-01
0.0058	6.99E-01
-0.0273	1.21E-02
0.0065	6.96E-01
-0.0548	6.81E-02
-0.0144	1.77E-01
NA	NA
-0.0010	9.24E-01
-0.0148	4.04E-01
-0.0115	2.94E-01
-0.0365	3.37E-03
-0.0365	4.13E-03
0.0211	9.86E-02
-0.0081	4.55E-01
-0.0083	4.32E-01
-0.0085	4.38E-01
-0.0470	3.75E-06
0.0106	4.06E-01
-0.0144	3.73E-01
-0.0120	4.77E-01
-0.0270	2.01E-02
-0.0332	8.62E-02
0.1027	4.23E-16
0.0026	8.26E-01
0.0323	6.43E-01
0.0147	1.55E-01
-0.0423	1.02E-04
-0.0063	5.91E-01
-0.0036	7.28E-01
0.0241	2.89E-02
0.0155	1.73E-01
0.0169	1.91E-01
-0.0092	6.03E-01

0.0042	7.99E-01
0.0033	8.24E-01
-0.0256	2.26E-02
0.0264	3.83E-01
0.0031	8.48E-01
0.0438	1.00E-01
0.0236	2.01E-01
0.0051	7.97E-01
0.0051	7.12E-01
-0.0081	7.91E-01
-0.0076	5.65E-01
0.0044	6.70E-01
-0.0748	1.63E-10
0.0507	2.86E-06
-0.0205	2.02E-01
0.0236	1.37E-01
-0.0281	1.88E-02
0.0198	1.47E-01
-0.0028	8.05E-01
0.0102	3.83E-01
0.0509	2.07E-01
0.0282	4.07E-01
0.0741	5.77E-02
0.0045	6.78E-01
-0.0076	5.56E-01
0.0225	3.79E-02
-0.0089	4.02E-01
NA	NA
0.0077	5.82E-01
0.0442	2.94E-04
-0.0120	3.07E-01
-0.0135	2.16E-01
0.1004	3.32E-02
-0.0057	5.75E-01
0.0382	3.37E-01
0.0186	6.53E-01
-0.0092	3.83E-01
-0.0191	1.81E-01
0.0518	8.19E-06
0.0075	4.64E-01
-0.0786	9.97E-02
-0.0989	1.26E-07
-0.0278	1.51E-01
-0.0124	2.37E-01
-0.0211	2.48E-01
0.0029	7.97E-01
-0.0052	6.56E-01

-0.0134	3.31E-01
0.0219	8.52E-02
0.0063	5.58E-01
0.0035	7.71E-01
0.0060	8.51E-01
-0.0290	2.43E-02
-0.0111	3.58E-01
0.0128	2.11E-01
-0.0053	6.61E-01
0.0061	5.55E-01